

```
XX 10-FEB-1998; 98US-00021701.
PR
XX (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINCA/) KINCAID R H.
XX
XX Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
XX WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
XX nucleotide sequence comprises determining and evaluating for each
XX oligonucleotide a parameter predictive of the oligonucleotides ability to
XX hybridize with target.
XX
XX Example 2; SEQ ID NO 733; 423bp; English.
XX
XX The invention relates to a method of predicting the potential of
XX oligonucleotides to hybridize to target nucleotide sequences. The method
XX is useful for predicting the potential of an oligonucleotide to hybridize
XX to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
XX contains chemically modified nucleotides. The method is also useful for
XX predicting the potential of the oligonucleotides to hybridize to a
XX complementary target nucleotide sequence. The method is useful to predict
XX efficient hybridisation oligonucleotides for each of multiple target
XX sequences therefore very large arrays may be constructed and tested with
XX minimum synthesis of oligonucleotides. The present sequence represents a
XX HIV PRT antisense derived probe.
XX
XX Sequence 20 BP; 1 A; 8 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5700 TTGCTTCCTTTCTCTTC 5719
XX |||||
XX 1 TTCCCTTCCTTTCCATTTC 20
XX
XX RESULT 2557
XX ADD81659
XX ID ADD81659 standard; DNA; 20 BP.
XX
XX AC ADD81659;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE HIV PRT antisense derived probe #588.
XX
XX KW ss: oligonucleotide hybridisation potential; efficient hybridisation;
XX large array; minimum oligonucleotide synthesis; probe.
XX
XX OS Human immunodeficiency virus.
XX
XX US2003054346-A1.
XX
XX 20-MAR-2003.
XX
XX 15-FEB-2001; 2001US-00784674.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX (SHAN/) SHANNON K W.
XX (WOLB/) WOLBER P K.
XX (DELE/) DELENSTARR G C.
XX (WEBB/) WEBB P G.
XX (KINCA/) KINCAID R H.
XX
XX Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
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XX WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
XX nucleotide sequence comprises determining and evaluating for each
XX oligonucleotide a parameter predictive of the oligonucleotides ability to
XX hybridize with target.
XX
XX Example 2; SEQ ID NO 732; 423bp; English.
XX
XX The invention relates to a method of predicting the potential of
XX oligonucleotides to hybridize to target nucleotide sequences. The method
XX is useful for predicting the potential of an oligonucleotide to hybridize
XX to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
XX contains chemically modified nucleotides. The method is also useful for
XX predicting the potential of the oligonucleotides to hybridize to a
XX complementary target nucleotide sequence. The method is useful to predict
XX efficient hybridisation oligonucleotides for each of multiple target
XX sequences therefore very large arrays may be constructed and tested with
XX minimum synthesis of oligonucleotides. The present sequence represents a
XX HIV PRT antisense derived probe.
XX
XX Sequence 20 BP; 1 A; 7 C; 0 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5699 TTGCTTCCTTTCTCTTC 5718
XX |||||
XX 1 TTCCCTTCCTTTCCATTTC 20
XX
XX RESULT 2558
XX ADE50858/C
XX ID ADE50858 standard; DNA; 20 BP.
XX
XX AC ADE50858;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE ESE gene SNP primer #16.
XX
XX KW ss: single nucleotide polymorphism; immunosuppressive; antidiabetic;
XX neuroprotective; antireumatic; antiarthritic; thyromimetic;
XX antiaerotoxic; antineurotic; antineurotic; dermatological; antipsoriatic;
XX antiaerotoxic; diagnosis; autoimmune disease; ESE-3; ESE-2; ESE-1;
XX diabetes; multiple sclerosis; rheumatoid arthritis; lupus; psoriasis;
XX asthma; myasthenia gravis; Sjogren's syndrome; Hashimoto's thyroiditis;
XX Pemphigus vulgaris; atherosclerosis; rheumatoid arthritis; restenosis;
XX
XX OS Homo sapiens.
XX
XX WO2003034896-A2.
XX
XX 01-MAY-2003.
XX
XX 15-OCT-2002; 2002WO-US032116.
XX
XX 12-OCT-2001; 2001US-0329158P.
XX
XX 26-APR-2002; 2002US-0376139P.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Libermann T, Tautu O, Grall F, Gu X;
XX
XX WPI; 2003-441218/41.
XX
XX Diagnosing the presence, predisposition or susceptibility to an
XX autoimmune disease e.g. diabetes or multiple sclerosis, comprises
XX detecting a polymorphism in the ESE-3, ESE-1 or ESE-1 genes.
XX
```

PS Example 2; SEQ ID NO 72; 96bp; English.

XX The invention relates to the diagnosis of an autoimmune disease, a
 CC predisposition or a susceptibility to the disease, by detecting a
 CC polymorphism in the ESR-3, ESR-2 or ESR-1 genes, which is correlated with
 CC an alteration in the activity or expression of a polypeptide encoded by
 CC these genes. Detection of the polymorphism is indicative of the
 CC occurrence, predisposition or susceptibility to autoimmune disease. The
 CC method is useful for diagnosing the presence, predisposition to, or
 CC susceptibility to an autoimmune disease, e.g. diabetes (e.g. Type 1
 CC diabetes or Type II diabetes), multiple sclerosis, rheumatoid arthritis,
 CC lupus, psoriasis, asthma, myasthenia gravis, Sjogren's syndrome,
 CC Hashimoto's thyroiditis, pemphigus vulgaris, or inflammation (e.g.
 CC atherosclerosis, rheumatoid arthritis, or inflammation associated with
 CC restenosis). The method is also useful for preventing or treating any of
 CC these diseases. This sequence corresponds to a primer used in the method
 CC to detect the single nucleotide polymorphisms in the ESR genes,
 CC especially correlated with multiple sclerosis.

XX Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5581 CTTGGCTCATGTGATTTG 5600
 DB 20 CATTGGCTCATTTGATTTG 1

RESULT 2559
 ADE43461
 ID ADE43461 standard; DNA; 20 BP.

XX ADE43461;
 XX 29-JUN-2004 (first entry)

DE Human SNCG sequencing primer, SEQ ID 66.
 XX
 XX Neurodegenerative disease; uPA; SNCG; IDE; XNLS1; LIPA; TNFRSF6;
 KM Alzheimer's disease; neuroprotective; neurotrophic; gene therapy;
 KM Chromosome 10; PCR; primer; ss.

OS Homo sapiens.
 OS
 XX WO2003054143-A2.
 PN
 XX 03-JUL-2003.

PD 25-OCT-2002; 2002WO-US034679.
 PF
 XX 25-OCT-2001; 2001US-0339525P.
 PR 08-NOV-2001; 2001US-0336929P.
 PR 08-NOV-2001; 2001US-0338010P.
 PR 09-NOV-2001; 2001US-0338363P.
 PR 04-DEC-2001; 2001US-0337052P.
 PR 28-MAR-2002; 2002US-0368919P.

XX (NEUR-) NEUROGENETICS INC.
 PA (GENO) GEN HOSPITAL CORP.
 XX
 XX Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
 PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
 XX
 XX WPI; 2003-559131/52.

XX Determining a predisposition for or the occurrence of neurodegenerative
 PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
 PT the presence or absence of an allelic variant of one or more polymorphic
 XX regions.
 XX Example 2; Page 267; 848bp; English.

XX The present invention relates to a method (M1) for determining a
 CC predisposition for or the occurrence of neurodegenerative disease in a
 CC subject. The method comprises detecting in a target nucleic acid obtained
 CC from the subject the presence or absence of an allelic variant of one or
 CC more polymorphic regions of one or more genes selected from uPA
 CC (urokinase plasminogen activator), SNCG (gamma-gynuclein), IDE (insulin-
 CC degrading enzyme), XNLS1 (kinesin-like protein 1), LIPA (lysosomal acid
 CC lyase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 CC presence of at least one of the allelic variant of one or more
 CC polymorphic regions is indicative of a predisposition for or the
 CC occurrence of neurodegenerative disease. The genes are all located on
 CC chromosome 10. M1 is useful for determining a predisposition for or the
 CC occurrence of, and for treating neurodegenerative disease, particularly
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used
 CC in the method of the invention.

XX Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3627 GGGGCTGGAGAGAGAGTAG 3646
 DB 1 GGAGTGGCAGAGAGAGTAG 20

RESULT 2560
 AAQ29595/c
 ID AAQ29595 standard; DNA; 21 BP.

XX AAQ29595;
 XX 25-MAR-2003 (revised)
 DT 10-MAR-1993 (first entry)

DE Pol 67/70 region sequencing primer 90-417.
 XX
 XX Amplify; HIV; pol; resistance; azidothymidine; AZT; 3SR; probe;
 KM self-sustained sequence replication; mutation; inosine; ss.
 XX
 XX Synthetic.
 OS
 XX WO9216180-A2.
 PN
 XX 01-OCT-1992.

PD 12-MAR-1992; 92WO-US002037.
 PF
 XX 13-MAR-1991; 91US-0066549.
 PR 03-SEP-1991; 91US-00754146.

XX (SISK-) SISKRA DIAGNOSTICS INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Gingersas TR, Barringer KJ, Richman DD, Prodanovich PC, Davis GR;
 PI WPI; 1992-348902/42.

XX Assay for detecting genotype of AZT resistance - utilizes series of
 PT probes which anneal to amplified region of HIV-1 gene.
 XX
 XX Disclosure; Page 17; 57pp; English.

XX The sequences given in AAQ29591-601 are sequencing primers which were
 CC used in the method of the invention to determine the sequence of regions
 CC of the HIV pol gene which are involved with resistance to azidothymidine
 CC (AZT). Resistance to AZT is caused by the accumulation of four mutations
 CC grouped within two regions of the HIV pol gene. The primers AAQ29591-96
 CC are used to determine the sequence around the mutations at amino acids
 CC positions 67 and 70, and primers AAQ29597-601 are used to determine the
 CC sequence around the mutations at positions 215 and 219. The region of

CC interest was amplified by self-sustained sequence replication (3SR).
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 11 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5703 CCTTCCTTTCTCTCTCT 5722
 |||||
 DB 20 CCTTCCTTTCTCTCTCT 1

RESULT 2561

AAQ79211/c
 ID AAQ79211 standard; DNA; 21 BP.

AC AAQ79211;

DT 25-MAR-2003 (revised)
 DT 17-JUL-1995 (first entry)

DE Guanosine rich oligonucleotide used to treat viral infection.

KM Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;
 KM infection; herpes simplex virus; human papilloma virus;
 KM Epstein-Barr virus; HIV; adenovirus; respiratory syncytial virus;
 KM hepatitis B virus; human cytomegalovirus; ss.

XX Synthetic.

PH Key Location/Qualifiers
 FT misc_feature 21
 FT /tag= a
 FT /mod base
 FT /note= "Propanolamine group attached to this base."

XX W09425037-A1.

PD 10-NOV-1994.

PF 25-APR-1994; 94WO-US004529.

PR 23-APR-1993; 93US-00053027.

PR 28-OCT-1993; 93US-00145704.

PA (TRIP-) TRIPLEX PHARM CORP.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.

PI Rando RF, Fennwald S, Zendequi JG, Ojwang JO, Hogan ME;

XX WPI; 1994-357890/44.

DR Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used
 PT to treat viral infections, e.g. herpes-virus and HIV.

XX Claim 41; Page 49; 10pp; English.

CC The oligonucleotides (see AAQ79201-52) can be used to treat viral
 CC infections. The oligonucleotides inhibit viral replication by forming
 CC guanosine tetrads which form a stabilised 3D structure. Preferred
 CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases
 CC and may be capped at the 3' terminus with a modifier selected from
 CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also
 CC have a modified phosphodiester linkage or be modified to contain a
 CC phosphorothioate linkage. They are used to treat infections with viruses
 CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,
 CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human
 CC cytomegalovirus. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2398 CCCCCACCCCTCACCACATC 3017
 |||||
 DB 21 CCCCCACCCACACCCACAC 2

RESULT 2562

AAT16460
 ID AAT16460 standard; DNA; 21 BP.

AC AAT16460;

DT 05-SEP-1996 (first entry)

DE PCR primer, p53-BP2, for human p53 gene (position 805 to 825).

KM Polymerase chain reaction; p53; cancer; neoplasia; diagnosis; prognosis;
 KM tumour suppressor gene; Li-Fraumeni syndrome; sequencing; ss.

XX Synthetic.

PN W09602671-A1.

PD 01-FEB-1996.

PF 29-JUN-1995; 95WO-SE000804.

PR 15-JUL-1994; 94SE-00002487.

PR 16-NOV-1994; 94SE-00003953.

PA (PHAA) PHARMACIA BIOTECH AB.

PI Bywater M, Lindstroem P, Inganäs M;

XX WPI; 1996-105932/11.

DR Sequence-based diagnosis of a human neoplastic tissue, blood or body
 PT fluid - useful for the diagnosis or prognosis of neoplasia.

XX Example 1; Page 24; 46pp; English.

CC AAT16454-T16469 are PCR primers used to amplify human p53 genomic DNA.
 CC The primers are used to demonstrate a method of sequence-based diagnosis
 CC of a human neoplastic tissue, blood or other body fluid. The method
 CC determines the presence, nature and location of any mutations and their
 CC influence on the biological function of the p53 protein (or other cancer-
 CC related protein), and hence the properties of the neoplasia (e.g.
 CC metastatic potential). The method allows a reliable, accurate diagnosis
 CC of neoplasia, allowing clinicians to form a prognosis on the development
 CC of the neoplasia and guidance for its treatment

XX Sequence 21 BP; 1 A; 2 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7307 CTTTGAGATTGCTTTGCTG 7326
 |||||
 DB 2 CTTTGAGTGTGCTTTGCTG 21

RESULT 2563

AAT51629/c
 ID AAT51629 standard; DNA; 21 BP.

AC AAT51629;

DT 12-NOV-1997 (first entry)

DE Viral integrase inhibiting oligonucleotide.
 XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
 KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
 KM respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
 KM integrase inhibition; guanosine tetrad; ss.
 OS Synthetic.
 XX MO9703997-A1.
 XX 06-FEB-1997.
 PD 17-JUL-1996; 96MO-US011786.
 XX 19-JUL-1995; 95US-0001505P.
 PR 23-OCT-1995; 95US-00535168.
 PR 19-MAR-1996; 96US-0013688P.
 PR 25-MAR-1996; 96US-0014007P.
 PR 17-APR-1996; 96US-0015714P.
 PR 23-APR-1996; 96US-0016271P.
 XX (ARON-) ARONEX PHARM INC.
 XX Rando RF, Fennwald S, Zendequi JG, Ojwang JO, Hogan ME;
 PI Bommler Y, Mazumder A;
 DR WPI; 1997-132569/12.
 XX Oligo:nucleotide(s) capable of forming guanosine tetrad - inhibit viral
 PT enzyme responsible for integrating viral nucleic acid into the host
 PT genome.
 XX Claim 3; Page 145; 245pp; English.
 XX AAT51619-T51698 are oligonucleotides used to inhibit the production of
 CC viruses within a host cell. The oligonucleotides may form guanosine
 CC tetrads (structures formed of eight hydrogen bonds by coordination of the
 CC four oxygen atoms of guanine with alkali cations believed to bind to the
 CC centre of a quadruplex, and by strong stacking interactions) and are used
 CC to prevent the integration of viral nucleic acid into a host genome. The
 CC oligonucleotides inhibit functioning of the integrase enzyme and hence
 CC prevent viral infection. Viral infections that may be treated include
 CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes
 CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory
 CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),
 CC especially HIV-1 infection
 CC
 SQ Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2998 CCCCCCCTCACCCTCATC 3017
 Db 21 CCCCCCCTCACCCTCATC 2
 RESULT 2564
 AAT74344/C
 ID AAT74344 standard; DNA; 21 BP.
 XX AAT74344;
 AC
 XX 25-MAR-2003 (revised)
 DT 20-AUG-1997 (first entry)
 XX Oligo for use in piliin gene hybridisation assay.
 DE promoter; template probe; signal amplifier; hybridisation assay; detect;
 KW functional domain; DNA-dependent RNA polymerase; quantifying; analyte;
 KM ligand receptor; amplification; hepatitis B virus; Neisseria gonorrhoeae;

KM bacterial beta-lactamase TEM-1 gene; Chlamydia; HIV; hepatitis C virus;
 KW bacterial tet M determinant; consensus; T7 promoter; ss.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "N4-(6-aminocaproyl-2-aminoethyl) derivative of 5-
 FT methyl cytidine"
 XX US5629153-A.
 XX 13-MAY-1997.
 PD 08-MAR-1994; 94US-00207901.
 XX 10-JAN-1990; 90US-00463022.
 PR 10-JAN-1991; 91US-00639560.
 XX (CHIR) CHIRON CORP.
 XX Urdea MS;
 PI WPI; 1997-280266/25.
 XX DNA construct for use as signal amplifier in hybridisation assays -
 PT containing DNA-dependent RNA polymerase promoter and template sequences.
 XX Example 2; Col 25; 45pp; English.
 XX A novel DNA construct (referred to as a "template probe") for use as a
 CC signal amplifier in hybridisation assays to detect a target comprises 3
 CC functional domains (A, B and C) orientated A-B-C or B-C-A. (A) is single-
 CC stranded and is designed to hybridise to complementary target sequence.
 CC (B) is double-stranded and functions as a DNA-dependent RNA polymerase
 CC promoter. (C) is single- or double-stranded, and functions as a template
 CC for the promoter activity of domain B. It consists of a nucleotide
 CC sequence not found in the template. The DNA construct is used in a method
 CC for detecting and quantifying an oligonucleotide analyte or a ligand
 CC receptor by amplification of a biological signal in a nucleic acid
 CC hybridisation assay. The method is especially useful for determination of
 CC nucleic acid segments characteristic of hepatitis B virus, Neisseria
 CC gonorrhoeae, bacterial beta-lactamase TEM-1 gene, Chlamydia, bacterial
 CC tet M determinant, HIV or hepatitis C virus. A hybridisation assay for
 CC the piliin gene DNA of Neisseria gonorrhoeae was performed using a
 CC microtitre dish assay procedure and the T7 RNA polymerase. The present
 CC sequence is a 21 base oligomer synthesised for use in the assay. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 21 BP; 7 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 3609 TTCTTGGGAAATGGGGTGG 3628
 Db 20 TTCTTGGGAAATGGGGTGG 1
 RESULT 2565
 AAT95441/C
 ID AAT95441 standard; DNA; 21 BP.
 XX AAT95441;
 AC
 XX 25-MAR-2003 (revised)
 DT 10-MAR-1998 (first entry)
 XX Primer for breast cancer susceptibility gene BRCA2 exon 11-7.
 DE Human; breast cancer; susceptibility; gene; BRCA2; diagnosis; screening;

KM treatment; gene therapy; PCR primer; exon 11-7; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09722689-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 17-DEC-1996; 96WO-US019598.
 XX
 PR 18-DEC-1995; 95US-00573779.
 PR 20-DEC-1995; 95US-00575359.
 PR 21-DEC-1995; 95US-00576559.
 PR 11-JAN-1996; 96US-00585391.
 PR 29-APR-1996; 96US-00639501.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (UYBE-) UNIV PENNSYLVANIA.
 PA (HSCR-) HSC RES & DEV LP.
 PA (ENDO-) ENDO RECH INC.
 XX
 PI Tavligian SV, Kamb A, Simard J, Couch F, Rommens JM, Weber BL;
 DR WPI, 1997-341680/31.
 XX
 PT Human breast cancer susceptibility gene BRCA2 - useful for diagnosing
 PT breast cancer and screening for compounds to treat breast cancer.
 XX
 PS Example 3; Page 60; 189pp; English.
 XX
 CC The present sequence is a primer for the human breast cancer
 CC susceptibility gene BRCA2, which can be used to diagnose breast cancer
 CC and screen for compounds to treat breast cancer. BRCA2 can also be used
 CC in gene therapy to restore wild type BRCA2 gene function to a cell, which
 CC has lost its or has altered (i.e. by virtue of a mutation in BRCA2) BRCA2
 CC gene function. (updated on 25-MAR-2003 to correct PA field.)
 XX
 SO Sequence 21 BP; 9 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4947 TTACTTTTCTCTGCTGCT 4966
 DB 21 TAACTTTTTCCTCCGCTACT 2
 RESULT 2566
 AAT80147/c
 ID AAT80147 standard; DNA; 21 BP.
 XX
 AC AAT80147;
 XX
 DT 08-FEB-1998 (first entry)
 XX
 DE Immunoglobulin signal sequence reverse PCR primer.
 XX
 KW CTLA4; IgG1; immunoglobulin; antibody; autoimmune disease;
 KW diabetes mellitus; rheumatoid arthritis; multiple sclerosis;
 KW myasthenia gravis; systemic lupus erythematosus; thyroiditis;
 KW transplant rejection; graft versus host disease; allergy; therapy;
 KW immunosuppressant; human; primer; PCR; signal peptide; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09728267-A1.
 XX
 PD 07-AUG-1997.
 XX
 PF 03-FEB-1997; 97WO-US001698.
 XX

XX
 PR 02-FEB-1996; 96US-00595590.
 XX
 PA (REBP) REPLIGEN CORP.
 XX
 PI Gray GS, Carson J, Javaherian K, Jellis CL, Rennert PD, Silver S;
 DR WPI, 1997-402620/37.
 XX
 PT New CTLA4-modified immunoglobulin fusion proteins - used for e.g.
 PT treating auto-immune diseases and allergies, or for inhibiting
 PT transplantation rejection.
 XX
 PS Example 1; Page 46; 105pp; English.
 XX
 CC A forward primer (AAT80146) and a reverse primer (AAT80147) were used for
 CC the PCR amplification of the immunoglobulin (Ig) signal sequence from
 CC template plasmid pSP7219G1. The reverse primer corresponds to the C-
 CC terminal of the natural Ig signal peptide. The 208 bp PCR product
 CC contains the entire Ig signal sequence. Novel CTLA4-antibody fusions have
 CC the heavy and light chain variable domains of an antibody molecule
 CC replaced with the extracellular domain of CTLA4. The resulting antibody-
 CC like protein binds to B7-1, B7-2 and CTLA4 ligands with high affinity.
 CC Novel CTLA4-Ig constructs (see AAT80131-83) encode fusion proteins (see
 CC AAT80206-08) useful in claimed methods for suppressing an immune response
 CC in a subject
 XX
 SO Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6020 TTTCACACCTGTCCACTCC 6039
 DB 20 TTCCACAGGTCCACTCC 1
 RESULT 2567
 AAX79218/c
 ID AAX79218 standard; DNA; 21 BP.
 XX
 AC AAX79218;
 XX
 DT 31-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #11 forms an intramolecular stacked tetrad structure.
 XX
 KW Column; box; stacked tetrad; inhibition; replication; pathophysiological;
 KW herpes simplex virus; HSV; human papilloma virus; Epstein Barr Virus;
 KW HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCV;
 KW respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;
 KW human T-cell leukaemia virus; HTLV; ss.
 XX
 OS Synthetic.
 XX
 FH Key
 FH modified_base
 FT 1. .21
 FT /tag= a
 FT /note= "optionally contains phosphodiester
 FT internucleotide linkages"
 FT 1. .21
 FT /tag= b
 FT /note= "forms intramolecular stacked tetrad or 3D
 FT columnar box structure"
 XX
 PN W09833807-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 03-FEB-1998; 98WO-US001974.
 XX
 PR 04-FEB-1997; 97US-0037374P.
 XX

PR 09-DEC-1997; 97US-00987574.
XX (ARON-) ARONEX PHARM INC.
XX
XX Rando RF, Ojwang JO, Hogan ME, Wallace TL, Cossum PA;
PI WPI; 1998-446809/38.
XX
XX New guanosine-rich tetrad forming oligonucleotide(s) - used for
PT inhibiting virus replication for treating e.g. herpes simplex, papilloma,
PT HIV, adenovirus or hepatitis B virus infection.
XX
XX Disclosure; Page 137; 140pp; English.
XX
XX Sequences AAY79210-X79275 represent oligonucleotides (ON) which are able
CC to form a columnar box or "stacked tetrad" structure by intramolecular
CC internucleotide binding. The ONs are used to inhibit the replication of
CC viruses. They are able to suppress virus production for prolonged periods
CC after an initial short treatment regimen. They can be used for treating
CC pathophysiological states caused by viruses such as herpes simplex virus,
CC human papilloma virus, Epstein Barr Virus, HIV, adenovirus, respiratory
CC syncytial virus, hepatitis B virus, human cytomegalovirus and HTLV I and
CC II
XX
SQ Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2998 CCCCCACCCCTCACCCTGC 3017
DB 21 CCCCCACCCCTCACCCTGC 2
RESULT 2568
AAZ26573/C
ID AAZ26573 standard; DNA; 21 BP.
XX
XX AAZ26573;
AC
XX 30-NOV-1999 (first entry)
DT
XX Human polymorphic region 762.
DE
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX WO9841648-A2.
PN
XX 24-SEP-1998.
PD
XX 19-MAR-1998; 98WO-US005419.
PF
XX 20-MAR-1997; 97US-0041057P.
PR
XX (VARI-) VARIAGENICS INC.
PA
XX Housman D, Ledley FD, Stanton VP;
PI WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 14 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5744 TTTTCTCTATTCACCTGC 5763
DB 20 TTTTCTCTATTCACCTGC 1
RESULT 2569
AAZ26268
ID AAZ26268 standard; DNA; 21 BP.
XX
XX AAZ26268;
AC
XX 30-NOV-1999 (first entry)
DT
XX Human polymorphic region 457.
DE
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX WO9841648-A2.
PN
XX 24-SEP-1998.
PD
XX 19-MAR-1998; 98WO-US005419.
PF
XX 20-MAR-1997; 97US-0041057P.
PR
XX (VARI-) VARIAGENICS INC.
PA
XX Housman D, Ledley FD, Stanton VP;
PI WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is

CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AA25812-226825 represent
CC human polymorphic sites described in the method of the invention
SQ Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACCTTTTCTTTTCTTTT 4481
DB 1 AATTTTCTTTTCTTTTAT 20

RESULT 2570
AA226511
ID AA226511 standard; DNA; 21 BP.
XX
AC AA226511;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 700.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9841648-A2.
XX PD 24-SEP-1998.
XX PF 19-MAR-1998; 98WO-US005419.
XX PR 20-MAR-1997; 97US-0041057P.
XX PA (VARI-) VARIAGENICS INC.
XX PI Housman D, Ledley FD, Stanton VP;
XX DR WPI; 1998-521232/44.
XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
XX PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX PT dysplastic lesions, endometriosis or graft versus host disease.
XX PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene

CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AA25812-226825 represent
CC human polymorphic sites described in the method of the invention
SQ Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 558 GACATCCCTGGGAGGGA 577
DB 1 GAGATCCCTGGCAAGGGA 20

RESULT 2571
AA226572/c
ID AA226572 standard; DNA; 21 BP.
XX
AC AA226572;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 761.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9841648-A2.
XX PD 24-SEP-1998.
XX PF 19-MAR-1998; 98WO-US005419.
XX PR 20-MAR-1997; 97US-0041057P.
XX PA (VARI-) VARIAGENICS INC.
XX PI Housman D, Ledley FD, Stanton VP;
XX DR WPI; 1998-521232/44.
XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
XX PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX PT dysplastic lesions, endometriosis or graft versus host disease.
XX PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the

CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA225812-226825 represent
 CC human polymorphic sites described in the method of the invention

XX Sequence 21 BP, 13 A, 1 C, 3 G, 4 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5744 TTTTCTCTATTCACCTGCG 5763
 21 TTTTCTCTATTCACCTGCG 2

RESULT 2572
 AA226485
 ID AA226485 standard; DNA, 21 BP.
 XX
 AC AA226485;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human polymorphic region 674.
 XX
 KM Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KM cell viability; loss of heterozygosity; precancerous condition; ASI;
 KM allele specific inhibitor; somatic cell; diagnosis; prevention;
 KM atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KM dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KM graft versus host disease; malignant cell removal; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9841648-A2.
 XX
 PD 24-SEP-1998.
 XX
 PF 19-MAR-1998; 98WO-US005419.
 XX
 PR 20-MAR-1997; 97US-0041057P.
 XX
 PA (VARI-) VARIAGENICS INC.
 XX
 PI Houseman D, Ledley FD, Stanton VP;
 XX
 DR WPI; 1998-521232/44.
 XX
 PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 XX
 PS Disclosure; Fig 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and

CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA225812-226825 represent
 CC human polymorphic sites described in the method of the invention

XX Sequence 21 BP, 16 A, 0 C, 5 G, 0 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4020 AAAAAGAGGAAAAACAAA 4039
 1 AAGAGAGAGGAAAAAAA 20

RESULT 2573
 AA220460
 ID AA220460 standard; DNA, 21 BP.
 XX
 AC AA220460;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Forward PCR primer for microsatellite marker Bmag323.
 XX
 KM PCR primer; microsatellite marker; barley; chromosome 7 marker; cereal;
 KM fermentability; group 5 chromosome; ethyl carbanate production; Bmac213;
 KM wort fermentation; Triticaceae; Bmac36; epi-heterodendrin production;
 KM diagnosis; ss.
 XX
 OS Synthetic.
 OS Hordeum vulgare.
 XX
 PN WO9946404-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 01-MAR-1999; 99WO-GB000602.
 XX
 PR 10-MAR-1998; 98GB-00005087.
 XX
 PA (SCCR-) SCOTTISH CROP RES INST.
 XX
 PI Thomas WTB, Swanson JS, Powell W, Waugh R, Ramsey LD;
 XX
 DR WPI; 1999-551424/46.
 XX
 PT Screening cereals for fermentability, especially useful in barley.
 XX
 PS Claim 25; Page 23; 49pp; English.

XX This sequence represents a PCR primer for a barley chromosome 7
 CC microsatellite marker, and can be used in the method of the invention.
 CC The method is for screening cereal for fermentability, comprising
 CC analysing cereal genomic DNA to determine which allele(s) of a gene/gene
 CC complex affecting fermentability at a locus close to the centromere on
 CC homologous Triticaceae group 5 chromosome (barley chromosome 7) is/are
 CC present. The invention also relates to a method for screening cereal for
 CC ethyl carbanate production on wort fermentation and distillation,
 CC comprising analysing barley genomic DNA to determine which allele(s) of
 CC the locus, designated eph on the short arm of homologous Triticaceae group
 CC 1 chromosome (barley chromosome 5) is/are present. The methods and
 CC primers are useful for determining fermentability and/or epi-heterodendrin
 CC production in cereals, especially barley. Current methods for determining
 CC fermentability are difficult to apply within barley breeding programs.
 CC Prior art methods using molecular markers have difficulty in detecting
 CC levels of allelic variation

XX Sequence 21 BP, 7 A, 5 C, 3 G, 6 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

OY 1720 TTCCGCACTTCAGACAC 1739

Db 2 TTGTGACATCTCAAGAACAC 21

RESULT 2574

AA00040/c

ID AA00040 standard; DNA; 21 BP.

AC AA00040;

DT 16-MAR-1999 (first entry)

DE aGFP PCR antisense primer.

XX Neuroepithelial stem cell; lineage restricted intermediate precursor;

KM oligodendrocyte; astrocyte; self-renewal; neuron; differentiation; CNS;

KM neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS;

KM central nervous system; glial cell; PCR primer; amplification; ss.

XX Synthetic.

OS Homo sapiens.

XX MO9850526-A1.

XX 12-NOV-1998.

PF 07-MAY-1998; 98WO-US009630.

PR 07-MAY-1997; 97US-00852744.

PR 06-MAY-1998; 98US-00073881.

XX (UTAH) UNIV UTAH RES FOUND.

PI Rao MS, Mayer-Proschel M, Mujtaba T;

DR WPI; 1999-070093/06.

XX Mammalian neuroepithelial stem cells and glial restricted precursor - can

PT self-renew and differentiate into central nervous system cells, used for

PT generating various types of cells.

XX Example 26; Page 59; 78pp; English.

XX The present invention describes an isolated, pure population of mammalian

CC neuroepithelial stem cells, which are capable of self-renewal in adherent

CC feeder-cell-independent (NFICI) culture medium and differentiation to

CC central nervous system (CNS) neuronal or glial cells and to neuronal

CC crest stem cells. Also described is an isolated population of mammalian

CC APIC culture medium and can differentiate to CNS glial cells but not to

CC CNS neuronal cells. The stem cells can be used to generate a population

CC of mammalian motor neurons by incubating the stem cells in a medium

CC promoting cell proliferation and neuronal differentiation. The medium

CC comprises laminin-coated plates and NEP medium lacking chick embryo

CC extract. The stem cells can also produce neural crest stem cells by

CC inducing the cells to differentiate in vitro. The inducing step comprises

CC withdrawing a mitogen (preferably fibroblast growth factor; FGF) and

CC chick embryo extract. Inducing can also comprise adding a dorsalizing

CC agent to the cells, preferably a bone morphogenetic protein (BMP) such as

CC BMP-2, -4 or -7. The stem cells can be used to produce cells of the

CC peripheral nervous system, by inducing the stem cells to differentiate in

CC vitro to neural crest stem cells, and inducing these cells to

CC differentiate. AA00029 to AA00054 represent PCR primers which are used

CC in an example from the present invention to amplify different FGF and

CC FGFR genes

XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

OY 3683 GCCAGAAAGCCAGCTATT 3702

Db 21 GCCAGAAAGCCAGCTATT 2

RESULT 2575

AA295022

ID AA295022 standard; DNA; 21 BP.

AC AA295022;

DT 15-AUG-2000 (first entry)

DE Prostate cancer diagnostic marker Proll1 forward PCR primer.

XX Prostate cancer; cancer specific gene; CSG; expressed sequence tag; EST;

KM diagnosis; monitoring; staging; imaging; therapy; metastasis; marker;

KM human; Proll1; PCR primer; ss.

XX Homo sapiens.

XX MO200023111-A1.

XX 27-APR-2000.

PF 19-OCT-1999; 99WO-US024331.

PR 19-OCT-1998; 98US-0104737P.

XX (DIAD-) DIADEXUS LLC.

PI Salceda S, Recipon H, Cafferkey R;

DR WPI; 2000-339531/29.

XX Diagnosing, staging and monitoring the presence and metastases of

PT prostate cancer especially useful for treating prostate cancer comprises

PT measuring changes in cancer specific gene levels.

XX Example 2; Page 23; 74pp; English.

XX The present sequence is that of the forward primer used in the real-time

CC quantitative PCR amplification of cancer specific gene Proll1 (see

CC AA295002 and AA295003). Overexpression of Proll1 was found in 5 of 16

CC primary prostate cancer samples examined, indicative of it being a

CC diagnostic marker for prostate cancer. The invention provides ESTs and

CC full-length cDNAs for CSGs (see AA294998-295017). The CSGs,

CC polypeptides encoded by them, and antibodies that specifically bind CSG

CC are used in claimed methods for detecting, diagnosing, monitoring,

CC staging, imaging and treating prostate cancer

XX Sequence 21 BP; 5 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 21;

XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;

XX Matches 17, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

XX OY 5181 CTGCAATGTTCTCCACTTGA 5200

Db 2 CTGCAATGTTCTCCACTTGA 21

RESULT 2576

AA446283

ID AA446283 standard; DNA; 21 BP.

AC AA446283;

XX 04-SEP-2000 (first entry)


```
PD 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-1B000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 21-APR-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 1715; 2745pp; English.
XX
XX AA65654 to AA69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA69579 to AA77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 21 BP; 0 A; 8 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5707 CCTTTCCTCTCTCTCTT 5726
XX 1 CCTTTCCTCTCTCTCTCT 20
XX
XX Db
XX
XX RESULT 2579
XX AA276810
XX ID AA276810 standard; DNA; 21 BP.
XX
XX AC AA276810;
XX
XX DT 10-SEP-2001 (first entry)
XX
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:11166.
XX
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9954500-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 21-APR-1999; 99WO-1B000822.
XX
XX PR 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX PA
```

```
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 2611; 2745pp; English.
XX
XX AA65654 to AA69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA69579 to AA77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 21 BP; 6 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4635 CAACCTCAGTGTGGAATTTC 4654
XX 2 CAACCTCAGTGTATATTTC 21
XX
XX Db
XX
XX RESULT 2580
XX AAC60966/c
XX ID AAC60966 standard; DNA; 21 BP.
XX
XX AC AAC60966;
XX
XX DT 13-FEB-2001 (first entry)
XX
XX DE Tumour necrosis factor beta short tandem repeat primer SEQ ID NO:26.
XX
XX KW Short tandem repeat; primer; STR; susceptibility; HIV; infection; AIDS;
XX detection; polymorphism; interleukin 10 promoter; IL-10;
XX chromosome position 6p21.3; tumour necrosis factor beta; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200061811-A2.
XX
XX PD 19-OCT-2000.
XX
XX PF 06-APR-2000; 2000WO-US009355.
XX
XX PR 09-APR-1999; 99US-0128521P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Smith MW, Shin HD, O'Brien SJ;
XX
XX WPI; 2000-687051/67.
XX
XX Predicting susceptibility to HIV infection or progression useful for
XX selection of therapeutic treatment for persons infected with HIV virus,
XX comprises detecting polymorphism in human interleukin-10 promoter.
XX
XX Example 1; Page 12; 40pp; English.
XX
XX
```

CC The present invention describes a method for predicting susceptibility to
 CC HIV infection or HIV progression in a subject. The method involves
 CC detecting a polymorphism in a human interleukin-10 (IL-10) promoter,
 CC where the presence of the polymorphism indicates susceptibility to HIV
 CC infection or HIV progression. The method provides prognostic information
 CC to persons infected with HIV virus and is useful to help select
 CC treatments (such as administration of IL-10 or gene therapy with IL-10).
 CC The presence of polymorphism is useful as predictor that very aggressive
 CC treatment could substantially eradicate the virus from the infected
 CC person. The method is useful for the generation of normograms or other
 CC predictive algorithms that can be used, in association with allele
 CC status, to prognose probable survival or years to development of AIDS
 CC following HIV seroconversion. It indicates that increased expression of
 CC the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression
 CC and enables a variety of new therapeutic interventions in the treatment
 CC of HIV disease. The present sequence represents a short tandem repeat
 CC (STR) primer which is used in an example from the present invention
 XX

SQ Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Qy Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5179 CTCGACATGTTCCACTTG 5198
 21 CTCGACAGTTCTCCCATG 2

RESULT 2581
 AAC80269/c
 ID AAC80269 standard; DNA; 21 BP.
 AC AAC80269;
 XX
 DT 03-MAY-2001 (first entry)
 XX
 DE Reverse primer #97 used for amplification of HLA-A exon 3.
 XX
 KM HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200061795-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-EP002998.
 XX
 PR 09-APR-1999; 99EP-00870068.
 PR 11-JUN-1999; 99US-0138614P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI De Canck I, Rombout A, Rossau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
 PT primer sets, useful for subtyping or typing of HLA Class I alleles.
 XX
 PS Claim 4; Page 40; 128pp; English.
 XX
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method
 XX
 SQ Sequence 21 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 1 Other;

Qy Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5151 GGGAGGAGACTTCTCTGG 5170
 21 GGGAGAGAMTCTCTGGG 2

RESULT 2582
 AAF95320/c
 ID AAF95320 standard; DNA; 21 BP.
 AC AAF95320;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #81.
 XX
 KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KM polymorphism; vascular disease; coronary artery disease; forensics;
 KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KM pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 /standard_name= "single nucleotide polymorphism"

PN W0200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-015357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX
 DR WPI; 2001-226749/23.
 XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 PS Example; Page 52; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Qy Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
OY      4761 ATCCGCGCTGAGAGTTAG 4780
      |||||
      21 ATCCGCGCTGAGAGTTAG 2
Db

RESULT 2583
AAF95430/c
ID      AAF95430 standard; DNA; 21 BP.
XX
AC      AAF95430;
XX
DT      06-JUN-2001 (first entry)
XX
DE      Human gene single nucleotide polymorphism #191.
XX
KW      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW      polymorphism; vascular disease; coronary artery disease; forensics;
KW      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW      pulmonary embolism; paternity test; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Variation
FT      Location/Qualifiers
FT      replace(11,A)
FT      /*tag= a
FT      /standard_name="single nucleotide polymorphism"
XX
XX      WO200118250-A2.
XX
XX      15-MAR-2001.
XX
XX      07-SEP-2000; 2000WO-US024503.
XX
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX
XX      (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILLENNIUM PHARM INC.
XX
XX      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX      WPI; 2001-226749/23.
XX
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
XX      applications such as forensics, paternity testing, medicine, genetic
XX      analysis and phenotype correlations to diseases such as diabetes and
XX      atherosclerosis.
XX
XX      Example; Page 61; 242pp; English.
XX
XX      The present invention provides a method of diagnosing a vascular disease
XX      in an individual, involving determining the sequence at various
XX      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX      genes. The sequences at a number of polymorphic sites are also provided
XX      in the specification. In particular, the method can be used in the
XX      diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX      disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX      useful in forensics, paternity testing, genetic analysis and phenotype
XX      correlations to diseases. The present sequence is an example of one of
XX      the human gene SNPs shown in the specification
XX
XX      Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      7408 AACATCAGCAGCAGCAGCAG 7427
      |||||
      20 AACATCAGCAGCAGCAGCAG 1
Db

RESULT 2585
AAH22257
ID      AAH22257 standard; DNA; 21 BP.
XX
XX      64 GGCTGCGGCGGCGGCGGCGC 83
XX      |||||
XX      21 GGCTGCGGCGGCGGCGGCGC 2
XX
XX      AAF96888/c
XX      ID      AAF96888 standard; DNA; 21 BP.
XX
XX      AAF96888;
XX
XX      06-JUN-2001 (first entry)
XX
XX      Human gene single nucleotide polymorphism #1649.
XX
XX      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX      polymorphism; vascular disease; coronary artery disease; forensics;
XX      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX      pulmonary embolism; paternity test; ds.
XX
XX      Homo sapiens.
XX
XX      Key
XX      Variation
XX      Location/Qualifiers
XX      replace(11,T)
XX      /*tag= a
XX      /standard_name="single nucleotide polymorphism"
XX
XX      WO200118250-A2.
XX
XX      15-MAR-2001.
XX
XX      07-SEP-2000; 2000WO-US024503.
XX
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX
XX      (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILLENNIUM PHARM INC.
XX
XX      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX      WPI; 2001-226749/23.
XX
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
XX      applications such as forensics, paternity testing, medicine, genetic
XX      analysis and phenotype correlations to diseases such as diabetes and
XX      atherosclerosis.
XX
XX      Example; Page 159; 242pp; English.
XX
XX      The present invention provides a method of diagnosing a vascular disease
XX      in an individual, involving determining the sequence at various
XX      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX      genes. The sequences at a number of polymorphic sites are also provided
XX      in the specification. In particular, the method can be used in the
XX      diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX      disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX      useful in forensics, paternity testing, genetic analysis and phenotype
XX      correlations to diseases. The present sequence is an example of one of
XX      the human gene SNPs shown in the specification
XX
XX      Sequence 21 BP; 0 A; 13 C; 7 G; 1 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

XX AAH22257;
AC
XX
DT 21-AUG-2001 (first entry)
XX
DE Placental growth factor forward PCR primer SEQ ID NO.3.
XX
XX Human, differentially expressed gene; angiogenesis; diagnosis;
KW angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KW vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KW rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KW neovascularisation; restenosis; hypertension; aneurysm; angina;
KM myocardial infarction; chronic heart condition; osteoporosis; PCR primer;
KM hybridisation; probe; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX WO200132926-A2.
XX
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-US030051.
XX
XX 01-NOV-1999; 99US-0162699P.
PR 13-APR-2000; 2000US-0196802P.
PR 31-OCT-2000; 2000US-00703350.
XX
XX (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
XX
XX Mehrahan F, Gerritsen M, Rastelli L;
PI
XX WPI; 2001-291056/30.
XX
XX Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumours, atherosclerosis and/or restenosis
PT subsequent to balloon angioplasty.
XX
XX Example 19; Page 147; 182pp; English.
XX
XX The present invention describes differentially expressed genes involved
CC in angiogenesis (I), and the polypeptides that encode them. (I) have
CC cardiovascular activity, and can be used in the modulation of
CC angiogenesis. The nucleic acids and polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate angiogenesis. The polypeptides may also be used as antigens
CC in the production of antibodies against them and in assays to identify
CC modulators of their expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity and
CC modulate angiogenesis. The antibodies may also be used as diagnostic
CC agents for detecting the presence of the polypeptides in samples.
CC Disorders that may be prevented, diagnosed and/or treated by the above
CC methods include, for example vascular tumours, proliferative tumours,
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC associated with neovascularisation, restenosis subsequent to balloon
CC angioplasty, scar tissue over production, peripheral vascular disease,
CC hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, heart failure such as congestive heart failure, age-related
CC macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAH98322
CC to AAH98325 represent sequence used in the exemplification of the present
XX invention
XX
XX Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 958 ACGGACTCTACGCGCTCG 977
DB 2 ACGTCTCTACGACGCTTCG 21
RESULT 2586
AAH62597/C
ID AAH62597 standard; DNA; 21 BP.
XX
XX AAH62597;
AC
XX 12-SEP-2001 (first entry)
DT
XX CHRNA7 polymorphism containing DNA fragment #498.
DE
KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Variation /replce(11,A)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200138576-A2.
XX
XX 31-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US031639.
XX
XX 24-NOV-1999; 99US-0167334P.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
PI
XX WPI; 2001-367705/38.
XX
XX New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites, for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 69; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis
XX
XX Sequence 21 BP; 1 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7412 TCAGCAGCAGCAGCAGC 7431
DB 21 TCCCGAGAGCAGCAGCAGC 2

RESULT 2587
AAH62143/C
ID AAH62143 standard; DNA; 21 BP.
XX

```
AC AAH62143;
XX
XX 12-SEP-2001 (first entry)
XX
XX Solute carrier family 3 A1 polymorphism containing DNA fragment #44.
DE
XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KM heart disease; paternity testing; forensic science; ds.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Variation replace(11,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200138576-A2.
XX
XX 31-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US031639.
XX
XX 24-NOV-1999; 99US-0167334P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI; 2001-367705/38.
XX
XX New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites, for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 32; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotypic correlation, forensics, paternity testing,
CC medicine and genetic analysis
XX
XX Sequence 21 BP; 4 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1580 CCCAAACACAGTGTGAGAA 1599
DB 20 CCCAGAAACAGTGTCTAGCA 1
RESULT 2588
AAH91825
ID AAH91825 standard; DNA; 21 BP.
XX
XX AAH91825;
AC
XX 09-OCT-2001 (first entry)
DT
XX Human inflammatory bowel disease associated polymorphic site #900.
DB
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KM chromosome 5q31-33; forensic test; gene therapy; ds.
XX
```

```
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 11
FT /*tag= a
FT /note= "SNP, optionally T or A at this position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 76; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
XX Sequence 21 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 1 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4463 CTTTCTTTTCTTTTCTTTTCTTTT 4483
DB 1 CTTCTTTATCCTTTTCTTTTCTTTT 21
RESULT 2589
AAF87033
ID AAF87033 standard; DNA; 21 BP.
XX
XX AAF87033;
AC
XX 18-SEP-2001 (first entry)
DT
XX Anchored 3' oligo dt12 primer.
DB
XX Sequencing primer; definitive ectoderm equivalent cell; DEB cell;
KM cell preparation; early primitive ectoderm-like cell; EBL cell; human;
KM cell therapy; gene therapy; neuroectoderm cell; organ transplant;
KM neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KM stroke; spinal cord injury; therapy; ss.
XX
XX Synthetic.
OS
XX WO200151610-A1.
XX
XX 19-JUN-2001.
XX
XX 12-JAN-2001; 2001WO-AU000029.
XX
```

PR 14-JAN-2000; 2000AU-00005098.
 PR 20-APR-2000; 2000AU-00007045.
 PR 27-APR-2000; 2000AU-00007143.
 XX
 XX (BRES-) BRESAGEN LTD.
 PA (LONG/) LONG C L O.
 XX
 XX Long CLO, Rathjen PD, Rathjen J;
 PI WPI; 2001-432907/46.
 DR
 XX
 PT Preparing (M1) definitive ectoderm equivalent (DEE) cells in vitro for
 PT treatment of Parkinson's and Alzheimer's comprises culturing early
 PT primitive ectoderm-like cells in conditioned medium.
 XX
 XX Example; Page 37; 116pp; English.
 XX
 CC This sequence represents a sequencing primer used within the scope of the
 CC invention. The invention relates to a method for preparing definitive
 CC ectoderm equivalent (DEE) cells in vitro comprising providing: (a) early
 CC primitive ectoderm-like (EPL) cells; and (b) a conditioned medium or
 CC extract exhibiting neural inducing properties and culturing the EPL cells
 CC for a time to permit controlled differentiation to DEE cells. The DEE
 CC cells, or their differentiated or partially differentiated progeny are
 CC useful in human cell therapy or transgenic animal production and for use
 CC in human or animal gene therapy. The method is useful for preparing DEE
 CC cells in vitro. It can also be used for selectively producing
 CC neuroectoderm cells or surface ectoderm cells from DEE cells. The method
 CC can also be used to produce genetically modified DEE cells. It is also
 CC useful for preparing tissues or organ for transplant. The cells are
 CC useful for treating and curing neurodegenerative diseases such as
 CC Parkinson's disease and Alzheimer's disease and pathological conditions
 CC such as stroke and spinal cord injury by replacing or assisting the
 CC function of normal disease tissues. They are also useful for the
 CC treatment of corneal disorders. The methods are useful for producing
 CC cells as a source for reprogramming and for use in pharmaceutical or
 CC toxicological screening
 XX
 SQ Sequence 21 BP; 4 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTT 4477
 DB 1 ATGAACTCTTTTCTTTTCTTTT 20
 RESULT 2590
 ABK51835/c
 ID ABK51835 standard; DNA; 21 BP.
 XX
 AC ABK51835;
 XX
 DT 30-JUN-2002 (first entry)
 XX
 DE DNA probe #1 for human UGT8 gene.
 XX
 KM Human; enzyme classification; enzyme quantitative determination;
 KM glucuronic acid conjugation; UDP-glucuronosyltransferase; UGT8; probe;
 KM ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN JP2002085066-A.
 XX
 PD 26-MAR-2002.
 XX
 PF 07-SEP-2000; 2000JP-00272228.
 XX
 PR 07-SEP-2000; 2000JP-00272228.
 XX

PA (SAKA) OTSUKA SEIYAKU KOGYO KK.
 XX
 XX WPI; 2002-378271/41.
 DR
 XX
 PT Determination of enzymes participating in glucuronic acid conjugation in
 PT human being, comprises use of oligonucleotide probes.
 XX
 XX Claim 8; Page 13; 13pp; Japanese.
 PS
 CC The present invention relates to a method for classification and
 CC quantitative determination of enzymes participating in glucuronic acid
 CC conjugation. The method involves the use of oligonucleotide probes
 CC hybridizing to regions of the human UDP-glucuronosyltransferase (UGT)
 CC genes (e.g. UGT1, UGT1A7, UGT1A10, UGT1A9, UGT1A8, UGT2B10,
 CC UGT2B11, UGT2B15, UGT2B17, UGT8), and the DDOST gene. The method and
 CC probes are useful for the genetic determination of enzymes participating
 CC in glucuronic acid conjugation with catalysed UGT. The method is both
 CC rapid and accurate. ABK51813-ABK51836 represent oligonucleotide probes
 CC useful for human UGT or DDOST genes
 XX
 SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7250 TGGATGGGGAATGCTCTG 7269
 DB 20 TAGATGGGGAATGCTCTG 1
 RESULT 2591
 ABK8538/c
 ID ABK8538 standard; DNA; 21 BP.
 XX
 AC ABK8538;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human cholecystokinin associated PCR primer P2.
 XX
 KM Panic disorder; polymorphism; human cholecystokinin; upper stream; CCK;
 KM PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002171990-A.
 PD 18-JUN-2002.
 XX
 PF 08-DEC-2000; 2000JP-00375090.
 XX
 PR 08-DEC-2000; 2000JP-00375090.
 XX
 PA (RIKA) RIKAGAKU KENKYUSHO.
 XX
 DR WPI; 2002-569886/61.
 XX
 PT Diagnosis and identification of panic disorder caused by polymorphism of
 PT upper stream region of human cholecystokinin gene.
 XX
 XX Claim 6; Page 6; 13pp; Japanese.
 PS
 CC The invention describes a method of diagnosing a panic disorder with a
 CC polymorphism of the upper stream region of human cholecystokinin (CCK)
 CC gene. This sequence represents a human cholecystokinin gene associated
 CC PCR primer
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6914 TACTGACTTAGAGCCTCTGG 6933
DB 20 TACTGAATTAGAGCCTCTGG 1

RESULT 2592
ABK16848/c
ID ABK16848 standard; DNA; 21 BP.
XX
XX ABK16848;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human protein refolding PCR primer #71.
DE
XX Protein refolding; growth hormone supergene family; human; mouse; ss;
KW therapeutic half-life; PCR primer; anti-angiogenesis factor.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200187925-A2.
XX
XX 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US016088.
XX
XX 16-MAY-2000; 2000US-0204617P.
XX
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.
XX
XX Rosendahl MS, Cox GN, Doherty DH;
PI
XX WPI; 2002-089843/12.
XX
XX Making and refolding insoluble or aggregated proteins having free
PT cysteine by exposing host cell expressing protein to cysteine blocking
PT agent, and exposing to cysteine reactive group to increase their
PT effectiveness.
XX
XX Example 14; Page 52; 110pp; English.
XX
XX The invention relates to a host cell, made to express an insoluble or
CC aggregated protein having free cysteines residues. The cell is then lysed
CC by chemical, enzymatic or physical agents and solubilised by exposing it
CC to a denaturing agent, a reducing agent and a cysteine blocking agent,
CC and is refolded into a biologically active form by reducing the
CC concentrations of denaturing and reducing agents. The protein may belong
CC to the growth hormone supergene family or may be an anti-angiogenesis
CC factor. The method is useful for preparing a refolded, soluble form of an
CC insoluble or aggregated protein. The proteins of the invention can act as
CC delivery vehicles for enhancement of the circulatory half-life of the
CC therapeutics that are attached or for directing delivery of a specific
CC target within the body. Sequences ABK16774-ABK16852 represent PCR primers
CC used in synthesis of the proteins
XX
XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6435 ATTAGCTTAAGCAGCAGTGT 6454
DB 21 ATTATCTTCAGCAGCAGTGT 2

RESULT 2593
ABZ31311
ID ABZ31311 standard; DNA; 21 BP.
XX
XX ABZ31311;

XX 30-JAN-2003 (first entry)
DT
XX
XX Candida albicans GRACE strain PCR primer SEQ ID NO 5530.
DE
XX
XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
XX Candida albicans.
OS
XX WO200253728-A2.
XX
XX 11-JUL-2002.
XX
XX 26-DEC-2001; 2001WO-US049486.
XX
XX 29-DEC-2000; 2000US-0259128P.
XX
XX 20-FEB-2001; 2001US-0079202A.
XX
XX 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
PI
XX WPI; 2002-566694/60.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
XX Claim 36; SEQ ID NO 5530; 167bp + Sequence Listing; English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
XX Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5695 CTGTTTGCCCTTCCTTTCC 5714
DB 2 CTCTTTGGCTGCTTTTCC 21

RESULT 2594
ABS98398/c
ID ABS98398 standard; DNA; 21 BP.
XX
XX ABS98398;

AC ABS98398;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human multidrug resistance associated protein 3 polymorphic sequence #20.
 XX
 KM Human; db; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 KM cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTP;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydrolase 2; EPXH2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMNT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPAR;
 KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; SNP;
 KM single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN W0200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 PS Example 24; Page 152; 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPXH2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HMMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NMNT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPAR), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
 CC AHR, EPXH2, GST12, NMNT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug

CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function. In COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and NMNT for altered serine
 CC immunological or haematological function, in KLK2 for altered
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 3 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 15.2; DB 1; Length 21;
 XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;
 XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 Db 562 ATCCCTGGGAGGAGGAGG 581
 XX 20 ATCCTTGGGAGGAGGAGG 1
 XX
 RESULT 2595
 XX ABR94358/c
 XX ID ABR94358 standard; DNA; 21 BP.
 XX
 XX ABR94358;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #146.
 XX
 KM Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
 KM EDNR; signaling system; cardiovascular disease; coronary heart disease;
 KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
 KM diabetes; familial hypercholesterolemia; forensic marker;
 KM transgenic animal; solid support; cardiovascular regulator; SNP;
 KM single nucleotide polymorphism; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN W0200224747-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-EP010087.
 XX
 PR 19-SEP-2000; 2000EP-00120123.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Brinkmann U, Hoffmeyer S;
 XX
 DR WPI; 2002-435060/46.
 XX
 PT Novel polymorphic of the endothelin/endothelin converting
 PT enzyme/receptor of endothelin and endothelin converting enzyme signaling
 PT system associated with cardiovascular disease, useful for treating the
 PT disease.
 XX
 PS Example 6; Page 67; 190pp; English.
 XX
 CC The invention describes a polynucleotide (I) of the endothelin
 CC (EDN) endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a
 CC molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolemia. The gene or a polynucleotide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP; 4 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

688 GCCCTGATGTGGCCAG 707
20 GCCCTGATGTGGCCAG 1

RESULT 2596
ABK94357
ID ABK94357 standard; DNA; 21 BP.
AC ABK94357;
DT 27-AUG-2002 (first entry)
XX
XX Endothelin converting enzyme 1 (ECE-1) SNP detection primer #145.
DE
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KM EDNR; signaling system; cardiovascular disease; coronary heart disease;
KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KM diabetes; familial hypercholesterolemia; forensic marker;
KM transgenic animal; solid support; cardiovascular regulator; SNP;
KM single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
OS
XX WO200224747-A2.
PN
XX 28-MAR-2002.
PD
XX 31-AUG-2001; 2001WO-EP010087.
PF
XX 19-SEP-2000; 2000EP-00120123.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Brinkmann U, Hofmeyer S;
PI
XX WPI; 2002-435060/46.
DR
XX
XX Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling
PT system associated with cardiovascular disease, useful for treating the
PT disease.
XX
XX Example 6; Page 67; 190pp; English.
PS
XX The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

molecular variant gene comprising (I) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolemia. The gene or a polynucleotide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

688 GCCCTGATGTGGCCAG 707
2 GCCCTGATGTGGCCAG 1

RESULT 2597
ABK94084
ID ABK94084 standard; DNA; 21 BP.
AC ABK94084;
DT 27-AUG-2002 (first entry)
XX
XX Endothelin-1 (EDN-1) SNP detection PCR primer #28.
DE
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KM EDNR; signaling system; cardiovascular disease; coronary heart disease;
KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KM diabetes; familial hypercholesterolemia; forensic marker;
KM transgenic animal; solid support; cardiovascular regulator; SNP;
KM single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
OS
XX WO200224747-A2.
PN
XX 28-MAR-2002.
PD
XX 31-AUG-2001; 2001WO-EP010087.
PF
XX 19-SEP-2000; 2000EP-00120123.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Brinkmann U, Hofmeyer S;
PI
XX WPI; 2002-435060/46.
DR
XX
XX Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling
PT system associated with cardiovascular disease, useful for treating the
PT disease.
XX
XX Example 6; Page 55; 190pp; English.
PS
XX The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

or (ii) is useful for producing cells capable of expressing a molecular variant polypeptide which is associated with a cardiovascular disease. (ii), (iii), the EDN, ECE or EDNR polypeptide, or a cell expressing a molecular variant gene comprising (i) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolaemia. The gene or a polynucleotide fragment of the EDN/EDNR/ECE signaling system and in creation of a solid support creating a transgenic animal and vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP, 3 A, 3 C, 2 G, 12 T, 0 U, 1 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3722 TCCTCATTCATTGAGCTTTT 3742
1 TCCTGATTANTGATCTTTT 21

RESULT 2598

ABK94083/c
ID ABR94083 standard; DNA; 21 BP.

ABK94083;

27-AUG-2002 (first entry)

Endothelin-1 (EDN-1) SNP detection PCR primer #27.

Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor; EDNR; signaling system; cardiovascular disease; coronary heart disease; hypertension; atherosclerosis; angiogenesis; fatty acid metabolism; diabetes; familial hypercholesterolaemia; forensic marker; transgenic animal; solid support; cardiovascular regulator; SNP; single nucleotide polymorphism; PCR; primer; ss.

Synthetic.

WO200224747-A2.

28-MAR-2002.

31-AUG-2001; 2001WO-EP010087.

19-SEP-2000; 2000EP-00120123.

(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

Brinkmann U, Hoffmeyer S;

WPI; 2002-435060/46.

Novel polynucleotide of the endothelin/endothelin converting enzyme/receptors of endothelin and endothelin converting enzyme signaling system associated with cardiovascular disease, useful for treating the disease.

Example 6; Page 55; 190pp; English.

The invention describes a polynucleotide (i) of the endothelin

(EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR) signaling system which is associated with a cardiovascular disease. (i), the gene encoding EDN, ECE or EDNR (ii) or a vector (iii) expressing (i) or (ii) is useful for producing cells capable of expressing a molecular variant polypeptide which is associated with a cardiovascular disease. (ii), (iii), the EDN, ECE or EDNR polypeptide, or a cell expressing a molecular variant gene comprising (i) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolaemia. The gene or a polynucleotide fragment of the EDN/EDNR/ECE signaling system and in creation of a solid support creating a transgenic animal and vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP, 12 A, 2 C, 3 G, 3 T, 0 U, 1 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3722 TCCTCATTCATTGAGCTTTT 3742
21 TCCTGATTANTGATCTTTT 1

RESULT 2599

ABV74830/c
ID ABV74830 standard; DNA; 21 BP.

ABV74830;

28-MAR-2003 (first entry)

Murine OAS gene isoform L1 PCR primer SEQ ID 13.

Virucide; hepatotropic; antiinflammatory; antiviral; OAS; murine; 2'-5'-oligoadenylate synthase; Flavivirus infection; PCR; primer; ss.

Mus sp.

WO200281741-A2.

17-OCT-2002.

04-APR-2002; 2002WO-FR001169.

04-APR-2001; 2001FR-00004598.

(INSP) INST PASTEUR.

(CNRS) CNRS CENT NAT RECH SCI.

Guenet J, Mashimo T, Simon-Chazottes D, Montagueilli X;

Frenkel M, Despres P, Deubel V, Bonhomme F, Lucas M;

WPI; 2003-058566/05.

Identifying stimulators of oligoadenylate synthase family genes, useful as antiviral agents against Flavivirus, also mutated genes responsible for sensitivity to virus.

Claim 16; Page 80; 93pp; French.

The present invention relates to a method for identifying compounds (i)

CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)
CC family. The method comprises: (a) inducing expression of the OAS gene in
CC a culture of cells from a non-human mammal (PIV/PIVr or PIVr/PIVr);
CC indicating resistance or sensitivity to Flavivirus infection); (b)
CC treating cells with test compound; and (c) measuring activity of OAS gene
CC relative to a control. (1) are potentially useful as antiviral agents for
CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow
CC fever and various forms of encephalitis). Genomic OAS DNA and derived
CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus
CC infection; (b) in screening for anti-Flavivirus agents, and (c) for
CC evaluating sensitivity of subjects to Flavivirus infection and their
CC likely response to interferon treatment, e.g. to identify patients at
CC risk of developing severe forms of such infections. The present sequence
CC is a PCR primer for murine OAS, which was used in an example from the
CC invention
CC XX
SQ Sequence 21 BP; 4 A; 1 C; 9 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1866 CAGACCTCAGCTCAGACTC 1885
DB 20 CAGACCTCAGCTCAGACTC 1
RESULT 2600
ADC78764
ID ADC78764 standard; DNA; 21 BP.
XX
AC ADC78764;
XX
DT 01-JAN-2004 (first entry)
XX
DE Mouse BORIS identification PCR primer SEQ ID NO:44.
XX
KM human; brother of regulator of imprinted site; BORIS; cytoskeletal;
XX gene therapy; cancer; ss; PCR primer.
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX WO2003072799-A2.
XX
PD 04-SEP-2003.
XX
PE 21-FEB-2003; 2003WO-US005186.
XX
PR 22-FEB-2002; 2002US-035889P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lobanenko VV, Loukinov DI, Morse HC;
XX WPI; 2003-721780/68.
XX
PT New nucleic acid molecule encoding a human or non-human brother of
PT regulator of imprinted sites (BORIS), useful for preparing a composition
PT for treating or preventing cancer.
XX
PS Example 1; SEQ ID NO 44; 71bp; English.
XX
CC The present invention describes the human brother of regulator of
CC imprinted sites (BORIS) protein. Also described: (1) a vector comprising
CC an isolated nucleic acid encoding BORIS; (2) a cell comprising the vector
CC; (3) an isolated polypeptide molecule comprising a sequence encoding the
CC human BORIS or its fragment comprising at least 307 or 21 contiguous
CC amino acids, either one of which is optionally glycosylated, amidated,
CC carboxylated, phosphorylated, esterified, N-acylated or converted into an
CC acid addition salt and/or optionally dimerised or polymerised; (4) a cell
CC line that produces a monoclonal antibody that is specific for a region of

CC the isolated polypeptide, where the region comprises any region that is
CC recognisable by the monoclonal antibody other than one spanning a zinc
CC finger region; (5) diagnosing cancer or predisposition to cancer in a
CC male or female mammal; (6) predicting a predisposition to cancer in an
CC offspring of a male mammal; (7) prognosticating cancer in a mammal; (8)
CC assessing the effectiveness of treatment of cancer in a mammal; (9)
CC preventing or treating cancer that is due to the presence of BORIS
CC nucleic acid or polypeptide; and (10) a composition comprising an
CC inhibitor of BORIS and a carrier. BORIS has cytoskeletal activity, and can
CC be used in gene therapy. A nucleic acid encoding BORIS can be used for
CC preparing a composition for treating or preventing cancer. The present
CC sequence represents a PCR primer corresponding to human BORIS and murine
CC Ctrf used to identify murine BORIS, which is used in an example from the
CC present invention.
CC XX
SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7358 TTGTGAATATATCCAGCAG 7377
DB 1 TTGTGAGTTATGCCAGCAG 20
RESULT 2601
ADD56481/C
ID ADD56481 standard; DNA; 21 BP.
XX
AC ADD56481;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human gene expression analysis multiplex Start-PCR primer #1.
XX
KM Gene expression; multiplex standardised reverse transcriptase-PCR;
KM Start-PCR; high density oligonucleotide array; cDNA array;
KM small biological sample; fine needle aspirate biopsy;
KM laser captured microdissected material; human; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003186246-A1.
XX
PD 02-OCT-2003.
XX
PE 28-MAR-2002; 2002US-00109349.
XX
PR 28-MAR-2002; 2002US-00109349.
XX
PA (WILL/) WILLEY J C.
XX (CRAW/) CRAWFORD E L.
XX
PI Willey JC, Crawford EL;
XX WPI; 2003-811730/76.
XX
XX
PT Direct comparison of numerical gene expression values between samples of
PT genes comprises using multiplex standardized reverse transcription-
PT polymerase chain reaction.
XX
PS Example 1; SEQ ID NO 1; 59bp; English.
XX
CC The present invention relates to a method for the direct comparison of
CC numerical gene expression values between samples of genes. The method
CC comprises amplifying cDNA in the presence of a competitive template
CC mixture and primer pairs for several genes and then amplifying aliquots
CC of the PCR products using a primer pair specific for each gene. The
CC method of amplification is by multiplex standardised reverse
CC transcriptase-polymerase chain reaction (Start-PCR). High density
CC oligonucleotide or cDNA arrays are used to measure PCR products following
CC quantitative Start-PCR. The method is useful for the assessment of gene

expression in small biological samples such as fine needle aspirate biopsies, and laser captured microdissected materials. The method allows for the standardised measurement of hundreds of genes from the same sample, which in prior art, could only be assessed for one gene. The present sequence represents a multiplex Start-PCR primer which can be used in the method of the present invention.

Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6802 CAGATTGGGAGGAGTATT 6821
DB 20 CAGAAATGGGAGGAGTATT 1

RESULT 2602

ADD90708
ID ADD90708 standard; DNA; 21 BP.

AC ADD90708;

DT 29-JAN-2004 (first entry)

XX Mouse beta-actin PCR primer SEQ ID NO:18.

XX allergic disease; SOCS3; allergy; mouse; beta-actin; PCR primer; ss.

XX Synthetic.

OS Mus sp.

XX MO2003072778-A1.

XX 04-SEP-2003.

XX 23-JAN-2003; 2003MO-JP000600.

XX 27-FEB-2002; 2002JP-00052310.

XX (GENO-) GENOX RES INC.

XX (NIGE-) JAPAN GEN AGENCY NATION.

XX Nagata N, Oshida T, Sugita Y, Kubo M, Saito H;

XX WPI; 2003-671871/63.

XX Detecting allergic disease using SOCS3 as a marker for dermatitis.

XX Example 7; SEQ ID NO 18; 80pp; Japanese.

CC The present invention describes a method for detecting an allergic disease using SOCS3 as a marker. The method comprises determining the level of expression of the marker gene in the sample and comparing it with that of a healthy individual. Also described: (1) a reagent for detecting allergies; (2) method for screening for treatments for allergies; and (3) a kit for screening for treatments. The method can be used for detecting the presence of allergies and for screening for treatments. The present sequence represents a PCR primer for mouse beta-actin, which is used in an example from the present invention.

XX Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 527 CCATTGGCAAGGAGGCTC 546
DB 2 CTATTGGCAAGGAGGCTT 21

RESULT 2603

AAQ27806
ID AAQ27806 standard; DNA; 22 BP.

AC AAQ27806;

DT 25-MAR-2003 (revised)

XX 28-JAN-1993 (first entry)

XX APP exon 17 primer 4.

XX Beta-amyloid protein; amyloid precursor protein; isoform; ss.

XX Synthetic.

XX MO9213069-A1.

XX 06-AUG-1992.

XX 21-JAN-1992; 92MO-GB000123.

XX 21-JAN-1991; 91GB-00001307.

XX 28-AUG-1991; 91GB-00018445.

XX (UNLO) IMPERIAL COLLEGE SCI TECHN MED.

XX Hardy JA, Chartier-Harlin MC, Goate AM, Owen MJ, Mullan MJ;

XX WPI; 1992-284654/34.

XX Polynucleotide probe comprising nucleic acid encoding codon 717 mutant -

XX of human APP770, useful for determining genetic pre-disposition to

XX Alzheimer's disease.

XX Disclosure; Page 31; 127pp; English.

CC The sequences given in AAQ27805-7 are primers which are complementary to CC intronic sequences within the amyloid precursor protein gene (APP). They CC were used to amplify exon 17. APP encodes various isoforms which are CC precursors of beta-amyloid protein. The beta-amyloid protein is an CC approx. 4KD protein (39-42 amino acids) which is an internal cleavage CC product from APP. There are five distinct isoforms of APP containing 563, CC 695, 714, 751 and 770 amino acids. These are generated by alternative CC splicing of primary transcripts of APP which is located on human CC chromosome 21. The APP isoforms are glycosylated transmembrane proteins. CC (updated on 25-MAR-2003 to correct PN field.) (updated on 25-MAR-2003 to CC correct PI field.)

XX Sequence 22 BP; 8 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5617 TTACCCAGCTTCAGGAG 5636
DB 2 TAACCCAGCATCATGAG 21

RESULT 2604

AAQ78894
ID AAQ78894 standard; DNA; 22 BP.

AC AAQ78894;

DT 25-MAR-2003 (revised)

XX 27-JUL-1995 (first entry)

XX Synthetic EcoRI-BglII fragment from plasmid p7,582-S.

XX Hepatitis B virus pres2 gene; vaccine; ds.

XX Synthetic.

PT correct. DNA and nucleic acid constructs for inactivating the transferase
 XX gene; for eliminating hyperacute region in human transplants.
 PS Example 6; Page 58; 184pp; English.
 CC The primers given in AAQ93081-86 are based on conserved regions of mouse
 CC and cattle alpha-GalT genes and were used to isolate porcine alpha-1,3-
 CC GalT cDNA (AAQ93077) by PCR amplification. (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX
 SQ Sequence 22 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 2 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4459 TGGACCTTTTCTTTTCTTTT 4478
 DB 1 TTGAATCTCTTTTCTTTTCTTTT 20

RESULT 2607
 AAT78987/c
 ID AAT78987 standard; DNA; 22 BP.
 XX
 AC AAT78987;
 XX
 DT 13-JUN-1998 (first entry)
 XX
 DE Mouse Huntington's disease gene Intron 2 5' donor site.
 XX
 KM Huntington's disease; animal model; transgenic animal; mouse; therapy;
 KM drug screening; Hdh gene; ss.
 XX
 OS Mus musculus.
 XX
 PN CA2178022-A.
 XX
 PD 02-DEC-1996.
 XX
 PF 03-JUN-1996; 96CA-02178022.
 XX
 PR 01-JUN-1995; 95US-00457273.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 PI Hayden M, Lin B, Nasir J;
 XX
 DR WPI; 1997-298677/28.
 XX
 PT Mouse Huntington's Disease gene - useful for generating transgenic mice
 PT as a model of Huntington's Disease.
 XX
 PS Disclosure; Page 60; 69pp; English.
 XX
 CC This oligonucleotide comprises the 5' donor site of intron 2 of the mouse
 CC Huntington's disease (HD) gene (see also AAT78974). The splice site
 CC sequences for the first 5 exons of the mouse and human HD genes were
 CC compared (see AAT78985-799002). Targeted disruption of the murine HD
 CC gene, e.g. at exon 5, can be used to examine the function of the HD gene
 CC and its role in development. Transgenic mice can be used as models of HD
 XX
 SQ Sequence 22 BP; 10 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5474 TTTTGTAAAGATTAAT 5493
 DB 22 TTTTGTAAAGCAAT 3

RESULT 2608
 AAX78249/c
 ID AAX78249 standard; DNA; 22 BP.
 XX
 AC AAX78249;
 XX
 DT 24-AUG-1999 (first entry)
 XX
 DE Human cyclin T1 PCR primer 1.
 XX
 KM Cyclin T1; cyclin K; human; TAT protein; transcriptional coactivator;
 KM human immunodeficiency virus; HIV; Tat-associated kinase; TAT; TEFB;
 KM Transcription elongation factor subunit b; TAF/TEFB complex; cis-acting;
 KM transactivation response element; TAR; divalent cation metal; modulator;
 KM treatment; infection; immunogen; tissue localization; diagnosis;
 KM transgenic animal; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 EN WO9292730-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 11-DEC-1998; 98WO-US026470.
 XX
 PR 11-DEC-1997; 97US-0069341P.
 PR 30-JUL-1998; 98US-00126980.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Jones KA, Wei P, Garber M, Fang S;
 XX
 DR WPI; 1999-394960/33.

PT Cyclin T1, a transcriptional co-activator that interacts with Tat
 PT protein.
 XX
 PS Example 7; Page 103; 107pp; English.
 XX
 CC This invention describes a novel human transcriptional co-activator,
 CC designated cyclin T1 (also known as cyclin K), which interacts with the
 CC human immunodeficiency virus (HIV) Tat protein. Cyclin T1 is capable of
 CC participating as a constituent of the Tat-associated kinase
 CC (TAK). Transcription elongation factor subunit b (TEFB) complex. The
 CC polypeptide modulates Tat transactivation by enhancing the affinity of
 CC the Tat protein with the cis-acting transactivation response element
 CC (TAR) RNA. Compounds identified by methods of the invention that disrupt
 CC the association of divalent cation metal(s) with cyclin T1 and/or Tat
 CC protein are useful for the modulation of Tat transactivation in
 CC biological systems. Cyclin T1, or antibodies specific for it, can be used
 CC to treat a subject infected with HIV. Antibodies against cyclin T1 can be
 CC used as immunogens and also for studying tissue localization of protein
 CC and complexes, for purification of inhibitors and are useful in
 CC diagnostic applications. The probes and primers are useful for
 CC identification and amplification of the cyclin T1 DNA. The transgenic
 CC animals are useful for elucidating the physiological and behavioural
 CC roles of HIV infection
 XX
 SQ Sequence 22 BP; 10 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5695 CTGTTTGCCTTCTTTTC 5714
 DB 20 CTGTTTGCAGCTTTTC 1

RESULT 2609
 AAV99612
 ID AAV99612 standard; DNA; 22 BP.

```

XX AAV99612;
AC
XX 29-MAR-1999 (first entry)
DT
XX Maize c1p gene primer c1p#3.
DE
XX Promoter; nuclear encoded plastid RNA polymerase; NEP; c1p; chloroplast;
KW transgenic plant; maize; PCR; primer; ss.
XX
OS Synthetic.
OS Zea mays.
XX
PN W09655595-A1.
PD 10-DEC-1998.
XX
PF 03-JUN-1998; 98WO-US011437.
XX
PR 03-JUN-1997; 97US-0048376P.
PR 12-SEP-1997; 97US-0058670P.
XX
PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Maliga P, Silhavy D, Sritaman P;
XX
DR WPI; 1999-070262/06.
XX
PT Isolated nuclear-encoded plastid RNA polymerase promoter sequences -
PT useful for expressing exogenous protein in plant plastids such as
PT chloroplasts.
XX
PS Example 1; Page 17; 79pp; English.
XX
CC This is the nucleotide sequence of maize c1p gene primer c1p#3. The 5'
CC nucleotide of the primer corresponds to nucleotide 70549 of the
CC complementary strand of the maize plastid genome sequence. The primer was
CC designed to add a XhoI restriction site downstream of an amplified c1p
CC fragment following PCR amplification. The PCR product was cloned into
CC vector pBSKS+ and used to generate protecting RNA for use in vitro
CC capping experiments. The invention provides isolated rpoB, acpB, c1p and
CC 16S rDNA NEP and PEP promoter elements (see AAV99569-99) useful for
CC producing exogenous proteins of interest in plant plastids
XX
SQ Sequence 22 BP; 7 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3342 GAATCCAGTTGTGAGAGA 3361
DB 3 GAATTCGTGTGTAAGAAGA 22
RESULT 2610
AAK26493/C
ID AAK26493 standard; cDNA; 22 BP.
XX
AC AAK26493;
XX
DT 26-MAY-1999 (first entry)
XX
DE cDNA transcript resulting from reverse transcription of the test RNA.
XX
KW Isolation; nucleic acid; subtraction oligonucleotide;
KW selection oligonucleotide; structure probing; ss.
XX
OS Synthetic.
XX
PN W09907890-A1.
XX
DR 18-FEB-1999.

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XX 05-AUG-1998; 98WO-US016211.
PR
XX 05-AUG-1997; 97US-00906494.
PR
XX (UYMA-) UNIV MASSACHUSETTS.
PA
XX Stern S;
XX
DR WPI; 1999-167451/14.
XX
PT Nucleic acid isolation, quantification and structural probing - using new
PT hybridisation-based and ligation-dependent methods.
XX
PS Example 8; Fig 9B; 71pp; English.
XX
CC The specification describes a method for isolating a target nucleic acid
CC fragment from a mixture of nucleic acid fragments. The method comprises
CC removing a non-target fragment by hybridizing it to an immobilised
CC "subtraction" oligonucleotide that is complementary to a sequence present
CC in the non-target fragment but absent in the target fragment, repeating
CC this step until a known sequence in the target nucleic acid is unique and
CC then selecting the target fragment by hybridizing to a complementary
CC immobilised "selection" oligonucleotide. The method can be used in
CC structure probing experiments to determine whether a given nucleotide is
CC modified by a modifying agent, or whether a compound alters reactivity of
CC a nucleotide in a test nucleic acid toward a modifying agent. The present
CC sequence represents a cDNA transcript resulting from reverse
CC transcription of the test RNA (AAK26474)
XX
SQ Sequence 22 BP; 8 A; 2 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5702 GCCCTCCTTCTCTCTCTC 5721
DB 21 GCCCTCCCTTCTCTCTCTC 2
RESULT 2611
AAK32687
ID AAK32687 standard; DNA; 22 BP.
XX
AC AAK32687;
XX
DT 21-JAN-2000 (first entry)
XX
DE Human APP exon 17-specific PCR primer APP-17B.
XX
KW APP; amyloid precursor protein; Alzheimer's disease; transfection;
KW transgenic animal; animal model; disease; transgene; co-lipofection;
KW yeast artificial chromosome; YAC; lipid; cationic; selectable; exon; PCR;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5981175-A.
XX
PD 09-NOV-1999.
XX
PF 25-JAN-1994; 94US-00187161.
XX
PR 07-JAN-1993; 93US-00001493.
PR 18-JUN-1993; 93US-00079444.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Choi T, Loring JF;
XX
DR WPI; 1999-633306/54.

```

XX Production of transfectant mammalian cells by co-lipofection with multiple
PT DNA species, useful for the production of transgenic animals for use as
PT disease models.
XX
XX Example 2, Col 20; 29pp; English.
XX This sequence represents human APP (amyloid precursor protein) exon 17-
CC specific PCR primer APP-17B, used with PCR primer APP-17A (AA232686) to
CC amplify exon 17 of the human APP gene in murine embryonic stem cells
CC transfectant via a novel method with a YAC (yeast artificial chromosome)
CC containing the human APP gene. The novel method of transfection produces
CC a selectable co-lipofected mammalian cell incorporating multiple
CC heterologous DNA species. It comprises forming a co-lipofection complex
CC comprising a cationic lipid, a first polynucleotide larger than 50 kb,
CC and an unlinked second polynucleotide comprising a selectable marker gene
CC expression cassette, and transfecting mammalian cells with it. Both
CC heterologous nucleotides are integrated into the genome, forming
CC selectable co-lipofected mammalian cells which contain incorporated
CC multiple heterologous DNA species. The method can be used for
CC transferring large segments of DNA, such as large YAC clones, into
CC mammalian cells such as embryonic stem cells. The methods can be used to produce
CC transgenic mammalian cells which express APP which can be used to produce
CC transgenic animals as models for Alzheimer's disease. The methods can
CC also be used for producing transgenic animals as models for autoimmunity
XX
SQ Sequence 22 BP; 8 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5617 TTACCCAGCTTCAAGGAG 5636
DB 2 TAACCCAGCATCATGAG 21
RESULT 2612
AA237259 ID AA237259 standard; DNA; 22 BP.
XX
AC AA237259;
XX
DT 28-JAN-2000 (first entry)
XX
DE PCR primer for AV37 antigen coding sequence.
XX
KW AV37 antigen; monoclonal antibody; hybridoma AV37; vaccine; avian tumour;
KW oncogenic avian virus; Marek's disease virus; avian leucosis virus;
KW Rous-associated virus; reticuloendotheliosis virus; therapy; PCR primer;
KW ss.
XX
XX Synthetic.
OS Gallus sp.
XX
XX WO9955860-A1.
XX
XX 04-NOV-1999.
XX
XX 22-APR-1999; 99WO-GB001238.
XX
XX 29-APR-1998; 98GB-00009070.
XX
XX (ANIM-) INST ANIMAL HEALTH LTD.
XX
XX Burgess SC, Davison TF, Rose LJM;
XX
XX WPI; 2000-013437/01.
XX
XX New polypeptide, useful as a vaccine and to generate monoclonal
PT antibodies.
PT
PS Claim 31; Page 39; 63pp; English.

XX This sequence is a PCR primer for DNA encoding the AV37 antigen protein
CC of the invention. The protein is recognised by a monoclonal antibody
CC (MAb) secreted by the hybridoma AV37 deposited at the European Collection
CC of Cell Cultures (ECACC) accession number 98030304. The polypeptide can
CC be used to isolate a MAb, produce a hybridoma producing the MAb, and in a
CC composition for use as a vaccine. The vaccine can be used against
CC oncogenic avian viruses, including Marek's disease virus, avian leucosis
CC virus, Rous-associated virus and reticuloendotheliosis virus. The vector
CC can be used to treat avian tumours
XX
SQ Sequence 22 BP; 2 A; 11 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5734 TTCCTTCCCTTCTTCTTA 5753
DB 2 TTCCTTCCCTTCTTCTTCA 21
RESULT 2613
AAC61082 ID AAC61082 standard; DNA; 22 BP.
XX
AC AAC61082;
XX
DT 05-FEB-2001 (first entry)
XX
DE Primer BEK311 used in isolation of cDNA encoding nurse cell receptor.
XX
KW Mouse; nurse cell receptor; detection; DiGeorge's syndrome; primer; ss.
XX
XX Synthetic.
OS
XX JP2000236882-A.
XX
XX 05-SEP-2000.
XX
XX 24-FEB-1999; 99JP-00046603.
XX
XX 24-FEB-1999; 99JP-00046603.
XX
XX (SHIO) SHIONOGI & CO LTD.
XX
XX WPI; 2000-597089/57.
XX
XX A mouse nurse cell receptor gene.
XX
XX Claim 9; Page 7; 27pp; Japanese.
XX
XX This invention relates to a mouse nurse cell receptor. The invention
CC includes DNA and protein sequences for the receptor (AAC61078 and
CC AA85616). Also included in the invention is an antibody specific for the
CC murine nurse cell receptor. DNA encoding the receptor can be used to
CC detect DiGeorge's syndrome. The present sequence represents a primer used
CC in the isolation and characterisation of the receptor of the invention
XX
SQ Sequence 22 BP; 7 A; 7 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7405 AGCAACATCAGCAGCAGCAG 7424
DB 1 AGCAACATCAGCAGCAGCAG 20
RESULT 2614
AAA39764 ID AAA39764 standard; DNA; 22 BP.


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XX AA39764;
AC 15-SEP-2003 (revised)
XX 18-SEP-2000 (first entry)
XX H. polymorpha TP51 DNA primer F9.
DE Trehalose-6-phosphate synthase; TP51; heat shock inducible; promoter;
XX yeast; primer; 88.
XX Pichia angusta.
OS CH690127-A5.
XX 15-MAY-2000.
XX 11-FEB-1999; 99CH-00000279.
XX 11-FEB-1999; 99CH-00000279.
XX (RHEI-) RHEINBIOTECH GES NEUE BIOTECHNOLOGISCHE.
XX Ivano R, De Virgilio C;
XX WPI; 2000-329626/29.
XX Heat-inducible promoter from Hansenula polymorpha, useful for controlling
XX expression of foreign genes in yeast, contains no general stress response
XX elements.
XX Example 3; Page 12; 19pp; German.
XX This invention describes a novel heat-inducible promoter (I). (I) is used
XX to express foreign genes in fungi, particularly yeast and specifically
XX Hansenula polymorpha, especially proteins that require glycosylation and
XX cannot be expressed in bacteria. (I) is active even at high temperature,
XX allowing yeast to be cultured at higher than normal temperatures with
XX reduced contamination by other microorganisms and reduced need for
XX expensive cooling. (I) is selectively activated by heat (it contains no
XX general stress-responsive elements), so permits expression of foreign
XX genes to be suppressed during selected stages of growth, resulting in
XX less injury to cells and biomass. This sequence represents a primer used
XX in the isolation of the trehalose-6-phosphate synthase TP51 gene from
XX Hansenula polymorpha. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 22 BP; 2 A; 3 C; 8 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 7190 GTGTGACTACTCTGTGTTTC 7209
DB 3 GTGTGACTACTCTGTGTTTC 22
RESULT 2615
AA294181/c
ID AA294181 standard; DNA; 22 BP.
XX
AC AA294181;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human GABAB-R1a PCR primer.
XX
KW GABAB receptor 2; GABAB-R2; human; bladder disorder;
KW gastrointestinal disorder; central nervous system disorder;
KW lung disorder; spasticity; epilepsy; Alzheimer's disease; pain;
KW affective disorder; feeding disorder; diagnosis; gene therapy;
KW G-protein coupled receptor; GABA; gamma-aminobutyric acid;
KW signal transduction; PCR primer; GABAB-R1a; 88.

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XX Homo sapiens.
OS
XX WC200014222-A2.
XX 16-MAR-2000.
XX 03-SEP-1999; 99WO-GB002918.
XX 07-SEP-1998; 98GB-00019420.
XX 09-OCT-1998; 98US-0103670P.
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Barnes AA, Wise A, Marshall FH, Frazer NJ, White JHM, Foord SM;
XX WPI; 2000-256974/22.
XX
XX GABA-B receptor subtypes useful for identifying modulators of GABA-B
XX receptor activity that may be used for preventing and treating diseases
XX including Alzheimer's disease, epilepsy and spasticity.
XX Disclosure; Page 29; 67pp; English.
XX
XX The present sequence is that of a primer used in a PCR-RACE in order to
XX generate a 800 bp fragment of GABAB receptor GABAB-R1a cDNA. The
XX invention relates to novel GABAB subtypes GABAB-R1c and GABAB-R2 (see
XX AA79202). It also relates to variants of the receptors, nucleotide
XX sequences (see AA294168) encoding the receptors, vectors, stable cell
XX lines, antibodies, screening methods, methods of receptor production, and
XX methods of treatment or prophylaxis of a disorder that is responsive to
XX modulation of GABAB receptor activity. The disorder is especially a
XX central nervous system disorder, a gastrointestinal disorder, a lung
XX disorder or a bladder disorder, especially spasticity, epilepsy,
XX Alzheimer's disease, pain or an affective or feeding disorder (claimed)
XX
SQ Sequence 22 BP; 3 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 7417 AGCAGCAGCAGCAGCAGCAGC 7436
DB 21 AGCAGCAGCAGCAGCAGCAGC 2
RESULT 2616
AAC81233
ID AAC81233 standard; DNA; 22 BP.
XX
AC AAC81233;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human tyrosine phosphatase HD-PTP exon 2. PCR primer, SEQ ID NO.11.
XX
KW Human; histidine domain-protein tyrosine phosphatase; HD-PTP;
KW chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic;
KW lung cancer; tumour; gene therapy; diagnosis; recombinant production;
KW anticancer; PCR primer; 88.
XX
XX Homo sapiens.
OS
XX WC2000063392-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-JP002455.
XX
PR 16-APR-1999; 99JP-00108842.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.

```

XX Shimizu K;
 XX WPI; 2000-672740/65.
 DR Human tyrosine phosphatase with oncostatic activity encoded by a gene
 PT frequently deleted in lung cancer, useful for treatment and diagnosis of
 PT tumors.
 XX Example 3; Page 119; 134pp; Japanese.
 CC The invention relates to a novel human tyrosine phosphatase, histidine
 CC domain-protein tyrosine phosphatase (HD-PTP; AAB29661) and to human HD-
 CC PTP nucleic acids (AAC81224, AAC81225, AAC81262, AAC81263). The HD-PTP
 CC gene is located on chromosome 3p21.3. This region is frequently found to
 CC be deleted in lung cancers, and is therefore thought to contain a tumour
 CC suppressor gene. The invention also relates to expression vectors and
 CC host cells containing human HD-PTP nucleic acids; the recombinant
 CC production of HD-PTP; anticancer drugs containing HD-PTP; gene therapy
 CC compositions containing DNA encoding HD-PTP; diagnostic reagents
 CC containing HD-PTP oligonucleotides; antibodies specific for HD-PTP; and
 CC an immunoassay method using HD-PTP-specific antibodies for use in cancer
 CC diagnosis and investigation. HD-PTP proteins, nucleic acids and
 CC antibodies may be used in the treatment, investigation and diagnosis of
 CC cancers, particularly those of the lung. The present sequence represents
 CC a human HD-PTP PCR primer used in an exemplification of the invention
 CC
 XX Sequence 22 BP; 7 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2529 CACAGCAGATGAGCTCCAGA 2548
 DB 1 CACAGTAGATGACCTCCACA 20
 RESULT 2617
 AAC80270/c
 ID AAC80270 standard; DNA; 22 BP.
 AC AAC80270;
 AT 03-MAY-2001 (first entry)
 DE Reverse primer #98 used for amplification of HLA-A exon 3.
 XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200061795-A2.
 PN 19-OCT-2000.
 PD 05-APR-2000; 2000WO-EP002398.
 PF 09-APR-1999; 99EP-00870068.
 PR 11-JUN-1999; 99US-0138614P.
 XX (INNO-) INNOGENETICS NV.
 PA De Canck I, Rombout A, Rossau R;
 PI WPI; 2000-647426/62.
 DR Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
 PT primer sets, useful for subtyping or typing of HLA Class I alleles.
 XX Claim 4; Page 40; 128pp; English.

XX The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3 and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method
 XX
 XX Sequence 22 BP; 5 A; 9 C; 4 G; 3 T; 0 U; 1 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5151 GGGAGGGAGTTCTCCGGG 5170
 DB 22 GGGAGAGAAATCTCTCGGG 3
 RESULT 2618
 AAH26873/c
 ID AAH26873 standard; DNA; 22 BP.
 AC AAH26873;
 AT 21-DEC-2001 (first entry)
 DE Human prostate specific gene clone sqpro030 reverse PCR primer.
 XX Human prostate cancer; diagnosis; therapy; imaging; vaccine; PCR primer;
 XX ss.
 KM Homo sapiens.
 OS Homo sapiens.
 XX WO200170095-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US009217.
 PF 23-MAR-2000; 2000US-0191511P.
 PR (DIAD-) DIADEXUS INC.
 PA Ali S, Recipon H, Hu P, Caferkey R;
 PI WPI; 2001-611439/70.
 DR Novel prostate cancer specific genes and polypeptides encoded by the
 XX genes, useful for detecting, diagnosing, monitoring, staging,
 PT prognosticating, imaging and treating prostate cancer.
 PT
 XX Example 2; Page 56; 83pp; English.
 PS The present sequence is that of primer sqpro030 reverse, which was used
 CC with primer sqpro030 forward (see AAH26872) for the PCR amplification of
 CC novel human prostate cancer specific gene (PSG) clone sqpro030 (see
 CC AAH26855). A semi-quantitative PCR was performed to determine relative
 CC expression patterns of sqpro030 in multiple samples. High expression was
 CC observed in healthy lung, with very little expression in healthy
 CC prostate, high levels of expression in liver and pancreatic carcinomas
 CC and moderate expression in prostate, kidney and ovarian carcinomas, and
 CC at moderate levels in 2 of 6 prostate cancer samples. The 25 PSG
 CC polynucleotides of the invention (see AAH26845-69) are diagnostic markers
 CC for prostate cancer. The polynucleotides, antisense oligonucleotides,
 CC host cells, PSG polypeptides, and antibodies immunospecific for the
 CC polypeptides are claimed. Also claimed are methods and tools for using
 CC the markers for diagnosing prostate cancer, diagnosing metastasis of
 CC prostate cancer, staging prostate cancer, monitoring prostate cancer,
 CC identifying potential therapeutic agents, imaging prostate cancer,
 CC treating prostate cancer (using an antibody), PSG polypeptide agonists
 CC and antagonists, and a vaccine comprising a PSG polypeptide or a vector
 CC expressing a PSG polypeptide, as well as a method of treating prostate
 CC cancer using the vaccine


```
XX AAH28297;
AC 05-SEP-2001 (first entry)
DT 3' untranslated region sequence from neuronal cadherin gene.
DE mRNA protein complex; tumor development; cell aging; death.
KW ribonucleic profile; RNA-binding protein; ss.
KM Unidentified.
XX NO200148480-A1.
XX 05-JUL-2001.
XX 28-DEC-2000; 2000WO-US035583.
XX 28-DEC-1999; 99US-0173338P.
XX (KEEN/) KEENE J D.
XX Keene JD, Tenenbaum SA, Carson C;
XX WPI; 2001-425706/45.
XX
XX Particulating endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
XX Example 6; Page 31; 49pp; English.
XX
XX The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonucleic profile of a cell which has numerous
CC uses including monitoring of tumor development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonucleic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
XX Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4020 AAAAAAGAGAAACAAA 4039
DB 22 AAAAAATACAGAAATATAA 3
```

```
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; anticancer; cytostatic; antitumor; anti-HIV;
KW immunosuppressive; proto-oncogene; virulence; hepatotropic; gene therapy;
KW anti-inflammatory; antibacterial; ss.
XX
XX Synthetic.
FH Key Location/Qualifiers
FT misc_RNA 1..22
FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
XX NO200193902-A2.
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond J, Flora M, Kliman DM;
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
XX Example 11; Page 63; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
XX Sequence 22 BP; 1 A; 3 C; 2 G; 16 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5460 GTTCTTACTCTGATTTT 5479
DB 3 GTTCTTACTCTTTT 22
```

```
RESULT 2623
ABK97546
ID ABK97546 standard; DNA; 22 BP.
XX
XX ABK97546;
AC 07-OCT-2002 (first entry)
DT Human LCAT gene forward PCR primer #7.
XX
XX Lecithin-cholesterol acyltransferase; LCAT; Norum disease; gene therapy;
XX
```

KW fish-eye disease; atherosclerotic cardiovascular disease; forensic;
 KW population diversity; anthropological lineage; paternity testing; human;
 KW polymorphism; PCR; primer; ss.
 XX Homo sapiens.
 XX OS
 XX MO200253575-A1.
 XX
 XX 11-JUL-2002.
 PD
 XX
 XX 03-JAN-2001; 2001MO-US000092.
 PF
 XX 03-JAN-2001; 2001MO-US000092.
 PR
 XX (GENA-) GENA15555 PHARM INC.
 PA
 XX Chew A, Denton RR, Nandabalan K, Stephens JC;
 XX WPI; 2002-557737/59.
 XX
 XX
 XX Novel isolated polymorphic variant polynucleotide of lecithin-cholesterol
 PT acyltransferase gene, useful for studying expression and biological
 PT function of the gene, and for therapeutic, diagnostic or forensic
 PT purposes.
 PS
 XX Example 1; Page 27; 72pp; English.
 XX
 XX The present invention relates to a new polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of a reference
 CC sequence for lecithin-cholesterol acyltransferase (LCAT). The invention
 CC is useful for identifying an association between a trait (preferably a
 CC clinical response to drug targeting LCAT) and at least one genotype or
 CC haplotype of LCAT gene. The method of the invention has applicability in
 CC developing diagnostic tests and therapeutic treatments for Norm disease,
 CC fish-eye disease and atherosclerotic cardiovascular disease. The
 CC haplotyping and genotyping methods are useful for studying population
 CC diversity, anthropological lineage, the significance of diversity and
 CC lineage at the phenotypic level, paternity testing, forensic applications
 CC and for identifying association between the LCAT genetic variation and a
 CC trait such as level of drug response or susceptibility to disease. In
 CC addition, the methods for identifying the LCAT haplotypes present in
 CC individuals are useful in the development of drugs targeting LCAT. For
 CC example, determining the frequency of individual LCAT haplotypes in a
 CC population with a specific disease, e.g. Norm disease, will facilitate
 CC the development of drugs targeting the LCAT isoform(s) that are most
 CC frequent in that disease population. The present nucleic acid sequence
 CC represents one of a collection (ABK97534-ABK97573) of PCR primers that
 CC were used in the methods of the invention to detect polymorphisms in the
 CC human LCAT gene
 CC
 XX
 XX Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1849 CAGGTGAAGAACTGTCTCA 1868
 Db 2 CTGCTGCGAAGAACTGTCTCA 21
 RESULT 2624
 ID ABR40406 standard; DNA; 22 BP.
 XX ABR40406;
 AC
 XX 15-JUL-2002 (first entry)
 DT
 XX Probe for gene amplification analysis of human PRO7133.
 DB
 XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;

KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
 KW neuroprotective; probe; ss.
 XX Homo sapiens.
 XX OS
 XX MO200153486-A1.
 XX
 XX 26-JUL-2001.
 PD
 XX
 XX 11-FEB-2000; 2000MO-US003565.
 PF
 XX 08-MAR-1999; 99MO-US005028.
 PR 11-MAR-1999; 99US-0123972P.
 PR 11-MAY-1999; 99US-0133459P.
 PR 02-JUN-1999; 99MO-US012252.
 PR 22-JUN-1999; 99US-0140650P.
 PR 22-JUN-1999; 99US-0140653P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149395P.
 PR 31-AUG-1999; 99US-0151689P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021090.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 05-JAN-2000; 2000MO-US000219.
 XX
 XX (GENTH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Masters SA, Pan J, Pitli RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX WPI; 2002-205567/26.
 XX
 XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
 PT benign or malignant tumours, leukemias and lymphoid malignancies,
 PT inflammatory, angiogenic and immunologic disorders.
 PS
 XX Example 26; Page 143; 302pp; English.
 XX
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
 CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
 CC antibodies are useful for treating benign or malignant tumours (e.g.
 CC renal, kidney, bladder, breast, etc), leukemias and lymphoid
 CC malignancies, other disorders such as neuronal, glial, astrocytal,
 CC hypotlamic, glandular, macropagal, stromal and blastocoele disorders,
 CC inflammatory, immune and angiogenic disorders. The polynucleotide
 CC sequences are also useful in gene therapy. The present sequence
 CC represents a probe used in the methods of the present invention
 CC
 XX
 XX Sequence 22 BP; 0 A; 11 C; 2 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6893 TGCCTCTCCCTTACTCTACTC 6912
 Db 2 TGCCTCTCCCTTACTCTACTC 21
 RESULT 2625
 ID AAS16493/C standard; DNA; 22 BP.
 XX AAS16493;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX

DE Marmoset Type II GnRH-R PCR primer S1.
 XX Marmoset; ss; type II gonadotrophin-releasing hormone receptor; GnRH-R;
 KW contraceptive; neural development; sexual arousal; gene therapy;
 KM transgenic animal; PCR primer; S1.
 XX
 OS Callithrix jacchus.
 XX
 PN WO200178796-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-GB001755.
 XX
 PR 15-APR-2000; 2000GB-00009269.
 PR 17-JUN-2000; 2000GB-00014761.
 PR 30-JUN-2000; 2000US-0215232P.
 XX
 PA (MED1-) MEDICAL RES COUNCIL.
 XX
 PI Millar RP, Lowe S, Conklin D;
 XX WPI; 2002-041317/05.
 XX
 PT New polypeptide, useful in gene therapy, as contraceptive or for
 PT inhibiting endogenous Type II GnRH binding to its native receptor in
 PT vivo, comprises Type II gonadotrophin-releasing hormone receptor and
 PS polynucleotides encoding receptor.
 XX
 PS Example; Page 24; 92pp; English.
 XX
 CC The invention relates to an isolated functional Type II gonadotrophin-
 CC releasing hormone receptor (Type II GnRH-R), or a peptide comprising at
 CC least a portion of exon I of Type II GnRH-R, nucleic acid encoding the
 CC receptor, an expression vector comprising the nucleic acid, a host cell
 CC transformed with the vector, a transgenic animal having the construct
 CC stably integrated into its genome, an antibody able to bind specifically
 CC to Type II GnRH-R. The Type II GnRH-R is useful in gene therapy. The Type
 CC II GnRH-R is particularly useful for inhibiting endogenous Type II GnRH
 CC binding to its native receptor in vivo or as a contraceptive. The
 CC receptor may also have roles in neural development and sexual arousal.
 CC The present sequence is a PCR primer used to isolate a nucleic acid
 CC encoding marmoset type II GnRH-R
 CC
 SQ Sequence 22 BP; 6 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1976 CAGTGATTTCTCTGGAGCA 1995
 Db 22 CAGTGATTTCTCTGGAGCA 3
 RESULT 2626
 ABL55000/C
 ID ABL55000 standard; DNA; 22 BP.
 XX
 AC ABL55000;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Human lymphoma-specific immunoglobulin PCR primer VH1.
 XX
 KW Human; lymphoma; immunoglobulin; B-cell mediated pathology; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; neuroprotective;
 KW antidiabetic; antithyroid; autoimmune disease; B-cell lymphoma; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PD Homo sapiens.
 XX
 PN WO200213862-A2.

XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-US025204.
 XX
 PR 11-AUG-2000; 2000US-0224722P.
 PR 11-AUG-2000; 2000US-0224723P.
 PR 23-MAR-2001; 2001US-0279079P.
 XX
 PA (FAVR-) FAVRILE INC.
 XX
 PI Gold DP, Shopes RJ;
 XX
 DR WPI; 2002-280742/32.
 XX
 PT Composition for altering B-cell mediated pathology, has a chimeric
 PT protein having portion of variable region of heavy chain or light chain
 PT linked to portion constant region associated with patient B cell clone.
 XX
 PS Example 1; Page 43; 100pp; English.
 XX
 CC The sequence represents a PCR primer used in the invention to amplify
 CC lymphoma-specific immunoglobulin heavy and light chains. The invention
 CC relates to a novel composition for altering a B-cell mediated pathology
 CC in a patient. The composition contains a chimeric protein comprising at
 CC least a portion of a variable region of heavy chain or light chain (VH or
 CC VL) linked to at least a portion of an immunoglobulin constant region,
 CC where VH or VL region is associated with a B cell clone from the patient
 CC having the B cell mediated pathology. The composition of the invention
 CC has cytostatic, immunosuppressive, dermatological, antiinflammatory,
 CC neuroprotective, antidiabetic, and antithyroid activity. This
 CC is a vaccine useful for altering a B cell mediated pathology. This
 CC includes B cell lymphoma e.g. non-Hodgkins lymphoma, refractory low grade
 CC or follicular B-cell lymphoma; autoimmune disease e.g. multiple
 CC sclerosis, systemic lupus erythematosus, anti-Hu associated
 CC paraneoplastic neurological syndrome, autoimmune hepatitis, Type I
 CC diabetes, autoimmune thyroiditis and scleroderma. The pathology is
 CC treated by administering the composition to the patient, preferably with
 CC a cytokine e.g. granulocyte-macrophage-colony stimulating factor (GM-CSF)
 CC or chemokine e.g. monocyte chemoattractant protein 3 (MCP 3)
 CC
 SQ Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7344 CCTGTCTCAGTCCATTGTGA 7363
 Db 20 CCAAGTCCAGTCCATTGTGA 1
 RESULT 2627
 ABS67627
 ID ABS67627 standard; DNA; 22 BP.
 XX
 AC ABS67627;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Mouse casein kinase-2 RT-PCR primer #1.
 XX
 KW ss; antisense therapy; casein kinase-2 alpha; cytostatic; antidiabetic;
 KW antiinflammatory; diabetes; hyperproliferative disorder; cancer; PCR;
 KW breast cancer; prostate cancer; liver cancer; infection; inflammation;
 KW tumour; RT-PCR; reverse transcriptase PCR; primer; mouse.
 XX
 OS Mus musculus.
 XX
 PN WO200262818-A2.
 XX
 PD 15-AUG-2002.
 XX

PF 31-JAN-2002; 2002WO-US002942.
XX
PR 08-FEB-2001; 2001US-00780172.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Freier SM, Wyatt JR;
XX WPI; 2002-627521/67.
DR
XX
XX New antisense oligonucleotides targeted to nucleic acid encoding casein
PT kinase 2-alpha, useful in diagnostic and research applications, or for
PT treating a disease or condition associated with expression of casein
PT kinase 2-alpha.
XX
XX Example 13; Page 92; 166pp; English.
PS
XX
XX The invention relates to a compound 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding casein kinase 2-alpha. The compound
CC specifically hybridises with and inhibits the expression of casein kinase
CC 2-alpha, or specifically hybridises with at least an 8-nucleobase portion
CC of an active site on a nucleic acid molecule encoding casein kinase 2-
CC alpha i.e. an antisense oligonucleotide. Also included are: (1) a
CC composition comprising the compound and a carrier or diluent; (2)
CC inhibiting the expression of casein kinase 2-alpha in cells or tissues by
CC contacting the cells or tissues with the novel compound; and (3) treating
CC an animal having a disease or condition associated with casein kinase 2-
CC alpha by administering to the animal the compound cited above so that
CC expression of casein kinase 2-alpha is inhibited. The antisense compounds
CC are useful for modulating the expression of casein kinase 2-alpha and for
CC treating diseases or conditions associated with expression of casein
CC kinase 2-alpha, e.g. diabetes or hyperproliferative disorder,
CC particularly cancer, such as breast cancer, prostate cancer, or liver
CC cancer. The antisense compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
CC inflammation or tumour formation, as research reagents and kits, and in
CC distinguishing between functions of various members of a biological
CC pathway. The present sequence is a reverse transcriptase (RT)-PCR primer
CC used in an experiment to measure the levels of casein kinase-2 alpha mRNA
CC
SQ Sequence 22 BP; 8 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2408 CCACAGTGCACCAACATC 2427
DB |||||
2 CCACAGTGCACCAACATC 21
XX
XX
XX RESULT 2628
XX ABL45313
XX ID ABL45313 standard; DNA; 22 BP.
XX
XX ABL45313;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:2357.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JF2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX

XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX
XX Arraying genome clones.
XX
XX
PS Claim 4; Page 51; 528pp; Japanese.
PS
XX
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 22 BP; 6 A; 2 C; 8 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5265 AATGTCATAGGAGGAGGT 5284
DB |||||
3 AATGTCATAGGAGGAGGT 22
XX
XX
XX RESULT 2629
XX ABQ80518
XX ID ABQ80518 standard; DNA; 22 BP.
XX
XX ABQ80518;
XX
XX 31-OCT-2002 (first entry)
XX
XX HBP17 reverse PCR primer.
XX
XX PCR; primer; allergic disease; allergy; NB-1; B48 antigen; c-fos;
XX involucrin; BENE; HBP17; fibronectin; Id1; ss.
XX
XX Synthetic.
XX
XX JF2002191398-A.
XX
XX 09-JUL-2002.
XX
XX 26-DEC-2000; 2000JP-00396167.
XX
XX 26-DEC-2000; 2000JP-00396167.
XX
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX
XX WPI; 2002-594354/64.
XX
XX Inspection of allergic diseases, and a reagent for the inspection of
XX allergic diseases.
XX

PS Example 2; Page 13; 31pp; Japanese.

XX The present invention relates to a method for the inspection of allergic

CC diseases. The method involves measuring the expression level of a gene

CC selected from the group consisting of NB-1, E48 antigen, c-fos,

CC involucrin, BDNF, HSP17, fibronectin and id1 in a biopsy sample, and

CC comparing it with the expression level of the gene in a biopsy sample of

CC a healthy person. The present primer was used in an example from the

CC invention

XX

SQ Sequence 22 BP; 2 A; 6 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;

Best Local Similarity 85.0%; Pred. No. 1.9e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3849 GCCTCTTTCTCTCTATTC 3868

DB 3 GCCTGCTTTCTCTTATC 22

RESULT 2630

ABSS2976/c

ID ABSS2976 standard; DNA; 22 BP.

XX

AC ABSS2976;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human IGE receptor sequencing primer #13.

XX

KW Human; IGE receptor; FcεR1α; HSA; human serum albumin;

KW anti-allergic; dermatological; anti-inflammatory; antiasthmatic; 89;

KW IGE binding domain; systemic allergy; IGE-receptor-mediated disorder;

KW atopic dermatitis; atopic asthma; chronic urticaria; primer.

XX

OS Homo sapiens.

XX

XX US6423512-B1.

PN

PD 23-JUL-2002.

XX

PF 21-JUL-1997; 97US-00897956.

XX

PR 26-JUL-1996; 96US-0022689P.

XX

PA (NOVS) NOVARTIS AG.

XX

PI Digan ME, Lake P, Gram H;

XX

DR WPI; 2002-672940/72.

XX

PT New fusion IGE-binding polypeptide, useful for the prevention and

PT treatment of systemic allergy and/or other IGE-receptor-mediated

PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.

XX

PS Disclosure; Fig 7; 49pp; English.

XX

XX The invention relates to a new fusion polypeptide or its pharmaceutically

CC acceptable salt comprises at least one IGE-binding domain fused to at

CC least one human serum albumin (HSA) component, where the IGE-binding

CC domain is the sequence (a) defined residues Val26-Leu204 of the protein

CC sequence appearing as ABG32801, or a truncation at the carboxy terminus

CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined

CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a

CC polynucleotide sequence encoding the fusion protein; (3) a host cell

CC transformed with the polynucleotide; (4) a method of preparing the fusion

CC protein comprising transforming a host cell with a vector comprising a

CC polynucleotide encoding the fusion polypeptide, expressing the fusion

CC polypeptide in the cell, and recovering the fusion polypeptide from the

CC host cell, optionally in the form of its salt; and (5) a vector for

CC expressing a polynucleotide sequence encoding a fusion polypeptide of

CC formula (I), (II), (III), (IV), or (V) or its salts (R₁-L-R₂ (I), R₂-

CC L-R₁ (II), R₁-L-R₂-L-R₁ (III), R₁-L-R₁-L-R₂ (IV), R₂-L-R₁-L-R₁

CC (V) where R₁ = the polypeptide (a) or its truncation at the carboxy-

CC terminus by 1-12 amino acids and R₂ = a polypeptide selected from the

CC sequence defined by residues Asp25-Leu609 the human HSA sequence

CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10

CC amino acids and L = independently a chemical bond, where the vector is

CC PMWT3-Rla-HAS-11a). The compositions and methods of the present invention

CC are useful for the prevention and treatment of systemic allergy and other

CC IGE-receptor-mediated disorders such as atopic dermatitis, atopic asthma

CC and chronic urticaria. The IGE-binding polypeptide have a more prolonged

CC effective serum life, more improved clinical utility in the treatment of

CC allergy, as well as improved activity in a more efficient and cost-

CC effective manner. The present sequence is a sequencing primer for the IGE

CC receptor cDNA

XX

SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;

Best Local Similarity 85.0%; Pred. No. 1.9e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3704 CATTGAGGATTCCTTC 3723

DB 20 CATTGTGTGACTGACTTC 1

RESULT 2631

ABST71631

ID ABST71631 standard; DNA; 22 BP.

XX

AC ABST71631;

XX

DT 28-NOV-2002 (first entry)

XX

DE T cell receptor (TCR) variable alpha (AV) peptide RT-PCR primer #9.

XX

KW T cell receptor; TCR; receptor; variable alpha peptide; AV peptide; TCRV;

KW T cell variable gene; T cell regulatory activity; autoimmune disease;

KW multiple sclerosis; human; reverse transcriptase; RT-PCR; primer; 89.

XX

OS Homo sapiens.

XX

XX US2002107388-A1.

PN

PD 08-AUG-2002.

XX

PF 10-MAY-2001; 2001US-00853830.

XX

PR 12-MAY-2000; 2000US-0203984P.

XX

PA (VAND/) VANDENBARK A A.

XX

PI Vandenbark AA;

XX

DR WPI; 2002-697882/75.

XX

PT Identifying a T cell receptor variable gene expressed by target T cells

PT in an individual is useful to identify disease-associated T cells for

PT design of individualized therapies, particularly for autoimmune disease.

XX

PS Example 2; Page 11; 20pp; English.

XX

XX The invention relates to a method for identifying a T cell receptor

CC variable (TCRV) gene expressed by target T cells in an individual

CC comprising determining expression of TCRV genes by activated T cells from

CC the individual and determining regulatory activity elicited in response

CC to TCRV peptides from the individual. A preferentially expressed TCRV

CC gene whose TCRV peptide elicits low T cell regulatory activity is

CC identified as a variable gene expressed by target T cells. The method is

CC used to identify disease-associated T cells in an individual so that

CC individualised therapies can be designed to prevent or treat the disease,

CC particularly an autoimmune disease, especially multiple sclerosis. This

CC sequence represents a reverse transcriptase PCR (RT-PCR) primer used in

CC analysis of expression of DNA encoding TCR variable alpha (AV) peptides
 XX Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6195 GAGATGAGAGATTGGA 6214

DB 1 GTGATGAGAGATTGGA 20

RESULT 2632

AA167914
 ID AA167914 standard; DNA; 22 BP.

AC AA167914;

DT 13-MAR-2002 (first entry)

DE Human MFO-110 cDNA cloning primer 01.

XX Zinc finger protein; MFO-110; developmental disorder; neurodegenerative;

XX psychiatric; vascular disease; angiogenesis; cancer; PCR primer; ss.

OS Homo sapiens.

PN WO200185765-A2.

PD 15-NOV-2001.

PE 11-MAY-2001; 2001WO-EP005372.

PR 12-MAY-2000; 2000EP-00110089.

PA (MERB) MERCK PATENT GMBH.

P1 Rodas Gubern B, Messeguey Peypoch R, Masa Alvarez M;

DR Rosell Vives E;

WIPI; 2002-055583/07.

XX Identification of a new human C2H2-type zinc finger protein, MFO-110, which

PT may be useful in the treatment and diagnosis of disease such as

PT developmental disorders, neurodegenerative disease, vascular disease and

PT cancer.

XX Example 1; Page 62; 63pp; English.

XX The invention provides new human C2H2-type zinc finger proteins, MFO-110.

CC The MFO-110 polypeptides can be expressed by standard recombinant

CC methodology. The MFO-110 polypeptides and polynucleotides can be used in

CC diagnostic assays for detection of abnormally decreased or increased

CC levels of polypeptide or mRNA expression. This may be used for diagnosing

CC or determining susceptibility of a subject to diseases that include

CC developmental disorders, neurodegenerative disease, brain stroke,

CC psychiatric disorders such as schizophrenia, cardiac and vascular

CC disease, angiogenesis and cancer especially lymphomas. The polypeptides

CC may be used to identify membrane bound or soluble receptors and may be

CC used to identify agonists and antagonists which compete with receptor

CC binding. The polynucleotides may be used as diagnostic reagents through

CC detecting mutations in the associated gene, for chromosome localization

CC studies and tissue expression studies. Sequences AA167914-17 represent

CC primers for the PCR amplification and cloning of human MFO-110 cDNA

XX Sequence 22 BP; 4 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6670 CATTGGGAGACATTCTATT 6689

DB 2 CATTGGGAGACATTCTATT 21

RESULT 2633

ABK55618/c
 ID ABK55618 standard; DNA; 22 BP.

AC ABK55618;

DT 18-JUN-2002 (first entry)

DE Human NOV3a RT-PCR primer #1.

XX Human; ss; primer; NOVX; gene therapy; cardiomyopathy; atherosclerosis;

XX diabetes; cell signal processing; metabolic pathway modulation;

XX inflammation; autoimmune disorder; scleroderma; transplantation; allergy;

XX systemic lupus erythematosus; haemophilia; Alzheimer's disease;

XX graft versus host disease; Leech-Nyhan syndrome; periodontitis;

XX pancreatic; musculoskeletal disorder; Parkinson's disease;

XX Huntington's disease; behavioural disorder; pain; obesity; wound healing;

XX neurodegenerative disorder; neuropsychiatric disorder; hypertension;

XX growth disorder; reproductive disorder; lung disease;

XX reverse transcriptase PCR.

OS Homo sapiens.

PN WO200216600-A2.

PD 28-FEB-2002.

PE 27-AUG-2001; 2001WO-US026518.

PR 25-AUG-2000; 2000US-0227800P.

PR 25-AUG-2000; 2000US-0228205P.

PR 25-AUG-2000; 2000US-0228324P.

PR 30-AUG-2000; 2000US-0228987P.

PR 30-AUG-2000; 2000US-0229185P.

PR 01-SEP-2000; 2000US-0229780P.

PR 01-SEP-2000; 2000US-0229848P.

PR 22-JAN-2001; 2001US-0263337P.

PR 31-JAN-2001; 2001US-0265518P.

PR 15-MAR-2001; 2001US-0276451P.

PR 27-MAR-2001; 2001US-0279196P.

PR 24-AUG-2001; 2001US-00939398.

PA (CURA-) CURAGEN CORP.

P1 Gerlach V, MacDougall JR, Smithson G, Stone DJ, Ellerman K,

P1 Spytek KA, Zernusen BD, Raetelli L, Verney CM, Patrajan M,

P1 Tcherev VT, Padigaru M, Taupier RJ;

WIPI; 2002-292064/33.

XX Example 2; Page 207; 245pp; English.

XX New isolated cytoplasmic, nuclear, membrane bound and secreted

PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune

PT disorders, hemophilia, Leech-Nyhan syndrome, pancreatitis,

PT musculoskeletal disorders.

XX The invention relates to an isolated cytoplasmic, nuclear, membrane bound

CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,

CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a

CC mature form, or a variant of the mature form of NOVX. Also included are a

CC polynucleotide encoding NOVX (or its complement), a vector comprising the

CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,

CC determining the presence of NOVX in a sample using the antibody,

CC which binds to NOVX polynucleotide, identifying a sample using a probe

CC NOVX (including modulators of NOVX), NOVX, the polynucleotide and the

CC antibody are useful for diagnosing, treating or preventing a NOVX-

CC associated disorder selected from cardiomyopathy, atherosclerosis, diabetes, a disorder related to cell signal processing and metabolic pathway modulation, inflammation, autoimmune disorders, scleroderma, CC transplacental, allergies, systemic lupus erythematosus, haemophilia, CC graft versus host disease, Alzheimer's disease, stroke, Leisch-Nyhan CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders, CC Parkinson's disease, Huntington's disease, behavioural disorders, pain, CC neurodegenerative and neuropsychiatric disorders, hypertension, wound healing, obesity, growth and reproductive disorders, lung diseases and CC many other diseases and disorders listed in the specification. NOVX, the CC polynucleotide and the antibody are useful in screening assays, detection CC assays (e.g., chromosomal mapping, tissue typing, forensic biology), CC predictive medicine (e.g., diagnostic assays, prognostic assays, CC monitoring clinical trials and pharmacogenomic), and in methods of CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to CC screen for potential agonist and antagonist compounds, and as bait CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is CC useful for producing non-human transgenic animals. The antibody is useful CC for isolating, and purifying NOVX and to monitor protein levels in tissue CC as part of a clinical testing procedure. The present sequence is an RT CC (reverse transcriptase)-PCR primer used to quantitate mRNA encoding a CC NOVX protein

XX
SQ Sequence 22 BP; 8 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.24; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7080 CTGAGTCCCTGGGTAGTA 7039
DB 22 CTGAGTCCCTGGGTAGTA 3

RESULT 2634
ACD19520/c
ID ACD19520 standard; DNA; 22 BP.
XX
AC ACD19520;
XX
DT 25-AUG-2003 (first entry)
XX
DE Novel human protein associated PCR primer #19.

XX
KW Human; NOV; gene therapy; endocrine related disease; diabetes;
KW metabolic-related disease; obesity; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW stroke; infection; PCR; primer; ss.

XX
OS Homo sapiens.
XX
PN W02003023002-A2.
XX
PD 20-MAR-2003.
XX
PP 09-SEP-2002; 2002WO-US028539.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318130P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.

PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324699P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 17-APR-2002; 2002US-037312P.
PR 06-SEP-2002; 2002US-00236177.

XX
PA (CURA-) CURAGEN CORP.
XX
PI Szytek KA, Paturajan M, Gorman L, Li L, Anderson DM, Zhong M;
PI Gerlich VL, Verne CM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI Lepley DM, Edinger SR, Burgess CE;
DR WPI; 2003-313242/30.

XX
PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT and polynucleotides, useful in gene therapy, e.g. for treating or
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT stroke or infections.

XX
PS Example 92; Page 494; 586pp; English.

XX
CC The invention describes a new isolated polypeptide (NOVX). The NOVX
CC polypeptide, nucleic acid and antibody are useful as therapeutics,
CC particularly in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, which includes a pathology associated
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC therapy for treating the disease or condition. In particular, the NOVX
CC polypeptide or polynucleotide is useful for treating endocrine/
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC asthma, inflammatory bowel disease, rheumatoid arthritis or
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC These are also useful in developing powerful assay systems for functional
CC analysis of various human disorders, as well as in diagnostic
CC applications, and for monitoring the effects of drugs during clinical
CC trials. This sequence represents a primer used to isolate DNA encoding
CC novel human NOV proteins

XX
SQ Sequence 22 BP; 13 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.24; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3921 CTCCTGGCTTCTTTCTCC 3940
DB 22 CTCCTGGCTTCTTTCTCC 3

RESULT 2635
ACF03609
ID ACF03609 standard; DNA; 22 BP.
XX
AC ACF03609;
XX
DT 15-SEP-2003 (first entry)
XX
DE Human NOV6 forward PCR primer SEQ ID NO:179.

XX
KW Human; NOVX; cytosolic; cardiac; anti-inflammatory; immunosuppressive;
KW anti-allergic; haemostatic; anti-HIV; antidiabetic; antileukosclerotic;
KW anorectic; antilethargic; nephrotropic; antiarthritic; hepatotropic;
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;

KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;
 KW vulnerability; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
 KW muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO200294870-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-NOV-2001; 2001WO-US051580.
 XX
 PR 02-NOV-2000; 2000US-0245291P.
 PR 02-NOV-2000; 2000US-0245317P.
 PR 07-NOV-2000; 2000US-0246562P.
 PR 08-NOV-2000; 2000US-0246871P.
 PR 26-JAN-2001; 2001US-0264389P.
 PR 26-JAN-2001; 2001US-0264423P.
 PR 29-JAN-2001; 2001US-0264799P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Grose WM, MacDougall JR, Smlthson G, Mallet I, Stone DV;
 PI Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
 PI Spletke KA, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
 PI Guo X, Fernandes ER, Vernet CM, Tchernev VT, Casman SJ, Shenoy S;
 PI Mishra V, Putrak K, Baumgartner JC, Colman SD;
 XX
 DR WPI; 2003-140359/13.
 XX
 PT New NOXV polypeptide useful for preventing or treating NOXV-associated
 PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
 PT in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 2; Page 260; 346pp; English.
 XX
 CC AC03547 to AC03570 encode the human NOXV proteins (1) given in ABR57412
 CC to ABR57435. (1) have cytotoxic, cardiant, antiinflammatory, nootropic,
 CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
 CC antiatherosclerotic, anorectic, antiasthmatic, nephrotropic, virolytic,
 CC antiparasitic, hepatotropic, neuroprotective, antibacterial, relaxant,
 CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
 CC vulnerability, angiogenic and antiangiogenic activities, and can be used in
 CC gene therapy and vaccines. The NOXV polypeptides and their antibodies can
 CC be used to determine the presence or absence of (1) in a sample. The NOXV
 CC polypeptides, polynucleotides encoding them, and antibodies against them,
 CC are useful in manufacturing a medicament for treating or preventing a
 CC syndrome associated with a NOXV-associated disorder such as hypertension,
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
 CC autoimmune disorders, allergies, blood disorders, obesity, acquired
 CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) nephropathy,
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. AC03571 to AC03644 represent PCR primers and probes for NOXV
 CC sequence, which are used in an example from the present invention
 XX
 SQ Sequence 22 BP; 8 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 7413 CAGCAGCAGCAGCAGCAGCA 7432
 DB 2 CAGCAGCAGCAGCAGCAGCA 21

RESULT 2636
 ID ACC58206/C
 ID ACC58206 standard; DNA; 22 BP.
 XX
 AC ACC58206;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE PCR primer used in human FCGR2A-131H/R genotyping.
 XX
 KW Human; FCGR2A; Fc gammaRIIa; receptor; antibody;
 KW single nucleotide polymorphism; SNP; lymphoma; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO2003035904-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 11-OCT-2002; 2002WO-EP011397.
 XX
 PR 19-OCT-2001; 2001EP-00402718.
 XX
 PA (UYLI-) UNIV LITTLE CENT HOSPITALIER REGIONAL.
 PA (INNA-) INNATE PHARMA.
 XX
 PI Watier H, Cartton G, Colombat P;
 XX
 DR WPI; 2003-482053/45.
 XX
 PT Assessing the response of a subject having a tumor to a therapeutic
 PT antibody e.g., rituximab treatment, or selecting patients for therapeutic
 PT antibody treatment, comprises determining the FCGR3A158 genotype of the
 PT subject.
 XX
 PS Disclosure; Page 15; 53pp; English.
 XX
 CC The present sequence is that of a PCR primer used in human FCGR2A
 CC genotyping. Genotyping of FCGR2A-131H/R was performed in order to
 CC determine any correlation between genotype and response to therapeutic
 CC antibody treatment in non-Hodgkin's lymphoma (NHL) patients. The present
 CC (sense) primer was modified to create a BstUI site in case of R allele,
 CC and the antisense primer (see ACC58207) was modified to create a BstUI
 CC site that served as an internal control. PCR amplification of genomic DNA
 CC was performed. Amplified DNA was digested with BstUI and separated by
 CC electrophoresis, staining with ethidium bromide. The FCGR2A-131H and -
 CC 131R alleles were visualized as a 337 bp and 316 bp DNA fragment,
 CC respectively. There was no correlation between FCGR2A-131H/R genotype and
 CC response to treatment. In contrast, FCGR3A-158V/F genotyping revealed a
 CC correlation with antibody treatment response in NHL patients
 XX
 SQ Sequence 22 BP; 8 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 6005 GAGGTTTCTGGCATTTTCC 6024
 DB 20 GAGGATTTCTGGGATTTTCC 1
 XX
 RESULT 2637
 ACF57219
 ID ACF57219 standard; DNA; 22 BP.
 XX
 AC ACF57219;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE Human LAMB3 forward PCR primer SEQ ID NO:19.
 DE Human; mouse; skin structure; skin; laminin 5 chain gene; LAMB3;
 XX

KW LAMC2; extracellular matrix component; matrix metalloproteinase; MMP-1;
 KM MMP-2; MMP-3; MMP-9; TIMP-1; TIMP-2; TIMP-3; collagen; PCR primer; ss.
 OS Synthetic.
 XX Homo sapiens.
 XX JP2002330792-A.
 PN 19-NOV-2002.
 PD 15-JAN-2002; 2002JP-00006797.
 PF 15-JAN-2002; 2002JP-00006797.
 PR 15-JAN-2001; 2001JP-00006952.
 XX (SHIS) SHISEIDO CO LTD.
 PA WPI; 2003-407328/39.
 DR WPI; 2003-407328/39.
 XX A method and a kit for determination of expression of mRNA or cDNA of a
 PT protein participating in the maintenance of skin structure.
 PS Claim 1; Page 2; 34pp; Japanese.
 XX The present invention describes a method and a kit for determining the
 CC expression of mRNA or cDNA of a protein participating in the maintenance
 CC of skin structure. The method is quantitative, simple and accurate in the
 CC determination of extracellular matrix components of laminin 5 chain genes
 CC LAMV3, LAMB3 and LAMC2, matrix metalloproteinases MMP-1, MMP-2, MMP-3 and
 CC MMP-9, VII collagen, type I collagen alpha 1 chain, type I collagen alpha
 CC 2 chain, type III collagen alpha 1 chain, type IV collagen alpha 1 chain,
 CC type IV collagen alpha 2 chain, TIMP-1, TIMP-2 and TIMP-3. ACFS7201 to
 CC ACFS7290 represent PCR primers and probes used in the method of the
 CC invention
 XX Sequence 22 BP; 6 A; 3 C; 10 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4513 CAGGACTGGAGAGCTGTG 4532
 DB 3 CAGGACTGGAGAGCTGTG 22
 RESULT 2638
 ADB81310/c
 ID ADB81310 standard; DNA; 22 BP.
 XX ADB81310;
 AC ADB81310;
 XX 04-DEC-2003 (first entry)
 DT PCR primer 9 used to amplify F8 scfv antibody to generate anti-11gande.
 DE ss; PCR; primer; F8 scfv; antibody; anti-11gand library;
 KM site directed mutagenesis.
 KW Unidentified.
 OS Unidentified.
 XX WO2003064648-A1.
 PN 07-AUG-2003.
 PD 30-JAN-2003; 2003WO-EP000982.
 PF 31-JAN-2002; 2002GB-00002206.
 PR (BIOI-) BIOINVENT INT AB.
 XX Ohlin M;
 PI WPI; 2003-627612/59.
 DR

XX Making a library of anti-11gande having a cavity binding site for a
 PT 11gand, useful in screening for a 11gand.
 PS Example 1; Page 16; 65pp; English.
 XX This invention relates to a novel method of generating anti-11gand
 CC libraries that have a cavity binding site. The method comprises providing
 CC several novel anti-11gands having a cavity for binding a first 11gand,
 CC and differing from the first anti-11gand in that one or more of the amino
 CC acid residues which make up the 11gand binding surface of the cavity are
 CC varied. Diversification of the first anti-11gand is achieved by site
 CC directed mutagenesis, such that one or more of the amino acids that form
 CC the cavity binding surface are replaced by those having similar but
 CC different physicochemical properties. Preferably the anti-11gand is an
 CC antibody, or fragment thereof, where amino acid replacements are derived
 CC from a natural CDR (complementarily determining region) that makes up the
 CC cavity and which binds to the 11gand - an antigen. Specific anti-11gands
 CC from such a library can be used as a starting point for further evolution
 CC in order to improve their binding characteristics or to better correlate
 CC their final use. This oligonucleotide is PCR primer 9 used to amplify the
 CC F8 scfv antibody fragment in order to generate the anti-11gand library of
 CC the invention.
 XX Sequence 22 BP; 6 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1984 TTCTGGGAGCAGATGTTAC 2003
 DB 21 TTCTGGGAGCTGTGATAC 2
 RESULT 2639
 ADC10255
 ID ADC10255 standard; DNA; 22 BP.
 XX ADC10255;
 AC ADC10255;
 XX 18-DEC-2003 (first entry)
 DT Human NOVX polypeptide gene forward primer SEQ ID NO: 277.
 DE ss; primer; cytosstatic; antidiabetic; anorectic; cerebroprotective;
 KM neuroprotective; antiinflammatory; gene therapy; antisense therapy;
 KM thymimetic; NOVX; pathology; cancer; diabetes; obesity;
 KW endocrine disorder; CNS disorder; inflammatory disorder;
 XX chromosome mapping; tissue typing; predictive medicine.
 OS Homo sapiens.
 XX WO2003000842-A2.
 PN 03-JAN-2003.
 PD 04-JUN-2002; 2002WO-US017443.
 PF 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.

PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 28-JUN-2001; 2001US-0301550P.
 PR 03-JUL-2001; 2001US-0302951P.
 PR 31-JUL-2001; 2001US-0308890P.
 PR 14-SEP-2001; 2001US-0322297P.
 PR 25-SEP-2001; 2001US-0324669P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341562P.
 PR 21-FEB-2002; 2002US-0358656P.
 PR 21-FEB-2002; 2002US-0359122P.
 PR 22-FEB-2002; 2002US-0358978P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-035964P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.
 PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.

XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dippio VA, Edinger SR, Eissen A, Eilerman K, Gangoli EW,
 PI Gerlach VJ, Gorman L, Guo X, Hermann JT, Hjal T, Ji W, Kekuda R;
 PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Miller I;
 PI Ort T, Padigaru M, Paturajan M, Pena CE, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsbrook JP;
 PI Burgess CE, Lepley DM;

XX WPI; 2003-210149/20.

XX New isolated NOX polypeptides and nucleic acid molecules useful for
 PT tracing, preventing and diagnosing pathological conditions with NOX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.

XX Example B; SEQ ID NO 277; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to a primer used to
 CC amplify and isolate the coding sequence for one of the polypeptides of
 CC the invention.

XX Sequence 22 BP; 0 A; 7 C; 2 G; 13 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
 XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 5733 CTTCCTTCCCTTTCTCTCT 5752
 DB 1 CTGCTTTGCGCTTTCTCTCT 20

XX RESULT 2640

XX ADE76823/c
 XX ID ADE76823 standard; DNA; 22 BP.

XX AC ADE76823;

XX DT 29-JAN-2004 (first entry)

XX Pfiesteria shumwayae-specific PCR primer Seq ID4.

XX water-borne organism; algal bloom; ship ballast; dinoflagellate;
 KW Pfiesteria; Gymnodinium; Chattonella; Alexandrium; Aureococcus;
 KW zebra mussel; Dreissena; PCR; primer; ss.

XX Pfiesteria shumwayae.

XX WO2003053855-A2.

XX 03-JUN-2003.

XX 25-OCT-2002; 2002MO-US034123.

XX 30-OCT-2001; 2001US-0131335P.

XX 10-JUN-2002; 2002US-0394654P.

XX (UYDE) UNIV DELAWARE.

XX Cary SC, Coyne KJ;

XX WPI; 2003-618038/58.

XX Identifying water-borne organisms associated with harmful algal bloom
 PT comprises fractionating an aliquot of water, isolating DNA from
 PT fractions, amplifying DNA, contacting amplicon obtained with probe, and
 PT detecting amplicon.

XX Claim 17; SEQ ID NO 4; 36pp; English.

XX This invention relates to a novel method of identifying water-borne
 CC organisms associated with harmful algal bloom. The method comprises
 CC fractionating an aliquot of water by size to yield several fractions,
 CC isolating DNA from the fractions, amplifying DNA by high throughput, real
 CC time PCR comprising forward and reverse genus-specific primer to yield
 CC amplified DNA amplicon, contacting the amplicon with a species-specific
 CC labelled probe, and detecting the amplicon. The method is useful for
 CC identifying water-borne organisms associated with harmful algal bloom or
 CC transported in the ballast of a ship, where the water-borne organisms are
 CC dinoflagellates selected from Pfiesteria, Gymnodinium, Chattonella,
 CC Alexandrium and Aureococcus, or is a zebra mussel (Dreissena). The
 CC present sequence is that of a species-specific PCR primer which may be
 CC used in the method of the invention.

XX Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
 XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 2545 CAGATCCTGACGTACGAGCT 2564
 DB 20 CAGATTCTGACCTATGAGCT 1

XX RESULT 2641

XX ADE15462
 XX ID ADE15462 standard; DNA; 22 BP.

XX AC ADE15462;

XX 29-JAN-2004 (first entry)

XX T cell receptor variable region alpha, RT PCR primer #9.

XX Human; T cell receptor variable region alpha; TCRV alpha;
 KW cytokine response; CD4+ T cell; CD25+ T cell; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW type 1 diabetes; non-obese diabetes; myasthenia gravis; Grave's disease;
 KW Hashimoto's thyroiditis; PCR; primer; ss; RT-PCR;
 KW reverse transcriptase PCR.

OS Homo sapiens.
 XX US2003190665-A1.
 PN 09-OCT-2003.
 PD 14-MAY-2003; 2003US-00438729.
 PF 12-MAY-2000; 2000US-0203984P.
 PR 10-MAY-2001; 2001US-00853830.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA (USGO) US DEPT VETERANS AFFAIRS.
 PI Vanderbark AA;
 XX WPI; 2003-864176/80.
 DR
 XX Identifying T cell receptor variable peptides useful for treating
 PT autoimmune disease including multiple sclerosis, rheumatoid arthritis,
 PT lupus, diabetes, myasthenia gravis, Grave's disease, Hashimoto's
 PT thyroiditis and psoriasis.
 PS Example 1; SEQ ID NO 125; 68pp; English.
 XX The invention relates to identifying a T cell receptor (TCR) variable (V)
 CC peptide useful as a therapeutic agent in a subject with a disorder,
 CC comprising screening TCR V beta and/or TCR V alpha peptides to select a
 CC TCR V peptide that produces altered expression of a cytokine in response
 CC to the peptide by T cells from the subject, and determining a regulatory
 CC activity of CD4+CD25+ T cells isolated from the subject in response to
 CC the peptide. Also included are monitoring the efficacy of a TCR V peptide
 CC for treatment of a subject (comprising exposing CD4+ T cells from the
 CC subject to the peptide and determining a T cell regulatory activity of
 CC CD4+CD25+ T isolated from the subject, where induction or regulatory
 CC activity indicates the efficacy of the peptide for treatment of the
 CC subject), selecting a therapy for a subject (comprising: identifying a
 CC TCR V gene expressed by target T cells in the subject by screening for
 CC expression of a TCR V gene by activated T cells from the subject and
 CC determining expression of a cytokine elicited in response to one or more
 CC TCR V peptides corresponding to the TCR V gene by T cells from the
 CC subject, thereby identifying a TCR V gene expressed by target T cells)
 CC and identifying a TCR V peptide corresponding to the TCR V gene that
 CC elicits T cell regulatory activity by a T cell isolated from the subject.
 CC The method is useful for identifying a T cell receptor (TCR) variable (V)
 CC peptide useful as a therapeutic agent in a subject with a disorder. The
 CC peptide is used to treat an autoimmune disease, particularly multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus, type I
 CC diabetes, non-obese diabetes, myasthenia gravis, Grave's disease,
 CC Hashimoto's thyroiditis or psoriasis. The present sequence is a TCR V
 CC alpha reverse transcriptase (RT)-PCR primer used to measure TCR gene
 CC expression levels, in the method of the invention.
 XX
 SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6195 GAGNATGAGAGAAATTGAA 6214
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1 GTGATGAGAGAAATCTGGA 20
 RESULT 2642
 AAT05666/C
 ID AAT05666 standard; DNA; 23 BP.
 AC AAT05666;
 XX 20-JUN-1996 (first entry)
 DT
 XX PCR primer for nucleic acid encoding TNF microsatellite.
 DB

XX Tumour necrosis factor; TNF; microsatellite; Crohn's disease; allele;
 KM inflammatory bowel disease; diagnosis; therapeutic; ulcerative colitis;
 KW ss.
 OS Synthetic.
 XX WO9531575-A1.
 PN 23-NOV-1995.
 PD 17-MAY-1995; 95WO-US006107.
 PF 17-MAY-1994; 94US-00245297.
 PR (CEDA-) CEDARS SINAI MEDICAL CENT.
 PA Plevy SE, Rotter JI, Targan SR, Toyoda H, Yang H;
 PI WPI; 1996-010959/01.
 DR Screening for Crohn's disease - by detecting nucleic acid encoding
 PT particular tumour necrosis factor micro-satellite allele(s).
 PS Claim 10; Page 32; 43pp; English.
 XX AAT05661-T05670 are PCR primers used for the detection of a nucleic acid
 CC encoding tumour necrosis factor (TNF) microsatellite alleles a to e.
 CC These alleles are associated with Crohn's disease (CD). The presence of
 CC nucleic acid encoding 3 or more of the alleles in a subject is indicative
 CC of CD. The primers provide a reliable method of screening for CD and are
 CC useful for distinguishing between CD and ulcerative colitis patients. The
 CC presence of a nucleic acid carrying 3 or more of the alleles a2, b1, c2,
 CC d4 and e1 indicates a CD patient and in ulcerative colitis patients
 CC alleles a2, b1 and c2 are absent
 XX
 SQ Sequence 23 BP; 8 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5179 CTCTGATGTTCTCCACTTG 5198
 | | | | | | | | | | | | | | | | | | | | | |
 Db 21 CTCGACGGTTCCTCCCATG 2
 RESULT 2643
 AAT63128/C
 ID AAT63128 standard; DNA; 23 BP.
 AC AAT63128;
 XX 22-JUN-1997 (first entry)
 DT
 XX Glutathione S-transferase promoter PCR primer A12.
 DE Promoter; glutathione S-transferase; herbicide safener; gene switch;
 KM transcription factor; transgenic plant; maize; primer; PCR;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS
 XX WO9711189-A2.
 PN 27-MAR-1997.
 PD 30-AUG-1996; 96WO-GB002116.
 PF 22-SEP-1995; 95GB-00019404.
 PR 22-SEP-1995; 95GB-00019406.
 XX (ZENB) ZENECA LTD.
 PA

XX Jepsen I, Greenland AJ, Bevan M, Sheppard H;
 XX WPI; 1997-202896/18.
 XX Chemically inducible promoter from the glutathione S-transferase gene -
 PT provides inducible gene expression in plants, esp. with herbicide
 PT safeners as inducer.
 XX Disclosure; Page 12; 49pp; English.
 XX Preliminary deletion analysis of the maize glutathione S-transferase 27
 CC kda subunit gene promoter region (see also AAT63125) suggested that
 CC element(s) conferring inducibility lay within 900 bp immediately upstream
 CC of the transcription start point (TSP). A series of fine deletion
 CC constructs were made by fusing 200 bp deleted fragments of this 900 bp
 CC region to a beta-glucuronidase marker gene. PCR primer A12 (AAT63128) was
 CC designed to correspond to a PstI site adjacent to the TSP. It was used in
 CC combination with primers A13, A14, A15 and A16 (AAT63129-32) in PCR
 CC experiments to generate fragments of 217, 378, 570 and 760 bp,
 CC respectively. Transient transformation assays indicated that the
 CC inducible element(s) lay between -217 and -318 upstream of the TSP
 SQ Sequence 23 BP; 3 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 7411 ATCAGCAGCAGCAGCAGCAG 7430
 Db 23 ATAACTAGCAGCTGCAGCAG 4
 RESULT 2644
 AAV57842/c
 ID AAV57842 standard; DNA; 23 BP.
 XX AAV57842;
 XX 18-NOV-1998 (first entry)
 XX Human chromosome 18 PCR primer F for D18S996.
 DE Manic-depressive illness; susceptibility; genotype; diagnosis;
 KW chromosomal marker; polymorphic marker; chromosome 18; human;
 KW myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9818963-A1.
 XX 07-MAY-1998.
 PD 28-OCT-1997; 97WO-US019381.
 PP 28-OCT-1997; 97WO-US019381.
 XX 28-OCT-1996; 96US-0029278P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Deterra-Wadleigh SD, Gershon ES, Badner JA, Goldin LR;
 PI Berrettini WH, Yoshikawa T, Sanders AR, Esterling LE;
 XX WPI; 1998-272247/24.
 DR New isolated IMP-18p myo-inositol monophosphatase - used to develop
 PT products for determining susceptibility to manic depressive illness and
 PT as targets for preventive and therapeutic treatments.
 XX Disclosure; Page 3; 118pp; English.
 PS A method has been developed for determining a genotype associated with

CC increased susceptibility to manic-depressive (MD) illness. The method
 CC comprises determining the genotype of an affected individual with at
 CC least one polymorphic marker localised within the chromosomal region
 CC defined by and including markers D18S843 and D18S869 and determining the
 CC genotype associated with increased susceptibility to MD disorder. The
 CC method can be used for determining susceptibility to MD illness including
 CC bipolar disorder, genetic counseling of individuals from families
 CC affected with MD illness, and aid in the differential diagnosis of MD
 CC illness from other psychiatric pathologies. Products from the present
 CC invention can also be used to obtain modulators of IMP-18p myo-inositol
 CC monophosphatase protein activity and as targets for preventive and
 CC therapeutic treatments. The present sequence represents a PCR primer from
 CC Table 1 in the present invention (see AAV57798 to AAV57877)
 XX Sequence 23 BP; 6 A; 3 C; 4 G; 10 T; 0 U; 0 Other;
 SQ Sequence 23 BP; 6 A; 3 C; 4 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 7108 GAAATAATGAATTAATTCTTCC 7127
 Db 23 GAAATAATGAATTAATTCTTCC 4
 RESULT 2645
 AAV64634/c
 ID AAV64634 standard; DNA; 23 BP.
 XX AAV64634;
 XX 09-FEB-1999 (first entry)
 XX PCR primer for amplification of tumour necrosis factor locus c.
 DE Tumour necrosis factor; TNF; microsatellite allele; Crohn's disease;
 KW clinical subtype; anti-TNF cytokine therapy; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9847004-A1.
 XX 22-OCT-1998.
 PD 08-APR-1998; 98WO-US006991.
 PP 11-APR-1997; 97US-00837056.
 PR 12-MAY-1997; 97US-00855825.
 XX (CEDA-) CEDARS SINAI MEDICAL CENT.
 PA (PROM-) PROMETHEUS LAB INC.
 XX Plevy SE, Targan SR, Taylor K, Barry MJ;
 XX WPI; 1998-583296/49.
 DR Diagnosis of Crohn's disease subtypes - by detecting serological and
 PT genetic markers for identifying subtypes having characteristic
 PT responsiveness to anti-TNF cytokine therapy.
 XX Claim 37; Page 76; 117pp; English.
 PS PCR primers AAV64633-34 are used in PCR analysis of tumour necrosis
 CC factor (TNF) microsatellite alleles to identify TNF locus c. The
 CC specification describes a method for detecting the presence or absence of
 CC at least two TNF microsatellite alleles selected from TNFA10, TNFB4,
 CC TNFC1, TNFD3 and TNPE3 in a patient with Crohn's disease, where the
 CC presence of an allelic combination comprising at least two of the alleles
 CC indicates a clinical subtype of Crohn's disease having an inferior
 CC clinical response to anti-TNF cytokine therapy. The methods and the
 CC products can be used for diagnosing clinical subtypes of Crohn's disease,
 CC that affect the gastrointestinal tract and produce similar symptoms, with

CC characteristic responsiveness to anti-TNF cytokine therapies such as anti-TNF- α therapeutics

CC -TNF- α therapeutics

XX Sequence 23 BP; 8 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

XX

Query Match 0.2%; Score 15.2; DB 1; Length 23;

Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5179 CTCTGATGTTCTCCACTTG 5198

DB 21 CTTCGACAGTTCTCCCATG 2

RESULT 2646

AAV5546/c

ID AAV5546 standard; DNA; 23 BP.

XX

AC AAV5546;

XX

DT 09-MAR-1999 (first entry)

XX

DE PCR primer for creation of Human erythropoietin isoform.

XX

KM Erythropoietin; isoform; isoelectric point; sialic acid; PCR primer;

KW human; haematocrit level; 88.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN US5856298-A.

XX

PD 05-JAN-1999.

XX

PF 03-NOV-1994; 94US-00334882.

XX

PR 13-OCT-1989; 89US-00421444.

PR 12-OCT-1990; 90US-00598448.

PR 08-SEP-1992; 92US-00942126.

XX

PA (AMGE-) AMGEN INC.

XX

PI Strickland TW;

DR WPI; 1999-105163/09.

XX

PT New isolated erythropoietin isoforms - used for increasing haematocrit levels in mammals.

XX

PS Example 6; Col 15; 26pp; English.

XX

CC This sequence represents a PCR primer used in the creation of the human erythropoietin (EPO) isoforms of the invention. The isoforms have a single isoelectric point and have a specific number of sialic acids per molecule, the number being selected from 1-14, and the isoform being the product of the expression of an exogenous DNA sequence in a non-human eukaryotic host cell. The isolated EPO isoforms have a defined sialic acid content and biological activity, e.g. the relative in vivo specific activities increase stepwise from isoforms having 5 sialic acid residues to isoforms having 11 sialic acid residues. The EPOs can be used for increasing haematocrit levels in mammals

CC

XX

SO Sequence 23 BP; 4 A; 7 C; 9 G; 3 T; 0 U; 0 Other;

QY

Query Match 0.2%; Score 15.2; DB 1; Length 23;

Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1185 CTGCTACAGTTGGCCAGG 1204

DB 23 CTTCGACAGTTGGCCAGG 4

RESULT 2647

AAAX00262/c

ID AAAX00262 standard; DNA; 23 BP.

XX

AC AAAX00262;

XX

DT 25-MAR-1999 (first entry)

XX

DE TNF microsatellite loci c PCR primer #6.

XX

KM TNF microsatellite locus; tumour necrosis factor; human; PCR primer;

KW amplification; diagnosis; ulcerative colitis; TNF α 2b1c2d4e1 haplotype;

KW anti-inflammatory; anti-Saccharomyces cerevisiae antibody; colectomy;

KW immunosuppressant; 88.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9846997-A1.

XX

PD 22-OCT-1998.

XX

PP 09-APR-1998; 98WO-US006947.

XX

PR 11-APR-1997; 97US-00837302.

XX

PA (CEDA-) CEDARS SINAI MEDICAL CENT.

XX

PI Plevy SE, Targan SR;

DR WPI; 1999-095224/08.

XX

PT Diagnosing a resistant clinical subtype of ulcerative colitis - by detecting presence of anti-Saccharomyces cerevisiae antibodies or a particular combination of tumour necrosis factor alleles.

XX

PS Claim 25; Page 44; 65pp; English.

XX

CC A method has been developed for diagnosing a medically resistant subtype of ulcerative colitis (UC) by detecting anti-Saccharomyces cerevisiae by antibodies (Ab) in a patient. Alternatively, this subtype is diagnosed by detecting at least two of the tumour necrosis factor (TNF) alleles (microsatellite loci) TNF a2, b1, c2, d4 and e1, more specifically the TNF α 2b1c2d4e1 haplotype (A). Ab and haplotype (A) are useful as independent markers of the resistant subtype of UC. The methods identify a subset of UC patients who do not respond to treatment with anti-inflammatory and/or immunosuppressants, and who generally will eventually require colectomy. Early identification of the resistant CC subtype will allow aggressive treatments to be applied before inflammation has become refractory. The present sequence represents a specifically claimed PCR primer for amplifying TNF microsatellite loci

CC

XX

SO Sequence 23 BP; 8 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

QY

Query Match 0.2%; Score 15.2; DB 1; Length 23;

Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5179 CTCTGATGTTCTCCACTTG 5198

DB 21 CTTCGACAGTTCTCCCATG 2

RESULT 2648

AAAX18542/c

ID AAAX18542 standard; DNA; 23 BP.

XX

AC AAAX18542;

XX

DT 05-MAY-1999 (first entry)

XX

DE Mouse IMC carcinoma cell IMC-HA1 PCR primer SEQ ID NO:32.

KW Mouse; carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;
 KW cancer metastasis associated protein; PCR primer; ss.
 OS Synthetic.
 OS Mus musculus.
 XX MO9845431-A1.
 PN 15-OCT-1998.
 PD 07-APR-1998; 98WO-JP001592.
 PF 08-APR-1997; 97JP-00105333.
 PR (BANY) BANYU PHARM CO LTD.
 PA (BANY) BANYU PHARM CO LTD.
 PI Morita M, Arakawa H, Ohta M;
 XX WPI; 1999-080732/07.
 DR
 XX
 PT Protein associated with cancer metastasis and gene encoding it - useful
 PT for screening for potential inhibitors of cancer metastasis.
 PS Example 2; Page 20; 74pp; Japanese.
 CC The present invention provides gene sequences associated with cancer
 CC metastasis which are isolated from mouse IMC carcinoma cells by detection
 CC of their higher expression in IMC-HM cell lines than in IMC-IM cell lines
 CC using differential display of the mRNA in these cells. The gene sequences
 CC can be used for the screening of potential inhibitors of cancer
 CC metastasis by either: bringing into contact with the cancer metastasis
 CC associated protein (CMAP) and determining the degree of binding; or
 CC creating a transformant cell line which expresses CMAP and measuring the
 CC degree of expression of CMAP using an antibody recognising the protein,
 CC either in the presence or absence of the potential inhibitor. IMC-HM
 CC cells transformed with antisense CMAP DNA show a lowered ability to
 CC metastasise. The present sequence represents a PCR primer used in an
 CC example from the present invention
 CC
 XX
 SQ Sequence 23 BP; 5 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
 QY
 DB 3222 TGGGAGGAGGAGGAGATT 3241
 DB 23 TGGGAGGAGGAGGAGATT 4
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3222 TGGGAGGAGGAGGAGATT 3241
 DB 23 TGGGAGGAGGAGGAGATT 4
 RESULT 2649
 AAA13773/c
 ID AAA13773 standard; DNA; 23 BP.
 XX
 AC AAA13773;
 XX
 DT 26-JUL-2000 (first entry)
 DE Deleted GST promoter sequence PCR primer #2.
 XX
 KM Maize; glutathione-S-transferase; GST; promoter; plant; tuber; potato;
 KM expression; sprouting inhibition; storage; PCR primer; ss.
 OS Zea mays.
 OS WO200018930-A1.
 PN 06-APR-2000.
 PD 13-SEP-1999; 99WO-GB003021.
 PF 25-SEP-1998; 98GB-00020970.
 PR
 XX

PA (ZENNE) ZENNECA LTD.
 XX
 PI Robertson NM, Paine JM, Jepson I;
 DR WPI; 2000-293164/25.
 XX
 PT Constitutively expressing a target gene in a storage organ or stem of a
 PT plant comprises transfecting the plant with a gene promoter region for
 PT the 27 kD subunit of glutathione-S-transferase operably linked to a
 PT target sequence.
 XX
 PS Example 1; Page 15; 53pp; English.
 CC A method has been developed of constitutively expressing a target gene in
 CC a storage organ or stem of a plant by using the gene promoter region (1)
 CC for the 27 kD subunit of the glutathione-S-transferase (GST), isoform II,
 CC or its deleted fragment which retains the activity of (1), operably
 CC linked to and controlling a target sequence. The present invention also
 CC describes: (1) a DNA construct comprising (1) operably linked to and
 CC controlling a target gene sequence; (2) potato plant germ plasma
 CC comprising the DNA construct of (1); (3) a potato plant, potato seed or
 CC potato plant cell comprising a DNA construct of (1); and (4) a method for
 CC preventing or inhibiting sprouting in a potato tuber comprising causing
 CC the tuber to express a target sequence under the control of (1). The
 CC method is used for constitutively expressing a target gene in a storage
 CC organ or stem of a plant in order to prevent or inhibit sprouting of
 CC tubers. The method obviates the use of chemicals and their associated
 CC costs for inhibiting sprouting in potatoes. The present sequence
 CC represents a PCR primer used in the generation of the specifically
 CC claimed deleted GST promoter sequence comprising 693 bases
 CC
 XX
 SQ Sequence 23 BP; 3 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
 QY
 DB 7411 ATCAGCAGCAGCAGCAGCAG 7430
 DB 23 ATAGTAGCAGCTGCAGCAG 4
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7411 ATCAGCAGCAGCAGCAGCAG 7430
 DB 23 ATAGTAGCAGCTGCAGCAG 4
 RESULT 2650
 AAA59333/c
 ID AAA59333 standard; DNA; 23 BP.
 XX
 AC AAA59333;
 XX
 DT 07-NOV-2000 (first entry)
 DE PCR primer used to amplify the cDNA sequence of I-2 resistance gene.
 XX
 KM Regulatory activity; transcription; I-2 resistance gene; tomato;
 KM egg plant; potato; melon; tobacco; Arabidopsis; plant pathogen; fungi;
 KM tissue-specific; PCR primer; ss.
 OS Fusarium oxysporum.
 OS EP1024196-A1.
 PN 02-AUG-2000.
 PD 29-JAN-1999; 99EP-00400212.
 PF 29-JAN-1999; 99EP-00400212.
 PR 29-JAN-1999; 99EP-00400212.
 XX
 PA (KEYG-) KEYGENE NV.
 PI Haring MA, Cornelissen BJC, Mes JJ, Simons AFM;
 DR WPI; 2000-516034/47.
 XX
 PT New I-2 resistance gene tissue-specific regulatory sequence useful in

PT plant resistance mechanisms against plant pathogens such as fungi.
 XX
 PS Disclosure; Page 7, 47pp; English.
 XX
 CC PCR primers AAA59333-34 were used to amplify cDNA encoding an I-2
 CC resistance protein. The specification describes nucleotide sequences
 CC which have a regulatory activity on the transcription of the I-2
 CC resistance gene in plant host cells. The transgenic plants, especially
 CC tomato, egg plant, potato, melon, tobacco and Arabidopsis, are capable of
 CC expressing a gene mediating resistance to a plant pathogen, such as
 CC fungi, in a tissue-specific manner. The plant is capable of preventing
 CC infection by a plant pathogen, such as fungi. Inserting the regulatory
 CC activity polynucleotide into plant cell genomes is useful for providing
 CC plants with reduced susceptibility to plant pathogens, especially for
 CC protecting plants in cultivation
 XX
 SQ Sequence 23 BP; 2 A; 12 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 6989 GAATGAGGTGGAAGGAG 7008
 Db 21 GAGTGAGGTGGAAGGAG 2
 RESULT 2651
 AAC80271/c
 ID AAC80271 standard; DNA; 23 BP.
 XX
 AC AAC80271;
 XX
 DT 03-MAY-2001 (first entry)
 XX
 DE Reverse primer #99 used for amplification of HLA-A exon 3.
 XX
 KW HLA-A, HLA-B, HLA-C, typing; primer; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200061795-A2.
 PD 19-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-EP002398.
 XX
 PR 09-APR-1999; 99EP-00870068.
 PR 11-JUN-1999; 99US-0138614P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI De Canck I, Rombout A, Rosseau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
 PT primer sets, useful for subtyping or typing of HLA Class I alleles.
 XX
 PS Claim 4; Page 40; 128pp; English.
 XX
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method
 XX
 SQ Sequence 23 BP; 6 A; 9 C; 4 G; 3 T; 0 U; 1 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5151 GCGAGGAGCTTCTCTGGG 5170
 Db 23 GCGAGGAGMTCTCTCTGGG 4
 RESULT 2652
 AAH19012/c
 ID AAH19012 standard; DNA; 23 BP.
 XX
 AC AAH19012;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Forward primer used to amplify UCP3 gene exon 2.
 XX
 KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200118232-A2.
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-US024784.
 XX
 PR 08-SEP-1999; 99US-0152789P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA (STEP/) STEPHENS J C.
 XX
 PI Chew A, Choi JY, Denton RR, Nandabalan K;
 XX
 DR WPI; 2001-218562/22.
 XX
 DE Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
 PT useful for the design of drugs for treating obesity.
 XX
 PS Example 1; Page 33; 94pp; English.
 XX
 CC The present invention relates to the human uncoupling protein 3
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
 CC polymorphisms are associated with obesity, especially diabetes mellitus
 CC associated obesity. They polymorphisms may be identified and analysed to
 CC determine whether an individual is susceptible to obesity and may be used
 CC as the basis for targeted design of drugs to treat obesity. The present
 CC sequence was used in the identification and amplification of UCP3
 CC polymorphisms
 XX
 SQ Sequence 23 BP; 3 A; 11 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3202 GAGGCGCTTGAAGAAGTGGG 3221
 Db 23 GAGGCGCTTGAAGAAGGAG 4
 RESULT 2653
 AAF76321/c
 ID AAF76321 standard; DNA; 23 BP.
 XX
 AC AAF76321;
 XX
 DT 05-JUN-2001 (first entry)
 XX
 DE Human TNF α microsatellite marker reverse PCR primer.
 XX
 KW Autoimmune disease; diagnosis; susceptibility; 2-2-4 haplotype;

PD 07-SEP-2001.
 XX 01-MAR-2001; 2001MO-US006466.
 XX 01-MAR-2000; 2000US-0186199P.
 XX (YUSF-) UNIV SOUTH FLORIDA.
 PA Dalton WS, Damiano JS;
 XX WPI; 2001-582112/65.
 XX
 PT Use of bisphosphonate compounds for inhibiting cell adhesion mediated
 PT drug resistance and enhancing efficacy of chemotherapeutic and/or
 PT radiation treatments.
 XX
 XX Example 2; Page 32; 77pp; English.
 PS
 CC This invention relates to the use of bisphosphonate compounds for
 CC inhibiting cell adhesion mediated drug resistance and enhancing efficacy
 CC of chemotherapy and/or radiation therapy in the treatment of cancer by
 CC inhibiting integrin-mediated cell adhesion. Cell adhesion is required by
 CC many normal processes but in some circumstances is undesirable, being
 CC involved in many pathologies. Cancer cell interaction with the
 CC extracellular matrix prevents apoptosis and can result in cell adhesion
 CC mediated drug resistance. This nucleotide sequence represents a primer
 CC used for human alpha4 integrin subunit specific reactions
 CC
 XX
 SQ Sequence 23 BP; 2 A; 9 C; 2 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5729 CTGGCTTCCTTCCCTTC 5748
 |||||
 Db 3 CTGGCTTCCTTCCACTTC 22
 RESULT 2656
 AAC85127
 ID AAC85127 standard; DNA; 23 BP.
 XX
 AC AAC85127;
 XX
 XX 08-MAY-2001 (first entry)
 DT
 XX
 DE R. anatispestifer OmpA gene amplifying primer 4.
 XX
 KM OmpA; outer membrane protein; avian; immunization; poultry; vaccine;
 KM septicemia anserum exsudativa; antibacterial; PCR primer; ss.
 XX
 OS Riemerella anatispestifer.
 XX
 PN WO200104317-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 14-JUL-1999; 99WO-SG0000075.
 XX
 PR 14-JUL-1999; 99WO-SG0000075.
 XX
 PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
 XX
 PI Frey J, Sumathi S;
 XX
 DR WPI; 2001-138355/14.
 XX
 PT New OmpA gene of Riemerella anatispestifer for production of vaccines and
 PT for diagnosing septicemia anserum exsudativa of avian species.
 XX
 PS Disclosure; Page 12; 50pp; English.
 XX

CC The invention relates to a Riemerella anatispestifer outer membrane
 CC protein OmpA. The OmpA protein can be expressed by standard recombinant
 CC methodology. An antibody (Ab) specific to the OmpA polypeptide is useful
 CC for diagnosing an infection by R.anatispestifer in an avian species. The
 CC OmpA gene and protein are useful for the preparation of vaccines and
 CC serodetective diagnostic assays. A vaccine composition comprising the
 CC OmpA gene, protein or Ab is useful for effective immunization of poultry
 CC against R. anatispestifer infection, especially septicemia anserum
 CC exsudativa. Sequences AAC85124-139 represent PCR primers used for
 CC amplifying the R. anatispestifer OmpA gene
 CC
 XX
 SQ Sequence 23 BP; 2 A; 5 C; 2 G; 14 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6459 GGATCTTTTCTTCTGTT 6478
 |||||
 Db 4 GGATCCTTTCTTCTTTT 23
 RESULT 2657
 ABS73976/c
 ID ABS73976 standard; DNA; 23 BP.
 XX
 AC ABS73976;
 XX
 XX 09-DEC-2002 (first entry)
 DT
 XX
 DE Interleukin-3 mutant-associated DNA sequence #1.
 XX
 XX
 KM Interleukin-3; IL-3; ds; haematopoietic cell; haematopoietic disorder;
 KM acute myelogenous leukaemia; AML; bone marrow transplant; neutropaenia;
 KM thrombocytopenia; aplastic anaemia; Chediak-Higashi syndrome;
 KM systemic lupus erythematosus; leukaemia; myelodysplastic syndrome;
 KM myelofibrosis; viral infection; microbial infection; parasitic infection;
 KM stem cell; immune deficiency; immune disorder; rheumatoid arthritis;
 KM leukaemia.
 XX
 OS Unidentified.
 XX
 PN US6440407-B1.
 XX
 PD 27-AUG-2002.
 XX
 PF 09-DEC-1996; 96US-00764114.
 XX
 PR 24-NOV-1992; 92US-00981044.
 PR 22-NOV-1993; 93MO-US011197.
 PR 06-APR-1995; 95US-00411795.
 XX
 PA (SEAR/) SEARLE G D.
 XX
 PI Bauer SC, Abrams MA, Braford-Goldberg SF, Caparon MH, Easton AM,
 PI Klein BK, Mckearn JP, Oline PO, Paik K, Thomas JW;
 XX
 DR WPI; 2002-711523/77.
 XX
 XX Ex vivo expansion of stem cells e.g. hematopoietic stem cells for use in
 PT treating hematopoietic disorders, comprises culturing the cells in medium
 PT having human interleukin-3 mutant polypeptide and harvesting cultured
 PT cells.
 XX
 PS Disclosure; Col 21; 215pp; English.
 XX
 CC The invention relates to ex vivo expansion of stem cells, comprises
 CC culturing stem cells with a growth medium comprising a human interleukin-
 CC 3 (IL-3) mutant polypeptide or a polypeptide comprising an N-terminal
 CC methionine residue, alanine residue or methionine-alanine di-peptide
 CC preceding the IL-3 sequence, and harvesting the cultured stem cells. Also
 CC include are enhancing the efficiency of the transduction of cultured stem
 CC cells by a heterologous gene, comprising: (a) culturing the stem cells


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Query Match      0.2%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

5476 TTTTGTAAAAGATTAATTTT 5495

23 TTTTGGGAAGAAATTTT 4

RESULT 2660
ABZ57960
ABZ57960 standard; DNA; 23 BP.

C ABZ57960 ;

T 14-APR-2003 (first entry)

Human respiratory chemokine receptor forward PCR primer.

W G-protein coupled receptor; GPCR; receptor; chemokine; human; antiasthmatic; antiinflammatory; antitussive; vaccine; PCR; primer; ss

S Homo sapiens.

N WO2003002604-A2.

D 09-JAN-2003.

25-JUN-2002; 2002WO-EP007021.

26-JUN-2001; 2001US-0300944P.

A (NOVS) NOVARTIS AG.

(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

I Bhatia U, Jones CE, Bouhelal R, Seuwen K, Tenalllon L,

WPI; 2003-210243/20.

TT New polypeptide, useful for diagnosing or treating e.g., asthma, chronic obstructive pulmonary disease, emphysema, chronic bronchitis or acute respiratory distress syndrome.

Example 7; Page 44; 44pp; English.

The present sequence is a forward primer for a polynucleotide encoding a novel human G-protein coupled receptor (GPCR) that has been characterised as a respiratory chemokine receptor. RT-PCR was used to determine expression levels of the GPCR in different tissues. The receptor was expressed in respiratory tissues and tissues related to monocytic/macrophage migration/activation, airway remodeling, airway fibrosis, regulation of epithelial differentiation, regulation of mucus hypersecretion, regulation of mucociliary clearance, regulation of inflammation, modulation of neutrophil, T-cell and eosinophil migration and/or activation, and regulation of epithelial cell or mast cell activation. GPCR polypeptides (see ABP5845-53) and polynucleotides (see AB257956-57) of the invention may be useful in treatment of asthma, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, acute respiratory distress syndrome, cough and acute bronchitis, in diagnostic assays, and as vaccines.

Q Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match	0.2%;	Score 15.2;	DB 1;	Length 23;
Best Local Similarity	85.0%;	Pred. No. 2e+03;		
Matches 17;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

1189 CTACAACTTGGCCAGGACA 1208

b 3 CTTCA CGTGGCCATGACA 22

RESULT 2661
ADC03090/c
ID ADC03090 standard; DNA; 23 BP.

AC ADC03090;

DT 18-DEC-2003 (first entry)

DE Ex vivo stem-cell expansion related polynucleotide #1.

KM cyrostatic; antihaemic; immunomodulator; immunostimulant;
KM immunosuppressive; antiinflammatory; interleukin agonist 3;
KM interleukin antagonist 3; gene therapy; ex vivo expansion of stem cell;
KM modified human interleukin-3; cell proliferation;
KM acute myelogenous leukaemia cell proliferation; TF-1 cell proliferation;
KM methylcellulose assay; haematopoietic disorder; cancer;
KM acute myelogenous leukaemia; B lymphoid cancer; leukopenia; neutropenia;
KM aplastic anaemia; Chedak-Hisashi's syndrome;
KM systemic lupus erythematosus; myelodysplastic syndrome; myelofibrosis;
KM bone marrow; blood cell activation; blood cell growth; ds-

OS Synthetic

PN US6479261-B1.

PD 12-NOV-2002

PF 15-NOV-1995; 95US-00559390.

PR 24-NOV-1992; 92US-00981044.

PR 06-APR-1995; 95US-00411796.

PA (PHAA) PHARMACIA CORP.

PA (PHAA) PHARMACIA CORP.

PI Bauer SC, Abrams MA, Bratford-Goldberg SR, Caparon MH, Easton AM
PI Klein BK, McKearn JP, Olins P, Paik K, Polazzi J, Thomas JW;

DR WPI; 2003-655574/62.

PT Selective ex vivo expansion of stem cells, useful for treating a patient
PT having hematopoietic disorder, e.g. leukemia, neutropenia or aplastic
PT anemia, comprises using recombinant human interleukin-3 variant or mutant
PT proteins.

PS Example 1; SEQ ID NO 1; 288pp; English

The invention describes selective ex vivo expansion of stem cells comprising separating stem cells from other cells, culturing the cells with modified human interleukin-3 polypeptide with at least 3 times greater cell proliferative activity than native human interleukin-3 in at least one assay selected from the group of acute myelogenous leukaemia cell proliferation, T-1 cell proliferation, and methylcellulose assay, ex and harvesting the cultured cells. The method is useful for selective ex vivo expansion of stem cells. The recombinant human interleukin-3 variant or mutant proteins are useful for treating a patient having a haematopoietic disorder, such as cancer (e.g. acute myelogenous leukaemia or certain types of B lymphoid cancer), leukopenia, neutropenia, aplastic anaemia, Chediak-Higashi's syndrome, systemic lupus erythematosus, myelodysplastic syndrome, or myelofibrosis. The interleukin-3 muteins are also useful as antagonists for producing antibodies used in immunoassay and immunotherapy protocols, or for stimulating bone marrow and blood cell activation and growth before infusion into patients. This sequence represents an ex vivo stem cell expansion method associated polynucleotide.

SQ Sequence 23 BP; 6 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match	0.2%	Score 15.2	DB 1	Length 23
Best Local Similarity	85.0%	Pred. No. 2e+03		
Matches 17	Conservative 0	Mismatches 3	Indels 0	Gaps 0

3735 AGCTTTTAAAGATCACA 3754

Db 21 AGCTTATTAAAGATCGCTA 2

RESULT 2662
 ADC02390/c
 ID ADC02390 standard; DNA; 23 BP.

AC ADC02390;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX
 DE Ex vivo stem cell expansion related polynucleotide #1.

antianaemic; immunomodulator; dermatological; antiinflammatory;
 immunosuppressive; cytostatic; haemostatic; antithrombotic; antiarthritic;
 osteopathic; gene therapy; cell therapy; ex vivo expansion; stem cell;
 human interleukin-3 mutant; htl-3 mutant; haematopoietic disorder;
 aplastic anaemia; Chediak-Higashi syndrome; systemic lupus erythematosus;
 leukaemia; myelodysplastic syndrome; myelofibrosis; neutropenia;
 thrombocytopenia; radiation; chemotherapy; bone marrow suppression;
 haematopoietic deficiency; azidothymidine; AZT; alkylating agent;
 chloramphenicol; rheumatoid arthritis; immune disorder; infection; ds.

OS Synthetic.
 XX
 XX US2003103936-A1.
 PN
 XX
 PD 05-JUN-2003.
 XX
 XX 04-MAR-2002; 2002US-00090182.
 PF
 XX 24-NOV-1992; 92US-00981044.
 PR 22-NOV-1993; 93WO-US011197.
 PR 06-APR-1995; 95US-00411795.
 PR 09-DEC-1996; 96US-00764114.

XX
 PA (BAUER/) BAUER S. C.
 PA (ABRA/) ABRAMS M. A.
 PA (BRAFO/) BRAFORD-GOLDBERG S. R.
 PA (CAPA/) CAPARON M. H.
 PA (EAST/) EASTON A. M.
 PA (KLEI/) KLEIN B. K.
 PA (MCKE/) MCKEARN J. P.
 PA (OLIN/) OLINS P. O.
 PA (PAIK/) PAIK K.
 PA (THOM/) THOMAS J. W.

XX
 PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM,
 PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
 XX WPI; 2003-678181/64.
 DR
 XX
 XX Ex vivo expansion of stem cells (e.g. hematopoietic cells) for gene
 PT therapy, e.g. using expanded stem cells for treating thrombocytopenia, by
 PT culturing the cells in a growth medium containing a variant or mutant of
 PT human interleukin-3.
 PT
 XX
 XX Disclosure; SEQ ID NO 1; 242pp; English.

The invention describes ex vivo expansion of stem cells comprising
 CC culturing the stem cells with a growth medium containing a human
 CC interleukin-3 (hIL-3) mutant polypeptide. The hIL-3 mutant polypeptide
 CC has a 133, 111, 133 or 111 amino acid sequence (designated hIL-3a, hIL-
 CC 3b, hIL-3c and hIL-3d, respectively), given in the specification. The
 CC method is useful for ex vivo expansion of stem cells for gene therapy.
 CC The expanded stem cells are useful for treating patients with a
 CC hematopoietic disorder e.g. aplastic anaemia, Chediak-Higashi syndrome,
 CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome,
 CC myelofibrosis, neutropenia or thrombocytopenia. The method is
 CC particularly useful for ex vivo expansion of hematopoietic cells for use
 CC in: (a) restoring hematopoietic cells to normal amounts in those cases
 CC where the number of cells has been reduced due to diseases or to

therapeutic treatments (e.g. radiation or chemotherapy); (b) preventing
 CC or treating bone marrow suppression or haematopoietic deficiencies, which
 CC occur in patients treated with e.g. azidothymidine (AZT), alkylating
 CC agents or chloramphenicol; or (c) treating rheumatoid arthritis or other
 CC immune disorders resulting from viral, microbial or parasitic infection.
 CC This sequence represents an ex vivo stem cell expansion method associated
 CC polynucleotide.

XX
 XX Sequence 23 BP; 6 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3735 AGCTTTTAAAGATCAACA 3754
 Db 21 AGCTTATTAAAGATCGCTA 2

RESULT 2663
 ADE27638/c
 ID ADE27638 standard; RNA; 23 BP.

AC ADE27638;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX
 DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:582.

short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
 stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
 antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
 atherosclerosis; cancer; viral infection; drug screening;
 genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic.
 XX
 XX WO2003070885-A2.
 PN
 XX
 PD 28-AUG-2003.
 XX
 XX 13-FEB-2003; 2003WO-US004317.
 PF
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409233P.
 PR 20-SEP-2002; 2002US-0412304P.
 PR 15-JAN-2003; 2003US-0440129P.

XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswigen J, Beigelman L, Thompson J;
 PI WPI; 2003-721687/68.
 DR
 XX
 XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of obesity or diabetes, downregulates expression of the
 PT stearoyl-CoA desaturase gene.
 PT
 XX
 XX Example 3; SEQ ID NO 582; 139pp; English.

The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
 CC by RNA interference. Also described: (1) modulating expression of SCD
 CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
 CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
 CC virucide activities. The siNAs can be used to modulate expression of SCD
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
 CC They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents an SCD sRNA, which is
 CC used in the exemplification of the present invention.

XX Sequence 23 BP; 7 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7230 TATCCCTCTCAAGTCCAGCA 7249

DB 22 TCTCCATCTCATGTCAGCA 3

RESULT 2664

AAFe2506
 ID AAF62506 standard; DNA; 24 BP.

XX AAF62506;

DT 08-MAY-2001 (first entry)

DE Primer #5.

XX Guanosine 5'-diphosphofucose; GDP-fucose;

KM Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDM; immunotherapy;

KM cardiovascular; infection; ss.

OS Synthetic.

XX EPI076096-A1.

PD 14-FEB-2001.

PF 10-AUG-2000; 2000EP-00117167.

PR 10-AUG-1999; 99JP-00225889.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;

DR WPI; 2001-193203/20.

XX Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a substrate

PT of complex carbohydrates for immunotherapy comprises employing

PT microorganisms that convert guanosine 5'-diphospho-4-keto-6-deoxymannose

PS to GDP-fucose.

XX Example 2; Page 12; 19pp; English.

XX The present invention relates to producing guanosine 5'-diphosphofucose

CC (GDP-fucose) by employing an enzyme source that is a culture broth of

CC microorganisms. GDP-fucose is useful as a synthetic substrate of complex

CC carbohydrates that are useful e.g. for immunotherapy for protection

CC against cardiovascular diseases, or infections by bacteria or viruses.

CC Guanosine 5'-diphospho-4-keto-6-deoxymannose (GKDM) is useful as an

CC intermediate for the production of GDP-fucose

XX Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 24;
 Best Local Similarity 85.0%; Pred. No. 2.1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2665

AAH46618
 ID AAH46618 standard; DNA; 24 BP.

XX AAH46618;

DT 17-SEP-2001 (first entry)

DE Synthetic oligonucleotide #21.

XX Helicobacter pylori; alpha-1,2-fucosyltransferase;

KM fucose-containing sugar production; Lewis antigen; ss.

OS Synthetic.

XX WO200146400-A1.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-JP009033.

PR 21-DEC-1999; 99JP-00362243.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Endo T, Koizumi S, Tabata K, Ozaki A;

DR WPI; 2001-418061/44.

XX Modified alpha-1,2-fucosyltransferase gene and its expression product for

PT efficient production of fucose-containing sugars such as Lewis antigen.

PS Example 3; Page 63; 63pp; Japanese.

XX The invention relates to DNA encoding a modified form of the alpha-1,2-

CC fucosyltransferase of Helicobacter pylori. The polycytosine sequence, the

CC AAAAAG sequence and/or the number of TAA repeats has been modified in

CC the DNA sequence. The modified gene is useful in the production of large

CC amounts of fucose-containing sugars, such as Lewis antigens for medicinal

CC use. The present sequence is an oligonucleotide provided in the

XX specification

XX Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 24;
 Best Local Similarity 85.0%; Pred. No. 2.1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3109 AAGACTCATGCTTGACAGCT 3128

DB 5 AATTCATCTGTTTGACAGCT 24

RESULT 2666

ABA03363
 ID ABA03363 standard; DNA; 24 BP.

XX ABA03363;

DT 12-FEB-2002 (first entry)

DE B alpha1,2-fucosyltransferase coding sequence related DNA #7.

XX Alpha1,2-fucosyltransferase; fucose-containing carbohydrate; cytostatic;

KM virucide; antibacterial; microbial infection; anticancer; tumour marker;

OS Synthetic.

XX WO200177313-A1.

PD 18-OCT-2001.

```
XX 11-APR-2001; 2001WO-JP003109.
PP
XX
XX 11-APR-2000; 2000JP-00109148.
PR
XX (KYOM ) KYOMA HAKKO KOGYO KK.
PA
XX
XX Endo T, Koizumi S;
PI
XX WPI; 2002-034238/04.
DR
XX Expression of approximately 1,2 fucosyltransferase producing fucose-
PT containing complex carbohydrates as preventives or remedies of e.g.
PT microbial infections, comprises using a transformation procedure.
XX
XX Disclosure; Page 52; 56pp; Japanese.
PS
XX
XX The present invention relates to a method of producing a fucose-
CC containing complex carbohydrate, involving using a culture of a
CC transformant expressing a protein with Bacteroides-originate alpha1,2-
CC fucosyltransferase as enzyme source, receptor complex carbohydrate and
CC guanosine diphosphate fucose in an aqueous medium to transfer fucose to
CC the receptor complex carbohydrate to accumulate the product for
CC isolation. The resulting carbohydrates can be used as preventives or
CC remedies of microbial infections, as tumour markers and as anticancer
CC drugs. The present sequence is an oligonucleotide described in the
CC exemplification of the invention
XX
XX Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3109 AAGACTGATGCTTGACAGCT 3128
Db |||||
5 AATTCATGTTGACAGCT 24
RESULT 2667
AAF74926
ID AAF74926 standard; DNA; 27 BP.
XX
XX AAF74926;
AC
XX 23-MAY-2001 (first entry)
DT
XX
XX CD40L poly-A tract sequence SEQ ID NO:23.
DE
XX
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
KW antinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200119844-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 13-SEP-2000; 2000WO-US024966.
PF
XX
XX 13-SEP-1999; 99US-0153625P.
PR
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA
XX
XX Crow MK, Li Y;
PI
XX WPI; 2001-244776/25.
DR
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
```

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PS Example 1; Fig 3; 90pp; English.
XX
XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C (I) has antiarthritis;
CC antirheumatic, immunosuppressive and antinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
XX Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 27;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4020 AAAAAAGAGGAAAAACAAA 4039
Db |||||
1 AAAAAAACAACAAA 20
RESULT 2668
AAF74932
ID AAF74932 standard; DNA; 27 BP.
XX
XX AAF74932;
AC
XX 23-MAY-2001 (first entry)
DT
XX
XX CD40L poly-A tract sequence SEQ ID NO:29.
DE
XX
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
KW antinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200119844-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 13-SEP-2000; 2000WO-US024966.
PF
XX
XX 13-SEP-1999; 99US-0153625P.
PR
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA
XX
XX Crow MK, Li Y;
PI
XX WPI; 2001-244776/25.
DR
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
XX Example 1; Fig 3; 90pp; English.
PS
XX
XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritis;
CC antirheumatic, immunosuppressive and antinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
```

SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 0.24; Score 15.2; DB 1; Length 27;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4020 AAAAAAGAGAAAAACAAA 4039
 Db 1 AAAAAAAAAAAAAACAAA 20
 RESULT 2669
 AAF74931
 ID AAF74931 standard; DNA; 27 BP.
 AC AAF74931;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:28.
 XX
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200119844-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US024966.
 XX
 PR 13-SEP-1999; 99US-0153625P.
 XX
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX
 PI Crow MK, Li Y;
 XX
 DR WPI; 2001-244776/25.
 XX
 PT New altered CD40L promoter for use in the study, diagnosis and treatment
 of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX
 PS Example 1; Fig 3; 90pp; English.
 XX
 CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritis.
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 CC
 SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 0.24; Score 15.2; DB 1; Length 27;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4020 AAAAAAGAGAAAAACAAA 4039
 Db 1 AAAAAAAAAAAAAACAAA 20
 RESULT 2670
 AAF74934
 ID AAF74934 standard; DNA; 27 BP.

XX
 AC AAF74934;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:31.
 XX
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200119844-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US024966.
 XX
 PR 13-SEP-1999; 99US-0153625P.
 XX
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX
 PI Crow MK, Li Y;
 XX
 DR WPI; 2001-244776/25.
 XX
 PT New altered CD40L promoter for use in the study, diagnosis and treatment
 of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX
 PS Example 1; Fig 3; 90pp; English.
 XX
 CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritis.
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 CC
 SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 0.24; Score 15.2; DB 1; Length 27;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4020 AAAAAAGAGAAAAACAAA 4039
 Db 1 AAAAAAAAAAAAAACAAA 20
 RESULT 2671
 AAF74920
 ID AAF74920 standard; DNA; 28 BP.
 AC AAF74920;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:17.
 XX
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200119844-A1.

XX 22-MAR-2001.
 PD 13-SEP-2000; 2000WO-US024966.
 PF 13-SEP-1999; 99US-0153625P.
 XX (NPRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 PA Crow MK, Li Y;
 PI WPI; 2001-244776/25.
 DR New altered CD40L promoter for use in the study, diagnosis and treatment
 XX of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 PS Example 1; Fig 3; 90pp; English.
 XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 28;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4020 AAAAAAGAGAAAAACAAA 4039
 |||||
 Db 2 AAAAAAAGAAAAAAGAAAAA 21
 RESULT 2672
 AAF74906
 ID AAF74906 standard; DNA; 28 BP.
 XX AAF74906;
 XX 23-MAY-2001 (first entry)
 DT CD40L poly-A tract sequence SEQ ID NO:3.
 XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX Homo sapiens.
 OS WO200119844-A1.
 PN 22-MAR-2001.
 XX 13-SEP-2000; 2000WO-US024966.
 PF 13-SEP-1999; 99US-0153625P.
 XX (NPRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 PA Crow MK, Li Y;
 PI WPI; 2001-244776/25.
 DR New altered CD40L promoter for use in the study, diagnosis and treatment
 XX of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.

PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 PS Example 1; Fig 3; 90pp; English.
 XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15.2; DB 1; Length 28;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4020 AAAAAAGAGAAAAACAAA 4039
 |||||
 Db 2 AAAAAAAGAAAAAAGAAAAA 21
 RESULT 2673
 AAF74916
 ID AAF74916 standard; DNA; 28 BP.
 XX AAF74916;
 XX 23-MAY-2001 (first entry)
 DT CD40L poly-A tract sequence SEQ ID NO:13.
 XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX Homo sapiens.
 OS WO200119844-A1.
 PN 22-MAR-2001.
 XX 13-SEP-2000; 2000WO-US024966.
 PF 13-SEP-1999; 99US-0153625P.
 XX (NPRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 PA Crow MK, Li Y;
 PI WPI; 2001-244776/25.
 DR New altered CD40L promoter for use in the study, diagnosis and treatment
 XX of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 PS Example 1; Fig 3; 90pp; English.
 XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis.

CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 XX
 XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 SO
 Query Match 0.2%; Score 15.2; DB 1; Length 28;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 4020 AAAAAAGAGAAAAACAAA 4039
 Db 2 AAAAAAAAAAAAAAAAAACAAA 21

RESULT 2674
 AAF74927
 ID AAF74927 standard; DNA; 28 BP.
 XX
 AC AAF74927;
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:24.
 XX
 KM Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antirheumatic; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200119844-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US024966.
 XX
 PR 13-SEP-1999; 99US-0153625P.
 XX
 PA (NYRE-) NEW YORK SOC RELIUF RUPTURED & CRIPPLED.
 XX
 PI Crow MK, Li Y;
 XX
 DR WPI; 2001-244776/25.
 XX
 PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX
 PS Example 1; Fig 3; 90pp; English.
 XX
 CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antirheumatic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities,
 CC can be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 XX
 SO Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 28;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 4020 AAAAAAGAGAAAAACAAA 4039
 Db 2 AAAAAAAAAAAAAAAAAACAAA 21

RESULT 2675
 AAQ93201/c
 ID AAQ93201 standard; DNA; 29 BP.
 XX
 AC AAQ93201;
 XX
 DT 24-FEB-1996 (first entry)
 XX
 DE C. perfringens beta 1 toxin PCR primer Betatoxl.
 XX
 KM Enterotoxin; beta 1 toxin; food poisoning; faeces; contamination;
 KM Clostridium perfringens; polymerase chain reaction; primer; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN W09517521-A2.
 XX
 PD 29-JUN-1995.
 XX
 PF 22-DEC-1994; 94WO-EP004292.
 XX
 PR 22-DEC-1993; 93US-00172026.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNEVA-) CNEVA CENT NAT ETUD VETERINAIRES & ALIME.
 XX
 PI Fach P, Guillou J, Popoff M;
 XX
 DR WPI; 1995-240681/31.
 XX
 PT New primers for amplification of Clostridium perfringens toxin genes -
 PT and new beta 2 toxin gene, used to detect and quantify C. perfringens in
 PT e.g. food and faecal samples.
 XX
 PS Example 7; Page 28; 43pp; English.
 XX
 CC The presence of beta 1 and beta 2 toxin genes was examined by PCR in a
 CC series of type B and C Clostridium perfringens strains. For beta 2 gene
 CC amplification, primers P319 and P320 (AAQ93199-200) were used; primers
 CC Betatoxl and Betatoxr (AAQ93201-02) were used for the beta 1 gene. The 3
 CC B strains examined possessed the beta 1 gene. Type C strains had either
 CC the beta 2 gene, or the beta 1 gene, or both
 XX
 SO Sequence 29 BP; 5 A; 0 C; 6 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15.2; DB 1; Length 29;
 Best Local Similarity 71.4%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 OY 7017 CTTACGAGGAAATAGGAAACCTCC 7044
 Db 29 CTTCAAAAAAAAAATTAATAAAACCTCC 2

RESULT 2676
 AAQ20018/c
 ID AAQ20018 standard; DNA; 15 BP.
 XX
 AC AAQ20018;
 XX
 DT 01-APR-1992 (first entry)
 XX
 DE Cross-linking agent 132 binds to HIV target DNA.
 XX
 KM deoxyribonucleic acid; major groove; ethanoamino group;
 KM aziridinylcytosine; cross-linking group; human immunodeficiency virus;
 KM ss.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FH modified_base 2
 FT /*tag= a

```

FT      modified_base      /mod_base= m5c
FT      /*tag= b
FT      /mod_base= m5c
FT      modified_base      /tag= c
FT      /mod_base= m5c
FT      modified_base      /*tag= d
FT      /mod_base= m5c
FT      modified_base      /*tag= e
FT      /mod_base= OTHER
FT      /note= "NA4-ethanocytosine"
XX
XX      W09118997-A.
XX
XX      12-DEC-1991.
XX
XX      25-MAY-1990; 90US-00529346.
XX
XX      25-MAY-1990; 90US-00529346.
XX      25-MAY-1990; 90US-00529346.
XX      14-JAN-1991; 91US-00640654.
XX
XX      (GILE-) GILEAD SCIE INC.
XX
XX      Matteucci MD, Krawczyk S;
XX
XX      WPI; 1992-007480/01.
XX
XX      New sequence-specific non-photo-activated crosslinking agents - bind to
XX      the major groove of duplex DNA and are esp. useful for treating latent
XX      infections e.g. HIV.
XX
XX      Example 4; Page 24; 42pp; English.
XX
XX      This sequence is designed to bind to the HIV target sequence 5'-
XX      AGAGAGAAAAAGAG-3' and to covalently cross-link to it via the NA4-
XX      ethanocytosine (aziridiny1) group. See also AAQ20009-Q20025
XX
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4017 GAGAAAAAAGAGAGA 4031
Db      15 GAGAAAAAAGAGAGA 1
RESULT 2677
AAQ20017/C
ID      AAQ20017 standard; DNA; 15 BP.
XX
XX      AAQ20017;
XX
XX      01-APR-1992 (first entry)
XX
XX      Cross-linking agent 131 binds to HIV target DNA.
XX
XX      deoxyribonucleic acid; major groove; ethanoino group;
XX      aziridiny1cytosine; cross-linking group; human immunodeficiency virus;
XX      ss.
XX
XX      Synthetic.
XX
XX      Key
XX      modified_base      Location/Qualifiers
XX      /*tag= a
XX      /mod_base= m5c
XX      modified_base      4
XX      /*tag= b

```

```

FT      modified_base      /mod_base= m5c
FT      /*tag= c
FT      /mod_base= m5c
FT      modified_base      /tag= d
FT      /mod_base= m5c
FT      modified_base      /*tag= e
FT      /mod_base= m5c
XX
XX      W09118997-A.
XX
XX      12-DEC-1991.
XX
XX      25-MAY-1990; 90US-00529346.
XX
XX      25-MAY-1990; 90US-00529346.
XX      25-MAY-1990; 90US-00529346.
XX      14-JAN-1991; 91US-00640654.
XX
XX      (GILE-) GILEAD SCIE INC.
XX
XX      Matteucci MD, Krawczyk S;
XX
XX      WPI; 1992-007480/01.
XX
XX      New sequence-specific non-photo-activated crosslinking agents - bind to
XX      the major groove of duplex DNA and are esp. useful for treating latent
XX      infections e.g. HIV.
XX
XX      Example 4; Page 24; 42pp; English.
XX
XX      This sequence is designed to bind to the HIV target sequence 5'-
XX      AGAGAGAAAAAGAG-3'. See also AAQ20009-Q20025
XX
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4017 GAGAAAAAAGAGAGA 4031
Db      15 GAGAAAAAAGAGAGA 1
RESULT 2678
AAQ33752
ID      AAQ33752 standard; DNA; 15 BP.
XX
XX      AAQ33752;
XX
XX      25-MAR-2003 (revised)
XX      02-FEB-1993 (first entry)
XX
XX      Microsatellite sequence from clone TGLA162.
XX
XX      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX      genetic mapping; traits; amplification; ss.
XX
XX      Bos taurus.
XX
XX      W09213102-A1.
XX
XX      06-AUG-1992.
XX
XX      15-JAN-1992; 92MO-US000340.
XX      15-JAN-1991; 91US-00642342.
XX      (GENM-) GENMARK.
XX      George M, Massey JM;
PI

```



```

XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 231; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine Mbol DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100,000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX CC specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX CC required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX CC economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 15 BP; 5 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7415 GCACGACGACGACGA 7429
Db 1 GCACGACGACGACGA 15
RESULT 2679
AAQ30250/C
ID AAQ30250 standard; DNA; 15 BP.
XX AC AAQ30250;
XX DT 25-MAR-2003 (revised)
XX DT 07-DEC-1992 (first entry)
XX DE Oligomer HIV132 for forming triplex with HIV target duplex.
XX KW Human immunodeficiency virus; AIDS; modified; HIV; hepatitis; herpes;
XX KW hepatitis; malignancy; inflammation; ss.
XX OS Synthetic.
XX FH Key
XX FH modified_base 2 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= m5c
XX FT modified_base 4 /*tag= b
XX FT /mod_base= m5c
XX FT modified_base 6 /*tag= c
XX FT /mod_base= m5c
XX FT modified_base 13 /*tag= d
XX FT /mod_base= m5c
XX FT modified_base 15 /*tag= e
XX FT /mod_base= OTHER
XX FT /note= "OTHER= N4 N4 ethanocytosine"
XX PN WO9209705-A1.
XX PD 11-JUN-1992.

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XX PF 25-NOV-1991; 91WO-US008811.
XX PR 23-NOV-1990; 90US-00617907.
XX PR 18-JUN-1991; 91US-0064382.
XX PR 08-APR-1991; 91US-00683420.
XX PR 17-APR-1991; 91US-0068544.
XX PR 17-APR-1991; 91US-0068546.
XX PR 17-APR-1991; 91US-0068547.
XX PR 27-SEP-1991; 91US-00766733.
XX PA (GILE-) GILEAD SCI INC.
XX PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX DR WPI; 1992-217083/26.
XX PT New oligomers contg. modified bases - which form a triplex with G-C
XX PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX PT herpes malignancy and inflammation.
XX PS Claim 12; Page 65; 77pp; English.
XX CC The synthetic oligomer is capable of forming a triplex at physiological
XX CC pH with a purine rich target sequence by coupling into the major groove
XX CC of the duplex. The specific target sequence of this oligomer is an HIV
XX CC target duplex confg. a purine-rich region concentrated on one chain of
XX CC the duplex. The oligomer, and others like it are useful in diagnosis and
XX CC therapy of diseases characterised by specific DNA duplex targets, e.g.
XX CC HIV, hepatitis, herpes, malignant tumours and inflammation. The triple
XX CC helices form under mild conditions thus assays may be carried out without
XX CC subjecting the test specimen to harsh conditions. Additional
XX CC modifications, such as altered inter- nucleotide linkages may also be
XX CC incorporated, rendering the oligomer e.g. stable to nuclease activity.
XX CC The oligomer is able to inhibit gene expression, as verified by in vitro
XX CC systems. See also AAQ25452-25501 and AAQ3026-448. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
SQ Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4017 GAGAAAAAAGAGAGA 4031
Db 15 GAGAAAAAAGAGAGA 1
RESULT 2680
AAQ30249/C
ID AAQ30249 standard; DNA; 15 BP.
XX AC AAQ30249;
XX DT 25-MAR-2003 (revised)
XX DT 07-DEC-1992 (first entry)
XX DE Oligomer HIV131 for forming triplex with HIV target duplex.
XX KW Human immunodeficiency virus; AIDS; modified; HIV; hepatitis; herpes;
XX KW hepatitis; malignancy; inflammation; ss.
XX OS Synthetic.
XX FH Key
XX FH modified_base 2 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= m5c
XX FT modified_base 4 /*tag= b
XX FT /mod_base= m5c
XX FT modified_base 6

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FT      /*tag= c
FT      /mod_base= m5c
FT      modified_base
FT      13
FT      /*tag= d
FT      /mod_base= m5c
FT      modified_base
FT      15
FT      /*tag= e
FT      /mod_base= m5c
XX
XX      W09209705-A1.
XX
XX      11-JUN-1992.
XX
XX      25-NOV-1991; 91WO-US008811.
XX
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00686544.
XX      17-APR-1991; 91US-00686546.
XX      17-APR-1991; 91US-00686547.
XX      27-SEP-1991; 91US-007676733.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Proehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX
XX      Claim 12; Page 65; 77pp; English.
XX
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is an HIV
XX      target duplex contg. a purine-rich region concentrated on one chain of
XX      the duplex. The oligomer, and others like it are useful in diagnosis and
XX      therapy of diseases characterised by specific DNA duplex targets, e.g.
XX      HIV, hepatitis, herpes, malignant tumours and inflammation. The triple
XX      helices form under mild conditions thus assays may be carried out without
XX      subjecting the test specimen to harsh conditions. Additional
XX      modifications, such as altered inter-nucleotide linkages may also be
XX      incorporated, rendering the oligomer e.g. stable to nuclease activity.
XX      The oligomer is able to inhibit gene expression, as verified by in vitro
XX      systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-
XX      2003 to correct PN field.)
XX
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4017 GAGAAAAAAGAGAGA 4031
DB      15 GAGAAAAAAGAGAGA 1
RESULT 2681
AAQ79185/c
ID      AAQ79185 standard; DNA; 15 BP.
XX
XX      AAQ79185;
XX
XX      25-MAR-2003 (revised)
XX      21-JUN-1995 (first entry)
XX
XX      Nuclease resistant oligonucleotide.
XX
XX      Nuclease resistant oligonucleotide; inhibition of gene expression;

```

```

KM      9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX      Synthetic.
XX
XX      Key
XX      modified_base
XX      13
XX      Location/Qualifiers
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "9-methyl-acyclo-adenosine"
XX
XX      W09422864-A1.
XX
XX      13-OCT-1994.
XX
XX      21-MAR-1994; 94WO-US002995.
XX
XX      30-MAR-1993; 93US-00040326.
XX
XX      (STER ) STERLING WINTHROP INC.
XX
XX      Cook PD, Delecki DJ, Guinasso C;
XX      WPI; 1994-333078/41.
XX
XX      New acyclic nucleoside analogues - used to prepare nuclease resistant
XX      oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
XX      Example 11; Page 20; 37pp; English.
XX
XX      AAQ79182-079186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX      nucleoside analogues which inhibit nuclease degradation. The nuclease
XX      resistant oligonucleotides can themselves be used to inhibit gene
XX      expression as antisense agents, in nucleic acid sequencing and diagnostic
XX      assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4464 TTTT TTTT TTTT TTTT 4478
DB      15 TTTT TTTT TTTT TTTT 1
RESULT 2682
AAQ79184/c
ID      AAQ79184 standard; DNA; 15 BP.
XX
XX      AAQ79184;
XX
XX      25-MAR-2003 (revised)
XX      21-JUN-1995 (first entry)
XX
XX      Nuclease resistant oligonucleotide.
XX
XX      Nuclease resistant oligonucleotide; inhibition of gene expression;
XX      9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
XX      Synthetic.
XX
XX      Key
XX      modified_base
XX      14
XX      Location/Qualifiers
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "9-methyl-acyclo-adenosine"
XX
XX      W09422864-A1.
XX
XX      13-OCT-1994.
XX
XX      21-MAR-1994; 94WO-US002995.

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XX 30-MAR-1993; 93US-00040326.
XX (STER ) STERLING WINTHROP INC.
XX Cook PD, Delecki DJ, Guinasso C;
XX WPI, 1994-333078/41.
XX New acyclic nucleoside analogues - used to prepare nuclease resistant
XX oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX Example 10; Page 20; 37pp; English.
XX AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX nucleoside analogues which inhibit nuclease degradation. The nuclease
XX resistant oligonucleotides can themselves be used to inhibit gene
XX expression as antisense agents, in nucleic acid sequencing and diagnostic
XX assays. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 15 TTTT TTTT TTTT TTTT 1
RESULT 2683
AAT52136
ID AAT52136 standard; RNA; 15 BP.
XX
XX AAT52136;
AC
AC 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICM hammerhead ribozyme target sequence (nt. position 2910).
DE
DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KM gene expression; downregulation; interleukin-5; IL-5; ICM-1;
KM intercellular adhesion molecule; rel A; tumour necrosis factor;
KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KM Philadelphia chromosome; myelogenous leukaemia; CML; cancer;
KM atherosclerosis; myocardial infarction; autoimmune disease;
KM transplant rejection; rheumatoid arthritis; psoriasis;
KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KM human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KM ss.
XX
XX Homo sapiens.
OS
XX ID AAT52138 standard; RNA; 15 BP.
XX
XX W09523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.

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PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 94US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowtra B, Dizenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpelsky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Belgelman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Ueman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICM-1 target sequences and thereby
XX inhibit ICM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 UUUUUUUUUUUUUU 15
RESULT 2684
AAT52138
ID AAT52138 standard; RNA; 15 BP.
XX
XX AAT52138;
AC
AC 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICM hammerhead ribozyme target sequence (nt. position 2911).
DE
DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KM gene expression; downregulation; interleukin-5; IL-5; ICM-1;
KM intercellular adhesion molecule; rel A; tumour necrosis factor;
KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KM Philadelphia chromosome; myelogenous leukaemia; CML; cancer;
KM atherosclerosis; myocardial infarction; autoimmune disease;
KM transplant rejection; rheumatoid arthritis; psoriasis;
KM

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KV myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 XX ss.
 XX Homo sapiens.
 XX OS
 XX M09523225-A2.
 XX PN
 XX 31-AUG-1995.
 PD
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 PF
 XX 23-FEB-1994; 94US-00201109.
 XX 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00324847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DF, Chowrira B, Drenzo A, Draper KG, Dudycz LM;
 PI Grimm S, Pavlosky A, Kleich K, Matulic-Adamic J, McGwisgen JA;
 PI Modak A, Pavco P, Beggelman L, Sullivan SM, Svedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Wolff T;
 XX
 XX WPI; 1995-351090/45.
 DR
 XX
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX
 XX
 XX Claim 2; Page 175; 407pp; English.
 PS
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
 SQ
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 XX Best Local Similarity 0.0%; Pred. No. 1.3e+03;
 XX Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
 OY 4464 TTTT TTTT TTTT TTTT 4478

DB 1 UUUUUUUUUUUUUU 15
 RESULT 2685
 AAV06037
 ID AAV06037 standard; DNA; 15 BP.
 XX
 XX AAV06037;
 AC
 XX 25-MAR-2003 (revised)
 DT 08-APR-1998 (first entry)
 XX
 XX Oligonucleotide-anthracycline or anthracycline conjugate #3.
 DE Anthracycline conjugate; anthracycline; triple-helix; tumour; virus;
 KW intercalation; ss.
 KW
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /note= "conjugated via a linker molecule to anthracycline
 FT or anthracycline"
 XX
 XX M09733897-A1.
 XX
 XX 18-SEP-1997.
 PD
 XX
 XX 12-MAR-1997; 97MO-EP001246.
 PF
 XX
 XX 13-MAR-1996; 96IT-FI000044.
 PR
 XX (CMDR) CONSIGLIO NAZ DELLE RICERCHE.
 XX
 XX Garbei AM, Bonazzi S, Zanello S, Capobianco ML, Gianini G;
 PI Arcamone F;
 PI
 XX WPI; 1997-470805/43.
 DR
 XX
 XX New oligo:nucleotide-anthracycline or anthracycline conjugates - which
 PT form triple-helix complexes with DNA, used for targeting e.g. tumours or
 PT viruses.
 PT
 XX
 XX Claim 7; Page 19; 25pp; English.
 PS
 XX This sequence represents a specifically claimed example of a conjugate
 CC which consists of a natural or modified oligonucleotide capable of
 CC forming a triple-helix complex with a double stranded DNA, linked, via an
 CC appropriate linker, to the aglycone-moiety of an anthracycline or to an
 CC anthracycline. The conjugates form triple-helix complexes with DNA of
 CC higher stability compared with corresponding oligonucleotides, due to the
 CC intercalation of the aglycone moiety in the DNA target. They can be used
 CC against activated oncogenes in the treatment of tumours and against the
 CC proviral genome of retroviruses. (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC
 XX
 XX Sequence 15 BP; 10 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4017 GAGAAAAAAGAGAGA 4031
 XX 1 GAGAAAAAAGAGAGA 15
 DB
 XX
 XX RESULT 2686
 XX AAV06038/c
 XX ID AAV06038 standard; DNA; 15 BP.
 XX

AC	AAV06038;
XX	
DT	25-MAR-2003 (revised)
DT	08-APR-1998 (first entry)
XX	
DE	Oligonucleotide-anthracycline or anthracyclinnone conjugate #4.
XX	
KM	Anthracycline conjugate; anthracyclinnone; triple-helix; tumour; virus;
OS	intercalation; ss.
XX	
XX	Synthetic.
FH	
FT	Key
FT	modified_base
FT	1 Location/Qualifiers
FT	/tag= a
FT	/note= "Conjugated via a linker molecule to anthracycline or anthracylinnone"
FT	2
FT	/tag= b
FT	/note= "Methylated cytosine"
FT	4 /tag= c
FT	/note= "Methylated cytosine"
FT	6 /tag= d
FT	/note= "Methylated cytosine"
FT	13 /tag= e
FT	/note= "Methylated cytosine"
PN	
PN	WO9733897-A1.
PD	
PD	18-SEP-1997.
XX	
PX	
PX	12-MAR-1997; 97WO-EP001246.
PR	
PR	13-MAR-1996; 96IT-FI000044.
PA	(CNDR) CONSIGLIO NAZ DELLA RICERCA.
XX	
PI	Garbest AM, Bonazzi S, Zanella S, Capobianco ML, Gianini G;
PI	Arcamone F;
DR	
DR	WPI; 1997-470805/43.
XX	
PT	New oligo:nucleotide-anthracycline or anthracyclinnone conjugates - which
PT	form triple-helix complexes with DNA, used for targeting e.g. tumours or
PT	viruses.
PS	
PS	Claim 7; Page 19; 25pp; English.
XX	
CC	This sequence represents a specifically claimed example of a conjugate
CC	which consists of a natural or modified oligonucleotide capable of
CC	forming a triple-helix complex with a double stranded DNA, linked, via an
CC	appropriate linker, to the aglycone-moiety of an anthracycline or to an
CC	anthracyclinnone. The conjugates form triple-helix complexes with DNA of
CC	higher stability compared with corresponding oligonucleotides, due to the
CC	intercalation of the aglycone moiety in the DNA target. They can be used
CC	against activated oncogenes in the treatment of tumours and against the
CC	proviral genome of retroviruses. (Updated on 25-MAR-2003 to correct PR
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)
XX	
SQ	Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
	Query Match 0.2%; Score 15; DB 1; Length 15;
	Best Local Similarity 100.0%; Pred. No. 1.3e+03;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4017 GAGAAAAAAGGAGA 4031
DB	15 GAGAAAAAAGGAGA 1

ID	AAV01603	standard; DNA; 15 BP.
RESULT 2687		
AAV01604/c		
AAV01604; standard; DNA; 15 BP.		
AC	AAV01604;	
XX		
XX	25-MAR-2003 (revised)	
DT	31-MAR-1998 (first entry)	
XX		
XX	Oligonucleotide containing phosphoramidate linkages.	
DE		
XX	phosphoramidate linkage; solid phase synthesis; ss.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	misc_feature	1..15
FT		/*reg= "a
FT		/note= "these residues have N3'->P5' phosphoramidate
FT		linkages"
XX		
XX	WO9731009-A1.	
XX		
PD	28-AUG-1997.	
XX		
PF	14-JUN-1996;	96WO-US010418.
XX		
PR	21-FEB-1996;	96US-00603566.
XX		
PA	(LNNX-) LNNX THERAPEUTICS INC.	
XX		
PI	Hirschbein BL, Fearon KL, Gryaznov SM, McCurdy SN, Nelson JS;	
PI	Schultz RG;	
XX		
DR	WPI; 1997-435080/40.	
XX		
PT	Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting	
PT	immobilised 3'-amino nucleotide with new amino:nucleoside 5'-	
PT	phosphoramidate then oxidation, useful as research, diagnostic and	
PT	therapeutic agents.	
XX		
XX	Disclosure; Page 28; 60pp; English.	
XX		
CC	A new method is provided for the synthesis of oligonucleotides having N3'	
CC	->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-	
CC	protected amino nucleoside to a solid support; (b) deprotecting the 3'-	
CC	amino; (c) reacting with a 3'-protected amonucleoside-5'-	
CC	phosphoramidate monomer to form an internucleoside N3'-> P5'	
CC	phosphoramidate link; (d) oxidising this link to phosphoramidate; and	
CC	optionally repeating steps (b)-(d) until the required oligonucleotide is	
CC	completed. This method provides better yields with lower reagent	
CC	consumption than known processes, and can be operated on a large scale.	
CC	The obtained oligos, containing phosphoramidate linkages, have favourable	
CC	binding properties, nuclease resistance and solubility, and are useful as	
CC	research, diagnostic and therapeutic agents. The present sequence is an	
CC	example of an oligonucleotide in which N3'->P5' phosphoramidate linkages	
CC	have been introduced by the new method. (updated on 25-MAR-2003 to	
CC	correct PR field.)	
XX		
XX		
SQ	Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
XX		
Query Match	0.2%; Score 15; DB 1; Length 15;	
Best Local Similarity	100.0%; Pred. No. 1.3e+03;	
Matches 15; Conservative	0; Mismatches 0; Indels 0;	
QY	4464 TTTT TTTT TTTT TTTT TTTT 4478	
DB	15 TTTT TTTT TTTT TTTT 1	
RESULT 2688		
AAV01603		
AAV01603 standard; DNA; 15 BP.		

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XX AC AAV01603;
XX DT 25-MAR-2003 (revised)
XX DT 31-MAR-1998 (first entry)
XX DE Oligonucleotide containing phosphoramidate linkages.
XX KM phosphoramidate linkage; solid phase synthesis; ss.
XX OS Synthetic.
XX FH Key location/Qualifiers
XX FT misc_feature 1..15
XX FT /*tag= a
XX FT /note= "these residues have N3'->P5' phosphoramidate
XX FT linkages"
XX PN WO9731009-A1.
XX PD 28-AUG-1997.
XX PF 14-JUN-1996; 96WO-US010418.
XX PR 21-FEB-1996; 96US-00603566.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
XX PI Hirschbein BL, Fearon KL, Gyzanov SM, Mcurdy SN, Nelson JS;
XX PI Schultz RG;
XX DR WP1, 1997-435080/40.
XX PT Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting
XX PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
XX PT phosphoramidite then oxidation, useful as research, diagnostic and
XX PT therapeutic agents.
XX PS Disclosure; Page 28; 60pp; English.
XX CC A new method is provided for the synthesis of oligonucleotides having N3'
XX CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
XX CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-
XX CC amino; (c) reacting with a 3'-protected aminonucleoside 5'-
XX CC phosphoramidite monomer to form an internucleoside N3'-> P5'-
XX CC phosphoramidite link; (d) oxidising this link to phosphoramidate; and
XX CC optionally repeating steps (b)-(d) until the required oligonucleotide is
XX CC completed. This method provides better yields with lower reagent
XX CC consumption than known processes, and can be operated on a large scale.
XX CC The obtained oligos, containing phosphoramidate linkages, have favourable
XX CC binding properties, nuclease resistance and solubility, and are useful as
XX CC research, diagnostic and therapeutic agents. The present sequence is an
XX CC example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
XX CC have been introduced by the new method. (Updated on 25-MAR-2003 to
XX CC correct PR field.)
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX QY Query Match 0.2%; Score 15; DB 1; Length 15;
XX DB Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX DB Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15
XX RESULT 2689
XX ID AAV07431 standard; DNA; 15 BP.
XX AC AAV07431;
XX KM
XX XX

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XX DT 27-OCT-1998 (first entry)
XX DE Synthetic peptide-labeled oligonucleotide primer.
XX KM oligonucleotide; peptide; conjugate; release tag compound;
XX KM mass spectrometry; detection; identification; diagnosis; primer; ss.
XX OS Synthetic.
XX PN WO9826095-A1.
XX PD 18-JUN-1998.
XX PF 10-DEC-1997; 97WO-US022639.
XX PR 10-DEC-1996; 96US-0033037P.
XX PR 16-MAY-1997; 97US-0046719P.
XX PA (GENE-) GENETRACE SYSTEMS INC.
XX PI Montforte JA, Becker CH, Pollart DJ, Shaler TA;
XX PI WP1, 1998-348547/30.
XX DR WP1, 1998-348547/30.
XX PT New release tag compounds for detecting target molecule(s) - comprising a
XX PT reactive group, a release group and a releasable non-volatile mass label
XX PT detectable by mass spectrometry.
XX PS Example 3; Page 92; 170pp; English.
XX CC The sequence is that of an oligonucleotide primer which was produced as
XX CC part of an oligonucleotide peptide conjugate as an example of a release
XX CC tag compound (RTC). These comprise a reactive group, a release group and
XX CC a non-volatile mass label comprising a synthetic polymer or biopolymer
XX CC detectable by mass spectrometry. The RTCs can be used as probes for the
XX CC detection of TMs. They can be used for e.g. identification of gene
XX CC sequences, identification of non-coding nucleotide sequences,
XX CC identification of mutations within a gene or protein sequence, detection
XX CC of metals, detection of toxins, detection of receptors on an organism or
XX CC a cell, characterisation of antibody-antigen interactions, enzyme-
XX CC substrate interactions and characterisation of ligand interactions.
XX CC Multiple applications include multiple pathogen diagnostics, multigene
XX CC genetic polymorphism screening, single nucleotide polymorphism (SNP)
XX CC genotyping, clone and gene mapping, and gene expression analysis. The
XX CC RTCs permit the ready detection of releasable mass labels by mass
XX CC spectroscopy. The releasable mass labels permit the multiplexing of tens,
XX CC hundreds and perhaps even thousands of different mass labels that can be
XX CC used to uniquely identify each desired target
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX QY Query Match 0.2%; Score 15; DB 1; Length 15;
XX DB Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX DB Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15
XX RESULT 2690
XX ID AAT86675 standard; DNA; 15 BP.
XX AC AAT86675;
XX DT 04-JUN-1998 (first entry)
XX DE Oligonucleotide linked to polyacrylamide.
XX KM Capillary affinity gel electrophoresis; separation; polymer-gel;
XX KM polyacrylamide; ss.
XX XX
XX 1

```

OS Synthetic.
 XX Key Location/Qualifiers
 FT modified_base 1
 FT /*cag= a
 FT /note= "Tytymine at 5' end attached to a polyacrylamide
 FT gel via a linking group"
 XX
 XX MO9745721-A1.
 XX
 XX 04-DEC-1997.
 XX
 XX 23-MAY-1997; 97MO-EP002647.
 XX
 XX 24-MAY-1996; 96CH-00001320.
 XX
 XX (NOVS) NOVARTIS AG.
 XX
 XX Muscate A, Paulus A, Natt F;
 XX
 XX WPI; 1998-041763/04.
 XX
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 XX
 XX Example A1; Page 22; 41pp; English.
 XX
 XX This sequence represents an oligonucleotide receptor molecule covalently
 CC bound to a polyacrylamide gel via a linking group. The invention relates
 CC to selective separation of electrically charged target molecules in an
 CC analytical mixture. It comprises capillary affinity gel electrophoresis
 CC using a capillary tube which is at least partly filled with a polymer
 CC gel. Receptors for target molecules are covalently bound to the polymer.
 CC An electric field of at least 50 volts/cm is applied. The capillary tube
 CC is charged with the analytical mixture. In a first separation stage, the
 CC target molecules in the mixture are bound to the receptors and the
 CC remaining components are eluted, optionally whilst splitting open. In a
 CC second stage, the elution conditions are changed, optionally whilst
 CC so that the affinity of the target molecules for the receptor is
 CC eliminated and the target molecules are eluted and detected, optionally
 CC whilst splitting open. The process is useful for selective separation
 CC and/or determination of charged organic compounds, such as
 CC oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
 CC isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 CC
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 DB 1 TTTT TTTT TTTT TTTT 15
 RESULT 2691
 ID AAT86605 standard; DNA; 15 BP.
 XX
 XX AAT86605;
 AC
 XX 04-JUN-1998 (first entry)
 DT
 XX Oligonucleotide separated by capillary affinity gel electrophoresis.
 DE
 XX

KM Capillary affinity gel electrophoresis; separation; polymer-gel;
 KM polyacrylamide; ss.
 XX
 XX Synthetic.
 OS
 OS MO9745721-A1.
 XX
 XX 04-DEC-1997.
 XX
 XX 23-MAY-1997; 97MO-EP002647.
 XX
 XX 24-MAY-1996; 96CH-00001320.
 XX
 XX (NOVS) NOVARTIS AG.
 XX
 XX Muscate A, Paulus A, Natt F;
 XX
 XX WPI; 1998-041763/04.
 XX
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 XX
 XX Example D3; Page 25; 41pp; English.
 XX
 XX A mixture of oligonucleotides (AAT86604-7) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel
 CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied. The
 CC capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
 CC for isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 CC
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 DB 1 TTTT TTTT TTTT TTTT 15
 RESULT 2692
 ID AAX00787 standard; DNA; 15 BP.
 XX
 XX AAX00787;
 AC
 XX 13-APR-1999 (first entry)
 DT
 XX N3-P5 phosphoramidate oligonucleotide #3.
 DE
 XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
 KM
 XX Synthetic.
 OS


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XX Key Location/Qualifiers
FT misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX
PN US5659233-A.
XX
PD 12-JAN-1999.
XX
PF 20-DEC-1996; 96US-007711789.
XX
PR 21-FEB-1996; 96US-00603566.
PR 14-JUN-1996; 96US-00663918.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Gyzarov SM, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;
PI Fearon KL;
XX
DR WPI; 1999-120007/10.
XX
PT New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT the synthesis of oligo-nucleotide(s).
XX
PS Example 10; Col 33; 34pp; English.
XX
CC This sequence represents an example of an oligonucleotide containing
CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC sequence is generated synthetically by using an amine-exchange reaction
CC of phosphoramidites in which a deprotected 3'-amino group of a 5'-
CC oligonucleotide chain is exchanged for the amino portion of a 5'-
CC phosphoramidite with a protected 3' amino group. The resulting
CC phosphoramidite internucleotide linkage is oxidised to form a stable
CC protected phosphoramidate linkage
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2693
AAx00788/c
ID AAx00788 standard; DNA; 15 BP.
XX
AC AAx00788;
XX
DT 13-APR-1999 (first entry)
XX
DB N3-P5 phosphoramidate oligonucleotide #4.
XX
KM Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX
PN US5659233-A.
XX
PD 12-JAN-1999.
XX
PF 20-DEC-1996; 96US-007711789.

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XX 21-FEB-1996; 96US-00603566.
PR 14-JUN-1996; 96US-00663918.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Gyzarov SM, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;
PI Fearon KL;
XX
DR WPI; 1999-120007/10.
XX
PT New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT the synthesis of oligo-nucleotide(s).
XX
PS Example 10; Col 33; 34pp; English.
XX
CC This sequence represents an example of an oligonucleotide containing
CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC sequence is generated synthetically by using an amine-exchange reaction
CC of phosphoramidites in which a deprotected 3'-amino group of an
CC oligonucleotide chain is exchanged for the amino portion of a 5'-
CC phosphoramidite with a protected 3' amino group. The resulting
CC phosphoramidite internucleotide linkage is oxidised to form a stable
CC protected phosphoramidate linkage
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 15 TTTT TTTT TTTT TTTT 1

RESULT 2694
AAx84262/c
ID AAx84262 standard; DNA; 15 BP.
XX
AC AAx84262;
XX
DT 08-SEP-1999 (first entry)
XX
DE PCR primer for human Nck associated protein 1 coding sequence.
XX
KW Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW therapy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9931239-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-JP005646.
XX
PR 15-DEC-1997; 97JP-00363183.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
PA (SAKA/) SAKAKI Y.
XX
PI Sakaki Y;
XX
DR WPI; 1999-395181/33.
XX
PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT Alzheimer's disease.
XX
PS Example 1; Page 77; 90pp; Japanese.
XX
CC This sequence represents a PCR primer used to isolate DNA encoding the

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CC human Nck associated protein 1 (Napl) of the invention. Nap1 inhibits
 CC apoptosis. The protein can be used in the investigation, diagnosis and
 CC treatment (e.g. by gene therapy) of Alzheimer's disease
 XX

SO Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7413 CAGCAGCAGCAGCAG 7427
 |||||
 DB 15 CAGCAGCAGCAGCAG 1

RESULT 2695
 AAX84261
 ID AAX84261 standard; DNA; 15 BP.

XX AAX84261;

AC 08-SEP-1999 (first entry)

XX PCR primer for human Nck associated protein 1 coding sequence.

DE Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
 KM therapy; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9931239-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-JP005646.

XX 15-DEC-1997; 97JP-00363183.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (SAKA) SAKAKI Y.

XX Sakaki Y;

PI WPI; 1999-395181/33.

DR WPI; 1999-395181/33.

XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of
 PT Alzheimer's disease.

XX Example 1; Page 77; 90pp; Japanese.

XX This sequence represents a PCR primer used to isolate DNA encoding the
 CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
 CC apoptosis. The protein can be used in the investigation, diagnosis and
 CC treatment (e.g. by gene therapy) of Alzheimer's disease

XX Sequence 15 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7413 CAGCAGCAGCAGCAG 7427
 |||||
 DB 1 CAGCAGCAGCAGCAG 15

RESULT 2696
 AAZ36369/c
 ID AAZ36369 standard; DNA; 15 BP.
 XX AAZ36369;
 AC
 XX

DT 22-FEB-2000 (first entry)
 XX PCR primer used to amplify mouse testatin cDNA.
 DE Mouse; cystatin-related protein; testatin; testis formation;
 XX foetal gonad; testis tumour growth; tumour inhibiting cystatin;
 KM genital tumour; testis malformation; PCR primer; ss.

XX Synthetic.
 OS Mus musculus.

XX WO958565-A1.

XX 18-NOV-1999.

XX 06-MAY-1999; 99WO-SF000764.

XX 08-MAY-1998; 98SE-00001617.

XX (KARO-) KAROLINSKA INNOVATIONS AB;

XX Nordqvist K, Toehonen V;

XX WPI; 2000-039071/03.

XX Novel cystatin-related protein used for testis tumor diagnostics and
 PT treatment.

XX Example 1; Page 15; 37pp; English.

XX The present sequence represents PCR primer used to amplify cDNA encoding
 CC a mouse cystatin-related protein, designated testatin. The protein is
 CC capable of inducing testis formation in foetal gonads. It is highly

CC probable that the protein inhibits testis tumour growth because of
 CC structural and functional similarities with tumour inhibiting cystatins.

CC The cystatin-related protein testatin may be useful for inducing testis
 CC formation in foetal gonads. Testatin polynucleotides are useful as a

CC source of primers and probes, which can be used to detect the presence of
 CC testatin nucleic acid molecules in a sample. The testatin

CC polynucleotides, polypeptides, and compositions can be used for treating
 CC genital tumours and may also be useful for creating a model for studying

CC testis malformations

XX Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7413 CAGCAGCAGCAGCAG 7427
 |||||
 DB 15 CAGCAGCAGCAGCAG 1

RESULT 2697
 AAZ61854
 ID AAZ61854 standard; RNA; 15 BP.

XX AAZ61854;

XX 28-MAR-2000 (first entry)

XX HCV 3' non core region substrate for Hammerhead ribozyme HCV-3-118.

XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KM cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KM autoimmune disease; ss.

XX Hepatitis C virus.

XX WO9955847-A2.

XX 04-NOV-1999.

XX

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XX 26-APR-1999; 99WO-US009027.
PE
XX 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Mcswigen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
DR
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 49; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC HCV sequence was screened for optimal ribozyme target sites using a
CC computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases. The
CC ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX
QY Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred.No.1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
XX
RESULT 2698
AAZ64910
ID AAZ64910 standard; RNA; 15 BP.
XX
AC AAZ64910;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
FN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PE 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
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```
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Mcswigen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
DR
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 102; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX
QY Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred.No.1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
XX
RESULT 2699
AAA46502
ID AAA46502 standard; cDNA; 15 BP.
XX
AC AAA46502;
XX
DT 04-SEP-2000 (first entry)
XX
DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
XX
OS Coffea arabica.
XX
FN WO200028046-A1.
XX
PD 18-MAY-2000.
XX
PE 28-OCT-1999; 99WO-EP008314.
XX
PR 11-NOV-1998; 98EP-00203742.
XX
PA (NEST ) SOC PROD NESTLE SA.
XX
PI Marracini P, Rogers J;
XX
DR WPI; 2000-399535/34.
XX
XX New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
PS Disclosure; Page 32; 41pp; French.
XX
CC PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
```

CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides
 CC that consist of molecules of mannan, either simple or branched, linked
 CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is
 CC used for in vitro modification of the coffee endo-beta-mannanase gene. It
 CC is also used to produce transgenic plant cells (especially coffee cells)
 CC which have modified properties of mannan polysaccharide, and thus altered
 CC flavour or structure. The enzyme is used for modification, degradation or
 CC synthesis of mannan polysaccharides in vitro, particularly to treat
 CC coffee beans to increase the percentage of dry matter extraction, and
 CC thus reduce the quantity of sediment

SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
 |||||
 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2700
 AAA75048
 ID AAA75048 standard; DNA; 15 BP.

XX AAA75048;

DT 15-JUN-2001 (first entry)

XX Primer used to reverse transcribe human RNA.

KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KW wound healing; infection; burn; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease;
 KW Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease; primer; ss.

XX Homo sapiens.

PN WO200052178-A1.

PD 08-SEP-2000.

PF 14-FEB-2000; 2000WO-US003542.

PR 01-MAR-1999; 99US-00258892.

PA (INST-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodavsky I, Feinstein B,

DR WPI; 2000-579289/54.

PT New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.

PS Disclosure; Page 44; 152pp; English.

XX The present primer was used to reverse transcribe human RNA, from which a
 CC cDNA sequence encoding a protein with heparanase catalytic activity was
 CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL-8), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or

CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections

SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
 |||||
 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2701
 AAA07792
 ID AAA07792 standard; DNA; 15 BP.

XX AAA07792;

DT 23-JUN-2000 (first entry)

XX Nucleic acid sequence of ODN-e.

KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW porriasis; duplex; ss.

XX Synthetic.

PN WO200011013-A1.

PD 02-MAR-2000.

PF 20-AUG-1999; 99WO-US019029.

PR 22-AUG-1998; 98US-0097712P.

PA (UYNE-) UNIV NEBRASKA.

PI Gold B;

DR WPI; 2000-246530/21.

PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.

PS Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, cytokines, hormones, growth factors and
 CC molecules, receptor molecules, cytochromes, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences
 CC
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15
 RESULT 2702
 AAA07794
 ID AAA07794 standard; DNA; 15 BP.
 AC AAA07794;
 XX
 DT 23-JUN-2000 (first entry)
 DE Nucleic acid sequence of ODN-g.
 XX
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US019029.
 XX
 PR 22-AUG-1998; 98US-0097712P.
 XX
 PA (UNNE-) UNIV NEBRASKA.
 XX
 P1 Gold B;
 P1
 DR WPI; 2000-246530/21.
 XX
 PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 20; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.3e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15
 RESULT 2703
 AAA07828
 ID AAA07828 standard; DNA; 15 BP.
 AC AAA07828;
 XX
 DT 23-JUN-2000 (first entry)
 DE Nucleic acid sequence of a strand of triplex oligomer 15.
 XX
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; triplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US019029.
 XX
 PR 22-AUG-1998; 98US-0097712P.
 XX
 PA (UNNE-) UNIV NEBRASKA.
 XX
 P1 Gold B;
 P1
 DR WPI; 2000-246530/21.
 XX
 PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 30; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07820-834 represent sequences forming triplex oligomers
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
|||||:|||||:|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2704
AAA07790
ID AAA07790 standard; DNA; 15 BP.
AC AAA07790;
XX
XX
XX 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-c.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KM viral infection; inflammatory response; cellular proliferation;
KM psoriasis; duplex; ss.
XX
OS Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
PI
DR WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX
PS Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
|||||:|||||:|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2705
AAA07789
ID AAA07789 standard; DNA; 15 BP.
XX
XX AAA07789;
XX
XX
XX 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-b.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KM viral infection; inflammatory response; cellular proliferation;
KM psoriasis; duplex; ss.
XX
OS Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
PI
DR WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX
PS Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
OY 4464 TTTTUUUUUUUUUU 4478
      |||||:|||||
      1 TTTTUUUUUUUUUU 15
DB

RESULT 2706
AAA07795
ID AAA07795 standard; DNA; 15 BP.
XX
XX AAA07795;
XX
XX 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of ODN-h.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 1.3e+03;
XX Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTUUUUUUUUUU 4478
XX |||||:|||||
```

```
DB 1 TTTTUUUUUUUUUU 15
      |||||:|||||
      1 TTTTUUUUUUUUUU 15
DB

RESULT 2707
AAA07797
ID AAA07797 standard; DNA; 15 BP.
XX
XX AAA07797;
XX
XX 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of ODN-j.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 1.3e+03;
XX Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTUUUUUUUUUU 4478
XX |||||:|||||
XX 1 TTTTUUUUUUUUUU 15
```


RESULT 2708

AAA07799 standard; DNA, 15 BP.

AAA07799;

23-JUN-2000 (first entry)

Nucleic acid sequence of ODN-1.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

proliferation; cellular proliferation; leukemias;

proliferation; cellular proliferation; leukemias;

Synthetic.

WO200011013-A1.

20-AUG-1999; 99WO-US019029.

22-AUG-1998; 98US-0097712P.

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic

oligomers used to inhibit expression of nucleic acids and in gene

regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.3e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2709

AAA07802 standard; DNA, 15 BP.

AAA07802;

23-JUN-2000 (first entry)

Nucleic acid sequence of ODN-0.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

proliferation; cellular proliferation; leukemias;

proliferation; cellular proliferation; leukemias;

Synthetic.

WO200011013-A1.

20-AUG-1999; 99WO-US019029.

22-AUG-1998; 98US-0097712P.

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic

oligomers used to inhibit expression of nucleic acids and in gene

regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.3e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2710

AAA07825 standard; DNA, 15 BP.

XX AAA07825;
AC 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of a strand of triplex oligomer 14.
DE
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KM psoriasis; duplex; triplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
PN
XX 02-MAR-2000.
PD
XX 20-AUG-1999; 99WO-US019029.
PF
XX 22-AUG-1998; 98US-0097712P.
PR
XX (UTNE-) UNIV NEBRASKA.
PA
XX Gold B;
PI
XX WPI; 2000-246530/21.
DR
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS
XX Disclosure; Page 30; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
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CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
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CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC infections, cardiovascular disorders, immune reactions, cancer, viral
CC conditions and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07820-834 represent sequences forming triplex oligomers
XX
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT 15
RESULT 2711
AAA07831
ID AAA07831 standard; DNA, 15 BP.
XX
XX AAA07831;
AC
XX

PT 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of a strand of triplex oligomer 16.
DE
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KM psoriasis; duplex; triplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
PN
XX 02-MAR-2000.
PD
XX 20-AUG-1999; 99WO-US019029.
PF
XX 22-AUG-1998; 98US-0097712P.
PR
XX (UTNE-) UNIV NEBRASKA.
PA
XX Gold B;
PI
XX WPI; 2000-246530/21.
DR
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS
XX Disclosure; Page 30; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutical acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC infections, cardiovascular disorders, immune reactions, cancer, viral
CC conditions and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07820-834 represent sequences forming triplex oligomers
XX
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT 15
RESULT 2712
AAA07803
ID AAA07803 standard; DNA, 15 BP.
XX
XX AAA07803;
AC
XX 23-JUN-2000 (first entry)
DE Nucleic acid sequence of ODN-P.

XX	Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	psoriasis; duplex; ss.
XX	Synthetic.
OS	
PN	WO200011013-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UTNE-) UNIV NEBRASKA.
XX	
B	Gold B;
P1	
XX	WPI; 2000-246530/21.
DR	
XX	
PT	Modified nucleonome, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
XX	regulation, antisense technology and diagnostics.
PS	
XX	Disclosure; page 20; 42pp; English.
CC	
CC	The invention provides modified nucleonome of specified formula and
CC	their pharmacologically acceptable salts. The nucleonome are used as
CC	monomers in oligomers, which are used in pharmaceutical compositions to
CC	inhibit expression of nucleic acid molecules including DNA and RNA in
CC	cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC	infected cells. They are used in oligomers for gene regulation, antisense
CC	technology, diagnostic applications to detect target sequences in
CC	biological samples such as those containing pathogenic bacteria, fungi
CC	and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC	encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC	molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC	interleukins associated with pathological conditions such as inflammatory
CC	conditions, cardiovascular disorders, immune reactions, cancer, viral
CC	infections and bacterial infections (see AA07786 for details of other
CC	uses for which the oligomers are suitable for). Oligomers comprising the
CC	nucleonome exhibit increased duplex DNA stability when hybridizing to
CC	target nucleic acid sequences, are physiologically stable, non-toxic and
CC	able to penetrate into cells while maintaining stringent base pair
CC	fidelity for target DNA sequences. The oligomers demonstrate significant
CC	single- or double-stranded target nucleic acid binding activity to form
CC	duplexes, triplexes or other forms of stable association. Sequences
CC	AA07788-803 represent oligonucleotides forming a third strand along with
CC	the duplex sequences
CC	
XX	
XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match	0.2%; Score 15; DB 1; Length 15;
Best Local Similarity	0.0%; Pred. No. 1.3e+03;
Matches	0; Conservative 15; Mismatches 0; Indels 0; Gaps 0
Oy	4464 TTTT TTTT TTTT TTTT 4478
Db	1 UUUUUUUUUUUUUUUUU 15
RESULT 2713	
ID	AAA07834
AC	AAA07834 standard; DNA; 15 BP.
XX	
XX	AAA07834;
DT	23-JUN-2000 (first entry)
DE	Nucleic acid sequence of a strand of triplex oligomer 17.
XX	
KW	Nucleonome; cancer; gene regulation; antisense technology; leukemia;

KM	vital infection; inflammatory response; cellular proliferation;
XN	pneumonia; duplex; triplex; ss.
XX	Synthetic.
OS	
PN	WO200011013-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UTNE-) UNIV NEBRASKA.
XX	
PI	Gold B;
XX	
DR	WPI; 2000-245530/21.
XX	
PT	Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.
XX	
PS	Disclosure; Page 30; 42pp; English.
CC	The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally- infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07820-834 represent sequences forming triplex oligomers
CC	
SC	Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
QY	
DB	
Query Match	0.2%; Score 15; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
4464 TTTTUUUUUUUUUUU 4478	
:	
1 TTTTUUUUUUUUUUU 15	
RESULT 2714	
AAA07796	
ID AAA07796 standard; DNA; 15 BP.	
XX	
AC	AAA07796;
XX	
DT	23-UUN-2000 (first entry)
XX	
DE	Nucleic acid sequence of ODN-1.
XX	
KM	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XN	viral infection; inflammatory response; cellular proliferation;
KW	pneumonia; duplex; ss.
XX	

PD 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
PF
XX 22-AUG-1998; 98US-0097712P.
PR
XX (UYNE-) UNIV NEBRASKA.
PA
XX Gold B;
PI
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
RESULT 2717
AAA07798
ID AAA07798 standard; DNA; 15 BP.
XX
XX AAA07798;
AC
XX 23-JUN-2000 (first entry)
DT
XX
DE Nucleic acid sequence of ODN-K.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX PD
XX

PF 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
PR
XX (UYNE-) UNIV NEBRASKA.
PA
XX Gold B;
PI
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
RESULT 2718
AAA07788
ID AAA07788 standard; DNA; 15 BP.
XX
XX AAA07788;
AC
XX 23-JUN-2000 (first entry)
DT
XX
DE Nucleic acid sequence of ODN-a.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX PD
XX 20-AUG-1999; 99WO-US019029.
XX PF
XX

PR 22-AUG-1998; 98US-0097712P.
XX
XX (UNNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT TTTT 15
RESULT 2719
AAA07791
ID AAA07791 standard; DNA; 15 BP.
XX
XX AAA07791;
AC
XX 23-JUN-2000 (first entry)
DT
XX
XX Nucleic acid sequence of ODN-d.
DE
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
PN
XX 02-MAR-2000.
PD
XX 20-AUG-1999; 99WO-US019029.
PF
XX 22-AUG-1998; 98US-0097712P.
PR
XX

PA (UNNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 1.3e+03;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 UTTT UTTT UTTT UTTT UTTT 15
RESULT 2720
AAA07801
ID AAA07801 standard; DNA; 15 BP.
XX
XX AAA07801;
AC
XX 23-JUN-2000 (first entry)
DT
XX
XX Nucleic acid sequence of ODN-n.
DE
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
OS
XX WO200011013-A1.
PN
XX 02-MAR-2000.
PD
XX 20-AUG-1999; 99WO-US019029.
PF
XX 22-AUG-1998; 98US-0097712P.
PR
XX (UNNE-) UNIV NEBRASKA.
XX

FT	/*tag= e	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R)-C,3'-N-ethanothymidine"	
FT	13	
FT	/*tag= f	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R)-C,3'-N-ethanothymidine"	
FT	15	
FT	/*tag= g	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R)-C,3'-N-ethanothymidine"	
PN	US6083482-A.	
PD	04-JUL-2000.	
PP	11-MAY-1999;	99US-00309742.
PR	11-MAY-1999;	99US-00309742.
PA	(ICMC) ICN PHARM INC.	
PI	Wang G;	
DR	WPI; 2000-451496/39.	
XX		
PT	New conformationally restricted 3',5'-bridged nucleosides and	
PT	oligonucleotides useful as antisense therapeutics or as gene-specific	
PT	diagnostics.	
PS	Example 20; Col 15; 10pp; English.	
XX		
CC	The present sequence is an oligonucleotide containing 3',-C-amino-5' (R)-	
CC	C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in	
CC	the sequence were incorporated by phosphoramidite chemistry using a DNA	
CC	synthesizer. Bicyclic sugar nucleosides are conformationally restricted	
CC	3',5'-bridged nucleosides which can be used as building blocks for	
CC	oligonucleotides. Oligonucleotides can be produced that have certain,	
CC	desired, geometrical shapes and entropy advantages. They may have	
CC	superior hybridisation to DNA and RNA, and excellent biological	
CC	stability. The conformationally-modified oligonucleotides may be useful	
CC	as antisense inhibitors of gene expression or as gene probes, and may	
CC	therefore be used in antisense therapeutics or gene-specific diagnostics	
XX		
SO	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;	
	Query Match	0.2%; Score 15; DB 1; Length 15;
	Best Local Similarity	100.0%; Pred. No. 1.3e+03;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	4464 TTTTTTTTTTTTTT 4478	
Db	1 TTTTTTTTTTTTTT 15	
	RESULT 2723	
	AAA62348	
ID	AAA62348 standard; DNA; 15 BP.	
AC	AAA62348;	
XX		
DT	06-NOV-2000 (first entry)	
DE	Oligonucleotide #4 containing 3'-C-amino-5' (R)-C,3'-N-ethanothymidine.	
XX		
KM	Conformationally-locked oligonucleotide; antisense inhibitor;	
XX	bicyclic sugar nucleoside analogue; gene probe; ds.	
OS		
XX	Synthetic.	
PH	Key	Location/Qualifiers
FT	modified_base	7
FT	/*tag= a	

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FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5' (R)-C,3'-3'-N-ethanothymidine"
FT      modified_base          9
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5' (R)-C,3'-3'-N-ethanothymidine"
XX
XX
XX      US6083482-A.
XX
XX
XX      04-JUL-2000.
XX
XX      11-MAY-1999;    99US-00309742.
XX
XX      11-MAY-1999;    99US-00309742.
XX
XX      (ICNC ) ICN PHARM INC.
XX
XX      Wang G;
XX
XX      WPI; 2000-451496/39.
XX
XX      New conformationally restricted 3',5'-bridged nucleosides and
PT      oligonucleotides useful as antisense therapeutics or as gene-specific
PT      diagnostics.
XX
XX      Example 20; Col 15; 10pp; English.
XX
XX      The present sequence is an oligonucleotide containing 3'-C-amino-5' (R) -
CC      C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC      the sequence were incorporated by phosphoramidite chemistry using a DNA
CC      synthesizer. Bicyclic sugar nucleosides are conformationally restricted
CC      3',5'-bridged nucleosides which can be used as building blocks for
CC      oligonucleotides. Oligonucleotides can be produced that have certain,
CC      desired, geometrical shapes and entropy advantages. They may have
CC      superior hybridisation to DNA and RNA, and excellent biological
CC      stability. The conformationally-modified oligonucleotides may be useful
CC      as antisense inhibitors of gene expression or as gene probes, and may
CC      therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
Query Match           0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY      4464 TTTTTTTTTTTTTTTT 4478
DB      1 TTTTTTTTTTTTTTTT 15
RESULT 2724
AAH20308
ID      AAH20308 standard; DNA; 15 BP.
XX
XX      AAH20308;
XX
XX      31-JUL-2001 (first entry)
XX
XX      Oligo dT15 EDTA labelled probe.
XX
XX      Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX      Synthetic.
XX
XX      Key Location/Qualifiers
XX      FH 1
XX      FT modified_base
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "Optionally thymidine has EDTA covalently attached
XX      at C-5"
XX      modified_base 5
XX      /*tag= b
XX      /mod_base= OTHER

```



```
FT /note= "Optionally thymidine has EDTA covalently attached
FT at C-5"
FT modified_base
FT 8 /*cag= C
FT /mod_base= OTHER
FT /note= "Optionally thymidine has EDTA covalently attached
FT at C-5"
XX
XX US2001002314-A1.
XX
XX 31-MAY-2001.
XX
XX 04-AUG-1998; 98US-00128732.
XX
XX 30-OCT-1987; 87US-00115922.
XX 16-NOV-1990; 90US-00614205.
XX 12-NOV-1993; 93US-00152250.
XX
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
XX Dervan PB, Moser HE;
XX
XX WPI; 2001-342909/36.
XX
XX New hybridization probe for specific triplex formation with large double
XX helices, useful e.g. for site-specific diagnostic cleavage, contains
XX attached functional residue.
XX
XX Example 1; Fig 3B; 20pp; English.
XX
XX This invention relates to hybridisation probes which target a specific
XX sequence within a large double-helical nucleic acid. The probe is
XX complementary to the target sequence and contains at least one nucleotide
XX with an attached molecule that is able to cleave double-helical DNA e.g.
XX EDTA-Fe(II) (ethylenediaminetetracetic acid-iron complex). The probes
XX where the attached molecule is a label or compound that alters gene
XX expression, are used for specific detection and/or cleavage of double-
XX helical DNA, e.g. for diagnosis, for treatment of disease (particularly
XX caused by viruses, genetic defects or oncogenes), for chromosomal
XX analysis, and for the isolation and mapping of genes. The present
XX sequence represents probe of the invention used in an example
XX illustrating how the probe binds to and cleaves double stranded DNA
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2725
XX AAF30882
XX ID AAF30882 standard; DNA; 15 BP.
XX
XX AAF30882;
XX
XX 09-JUL-2001 (first entry)
XX
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX Synthetic.
XX
XX WO200131063-A1.
XX
XX 03-MAY-2001.
XX
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PF 26-OCT-2000; 2000WO-US029786.
XX
XX 26-OCT-1999; 99US-00428236.
XX
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX Dempsy RO, Afonina IA, Vermeulen NMU;
XX
XX WPI; 2001-328656/34.
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component of an
XX ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX invention. MGBs bind in a non-intercalating manner to the minor groove of
XX non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX but in an intercalating manner, or lies in the minor groove, or is
XX oriented in some other way to the DNA molecule by MGB, such that it
XX becomes fluorescent (or its fluorescent properties change detectably).
XX The conjugates are used as hybridisation probes and amplification primers
XX for fluorescent detection of specifically hybridising sequences, for
XX analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX mismatch discrimination, target or signal amplification, array-based
XX assays and sequencing, including detection of double-stranded DNA by
XX triplex formation. Many different targets can be detected a single
XX reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX hybridisation-triggered fluorescence. Upon hybridisation to the
XX complementary target sequence there was an increase in fluorescence
XX yield, measured as the ratio of the fluorescence emitted by the hybrid
XX between the ODN-MGB-LF conjugate and its target sequence to the
XX fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX of 8.3
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2726
XX AAH20511
XX ID AAH20511 standard; DNA; 15 BP.
XX
XX AAH20511;
XX
XX 31-JUL-2001 (first entry)
XX
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..14 /*cag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate deoxynucleotides"
XX
XX DE10051726-A1.
XX
XX 10-MAY-2001.
XX
```

XX 18-OCT-2000; 2000DE-01051726.
 XX 30-OCT-1999; 99DE-01052376.
 XX (MERK) MERCK PATENT GMBH.
 XX Seliger H, Sobkowski M, Hinz M;
 XX WPI; 2001-336414/36.
 XX Intermediate for oligonucleotide synthesis comprises partially hydrolysed
 PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
 PT
 XX Example 2; Page 5; 8pp; German.
 XX This invention describes a novel chemical product comprising a partially
 CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
 CC with nucleotide derivative(s). The product is an intermediate for the
 CC large (gram) scale solid phase synthesis of modified oligonucleotides
 CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the
 CC treatment of AIDS and cancers. The presence of the partially hydrolysed
 CC copolymer facilitates the synthesis of larger amounts of oligonucleotides
 CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
 CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
 CC Oligonucleotides are obtained in very good quality and high yields. Also,
 CC the nucleosides do not display the reduced activity seen in some prior
 CC art procedures, less carrier material, reagents and solvent are required.
 CC Further, the carrier material is biodegradable and thus does not present
 CC disposal problems. It also swells uniformly in a range of solvents, which
 CC obviates expansion or contraction during use or solvent exchange.
 CC AAH20510-AAH20513 represent oligonucleotides containing modified
 CC deoxynucleotides which are used to illustrate the method of the invention
 CC
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 4464 TTTTTTTTTTTTTT 4478
 XX 1 TTTTTTTTTTTTTT 15
 XX
 XX RESULT 2727
 XX AAF49041
 XX ID AAF49041 standard; DNA; 15 BP.
 XX AC AAF49041;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #1.
 XX XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cyostatic; dermatological; cardiant; vinctide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KW
 XX Homo sapiens.
 XX OS
 XX PN MO200078341-A1.
 XX PD 28-DEC-2000.
 XX XX
 XX 21-JUN-2000; 2000MO-AU000693.
 XX PF
 XX 21-JUN-1999; 99US-0140345P.
 XX PR

XX (MURDOCH) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 8; Page 60; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 CC
 XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 15; DB 1; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 4470 TTTTTTTTTTTTGG 4484
 XX 1 TTTTTTTTTTTTGG 15
 XX
 XX RESULT 2728
 XX AAF45344/C
 XX ID AAF45344 standard; DNA; 15 BP.
 XX AC AAF45344;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGFBP2 oligonucleotide #183.
 XX XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cyostatic; dermatological; cardiant; vinctide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KW
 XX Homo sapiens.
 XX OS
 XX PN MO200078341-A1.
 XX PD 28-DEC-2000.
 XX XX
 XX 21-JUN-2000; 2000MO-AU000693.
 XX PF
 XX 21-JUN-1999; 99US-0140345P.
 XX PA (MURDOCH) MURDOCH CHILDRENS RES INST.
 XX PI Wright CJ, Werther GA, Edmondson SR;

```
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 35; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7414 AGCAGCAGCAGCAGC 7428
Db 15 AGCAGCAGCAGCAGC 1
XX
RESULT 2729
AAH18783/C
ID AAH18783 standard; DNA; 15 BP.
XX
AC AAH18783;
XX
DT 25-JUN-2001 (first entry)
XX
DE Human IL4 allele-specific primer SEQ ID NO: 42.
XX
KW Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;
KW inflammatory disorder; immune disorder; population diversity;
KW paternity test; forensic test; cytokine; chromosome 5q31.1; probe;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN MO200123404-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026608.
XX
PR 30-SEP-1999; 99US-0156825P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Denton RR, Mandabalan K, Stephens JC;
XX
DR WPI; 2001-316132/33.
XX
PT Polynucleotide comprising novel single nucleotide polymorphisms in human
PT interleukin-4 gene for use in studying expression, function of
PT interleukin-4, in developing drugs, diagnosis and treatment of immune
PT disorders.
XX
```

```
PS Claim 12; Page 16; 71pp; English.
XX
CC The present invention provides the protein, cDNA and gene of human
CC interleukin-4 (IL4). The coding sequences for this protein contain single
CC nucleotide polymorphisms (SNPs) which may be associated with differences
CC in susceptibility to atopy, inflammatory and immune diseases and
CC different drug responses. They may also be used in applications such as
CC forensic and paternity testing and studying population diversity and
CC anthropological lineage. The IL4 gene is found on human chromosome 5q31.1
XX
SQ Sequence 15 BP; 5 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5799 CCGGCTGCTGCTGCT 5813
Db 15 CCGGCTGCTGCTGCT 1
XX
RESULT 2730
AAH49243
ID AAH49243 standard; DNA; 15 BP.
XX
AC AAH49243;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #7.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9 /*tag= a
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "c-but"
FT modified_base 15 /*tag= b
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "t-hex"
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
XX
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 26; Page 40; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula P(DNA)-Li1q(PNA-
CC Li1)_r(DNA-Li1)_s(PNA)_t where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
```

CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (1) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC reesterases, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (1) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (1)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (1)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX

SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4478
|||||
1 TTTT TTTT TTTT TTTT 15

DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2731

ABL40743
ID ABL40743 standard; DNA; 15 BP.

AC ABL40743;

XX 03-JUL-2002 (first entry)

DE Chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.

XX Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;

KW anti-protoczoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.

XX Gallus gallus.

OS US2002034810-A1.

PN 21-MAR-2002.

PD 16-AUG-2001; 2001US-00930218.

PF 20-SEP-2000; 2000US-00663390.

PR (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX Goldsmith O, Becker I, Vlodevsky I, Michal I, Zeharia E;

XX WPI; 2002-338926/37.

PT Nucleic acid encoding avian and reptile heparanase polypeptide is useful
PT to treat various heparin-related disorders and the signal peptide is

PT useful in production of membrane-targeted or secreted recombinant
PT proteins.
XX
XX Disclosure; Page 13; 39pp; English.

CC The invention relates to an isolated avian and reptile nucleic acid,
CC encoding a polypeptide with heparanase catalytic activity. The signal
CC peptide of the nucleic acid can be used to express membrane-associated or
CC secreted proteins in heterologous expression systems. The encoded
CC polypeptides can be used to prevent tumor angiogenesis, metastasis and
CC invasion, and to intervene with pathologies associated with impaired
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoa and bacterial infections or
CC integration of neurodegenerative plaques. The present sequence
CC represents a chicken heparanase (hpa) cDNA cloning oligo dt(15) primer
XX

SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4478
|||||
1 TTTT TTTT TTTT TTTT 15

DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2732

ABA97403
ID ABA97403 standard; DNA; 15 BP.

AC ABA97403;

DT 18-JUN-2002 (first entry)

DE Nucleotide sequence of oligomer # 10 used to compare mismatches.

XX Protein nucleic acid molecule; PNA; ds.

XX Synthetic.

OS WO200168673-A1.

PN 20-SEP-2001.

PF 13-MAR-2001; 2001WO-US008111.

PR 14-MAR-2000; 2000US-0189190P.

PR 30-NOV-2000; 2000US-0250334P.

XX (ACTI-) ACTIVE MOTIF.

PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;

PI Chikhakhcheanu O, Buryakova A, Choob M, Hondorp K;

XX WPI; 2002-041177/05.

PT Oligonucleotides analogs useful in detection, separation and purification
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.

XX Example 20; Page 123; 197pp; English.

CC This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adaptors and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide

XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2735

AAD29506
ID AAD29506 standard; DNA; 15 BP.

AC AAD29506;

DT 17-MAY-2002 (first entry)

DE Primer used for the expression of adipocytes in human preadipose cells.

XX Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KM diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
SS.

XX Unidentified.

XX MO200206450-A1.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-EP008165.

XX 18-JUL-2000; 2000EP-00115489.

XX (NEST) SOC PROD NESTLE SA.

XX Darimont C, Mace K, Pfeifer A;

XX WPI; 2002-188539/24.

PT New human pre-adipose cell line capable of differentiating to adipose
cells, useful in developing drug, food ingredients, and supplements
against obesity, diabetes and cardiovascular diseases.

XX Example 5; Page 10; 30pp; English.

CC The present invention relates to new human pre-adipose cell lines capable
to differentiate to white adipose cells, exhibiting essentially the same
cellular properties of normal white adipose cells. The human pre-adipose
cell lines are useful for the identification of substances controlling
the regulation of lipid uptake and release by human white adipocytes, and
substances controlling the differentiation of preadipocytes into mature
adipocytes. They are useful for screening compounds capable to regulate
the secretion of any metabolites or hormones from human white adipocytes.
Sequences of the invention are useful for developing drugs, food
ingredients and supplements against obesity, diabetes and cardio-
vascular diseases. The present DNA sequence is a reverse transcription
(RT)-PCR primer which is used for the expression of adipocytes in
differentiated immortalised human preadipose cells. This primer is used
in the amplification of the invention

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2736

AAD22531/C
ID AAD22531 standard; RNA; 15 BP.

XX AAD22531;

XX 29-AUG-2003 (revised)

DT 07-AUG-2003 (revised)

DT 12-FEB-2002 (first entry)

DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.

XX RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
KM virucide; oncogene; cancer; transcription; translation; leukemia virus;
KM hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
XX poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.

XX Unidentified retrovirus.

XX US6291438-B1.

XX 18-SEP-2001.

XX 06-OCT-1998; 98US-00167375.

XX 24-FEB-1993; 93US-00022055.

XX 23-FEB-1994; 94US-0020650.

XX 22-FEB-1996; 96US-00604871.

XX (WANG/) WANG J H.

XX Wang JH;

XX WPI; 2002-009339/01.

PT Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
reverse transcriptase comprises at the 2'-O position of the
oligoribonucleotide, a hydrophobic carrier reagent containing a poly
substituted phenyl compound.

XX Example 3; Col 24; 56pp; English.

CC The invention relates to derivatised antisense oligoribonucleotides with
enhanced membrane permeability and stability. The derivatised antisense
oligoribonucleotide complementary to a sequence of nucleotides found in a
virus or a cell is useful for inhibiting e.g., viral reverse
transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
the 2'-O position with a hydrophobic carrier reagent containing a poly
substituted phenyl compound. The derivatised oligoribonucleotides are
used to decrease the expression of oncogenes and thereby decrease the
expression of cancer cells which rely upon oncogene expression for their
phenotypic and pathological properties. The oligoribonucleotides are also
used for increasing the effectiveness of antisense oligonucleotide
targeted to a gene associated with a disease or a condition in an
animal. To alter gene transcription and/or translation for any gene or
gene segment responsible for expression, to inhibit viral reverse
transcriptase, to inhibit the expression of leukemia virus, hepatitis
virus, oncogenes and human immunodeficiency virus. The present sequence
is a retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
which is used in the treatment of moloney murine leukemia virus (MuLV)
in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-
AUG-2003 to standardise OS field)

XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT TTTT 15

Db 15 TTTTTTTTTTTTTT 1

RESULT 2737
ABQ82140/c
ID ABQ82140 standard; DNA; 15 BP.

XX
AC ABQ82140;
XX
DT 11-DEC-2002 (first entry)

XX
DE Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.

XX
KM Chimeric nucleic acid construct; recombinational cloning; silencing;
KM recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.

XX
PN W0200259294-A1.
XX
PD 01-AUG-2002.

XX
PF 24-JAN-2002; 2002WO-AU000073.

XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.

XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Weeley S, Waterhouse P, Helliwell C;
XX
DR WPI; 2002-682669/73.

XX
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.

XX
PS Claim 14, Page 74; 104pp; English.

XX
CC The present invention describes a vector (1) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC a selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (1) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (1i) first, second, third and
CC fourth recombination sites; (1ii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention

XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478
DB 15 TTTTTTTTTTTTTT 1

RESULT 2738
ABX00240
ID ABX00240 standard; RNA; 15 BP.

XX
AC ABX00240;
XX
DT 23-DEC-2002 (first entry)

XX
DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.

XX
KM Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KM HCV ribozyme; HCV expression; HCV replication; cirrhosis; viremia;
KM liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KM type I interferon; interferon alpha; interferon beta; cytostatic;
KM interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KM substrate; hammerhead ribozyme; HH ribozyme; ss.

XX
OS Hepatitis C virus.

XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.

XX
PF 23-MAR-1999; 99US-00274553.

XX
PR 23-MAR-1999; 99US-00274553.

XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVCO/) PAVCO P A.
PA (MACE/) MACEJACK D.

XX
PI Blatt L, Mewiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.

XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.

XX
PS Claim 1, Page 21; 80pp; English.

XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC : (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/patididentry.html

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478
DB 1 UUUUUUUUUUUUUU 15

RESULT 2739

ABX03406
ID ABX03406 standard; RNA; 15 BP.
AC
XX
AC ABX03406;
XX
DT 24-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KM Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KM HCV ribozyme; HCV expression; HCV replication; cirrhosis; virology;
KM liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KM type I interferon; interferon alpha; interferon beta; cytosolic;
KM interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KM substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLATT) BLATT L.
PA (MCSW) MCSWIGEN J A.
PA (ROBE) ROBERTS B.
PA (PAVC) PAVCO P A.
PA (MACE) MACEJACK D.
XX
P1 Blact L, Mcawigen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 64; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/patseqidentry.html
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
CY 4464 TTTT TTTT TTTT TTTT 4478
DB 1 UUUUUUUUUUUUUUU 15

ABL57064;
AC
XX
AC ABL57064;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide 035.
XX
KM Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key
FH modified_base
FT 1. .15
FT /*cag= b
FT /note= "phosphoramidite linkage"
FT modified_base
FT 1
FT /*cag= a
FT /mod_base= OTHER
FT /note= "diethyl 5-((2-cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)methyl) isophthalate, synthetic branching
FT amidite"
FT modified_base
FT 15
FT /*cag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
PN W0200214558-A2.
XX
PD 21-FEB-2002.
XX
PE 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
P1 Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TV, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 4; Page 44; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo 035, which was produced in an
CC example from the invention and which includes a synthetic branching
CC amide compound. The invention describes an improved process for
CC immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC molecules, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4464 TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2740
ABL57064
ID ABL57064 standard; DNA; 15 BP.

RESULT 2741
ABL57054


```

XX ID ABL57054 standard; DNA; 15 BP.
XX AC ABL57054;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide phosphoramidite oligonucleotide 09.
XX KM Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base 1.15
XX FT /tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "6-(2-cyanoethoxy) (diisopropylamino)
XX FT phosphanyloxy)-N'-tritylhexanohydrazide"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 2; Page 40; 120pp; English.
XX CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
XX CC 15-mer, designated oligo 09, which was produced in an example from the
XX CC invention. The invention describes an improved process for immobilisation
XX CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX CC RNA and peptides, especially macromolecules containing multiple reactive
XX CC sites, to a substrate surface or other conjugation target. It also
XX CC describes the preparation of oligos containing one or more hydrazides,
XX CC which can be used for conjugation to surface binding moieties, or for
XX CC other conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

```

RESULT 2742
ABL57063
ID ABL57063 standard; DNA; 15 BP.

ABL57063;
22-JUL-2002 (first entry)

```

XX DE Hydrazide precursor phosphoramidite oligonucleotide 039.
XX KM Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base 1.15
XX FT /tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "1,3-Bis-(3',5'-bis(ethyloxy-carbonyl) benzyloxy)-5
XX FT -(2'-cyanoethyl) (diisopropylamino) phosphanyloxy-methyl)-
XX FT benzene"
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo 039, which was produced in an
XX CC example from the invention. The invention describes an improved process
XX CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX CC multiple reactive sites, to a substrate surface or other conjugation
XX CC target. It also describes the preparation of oligos containing one or
XX CC more hydrazides, which can be used for conjugation to surface binding
XX CC moieties, or for other conjugation reactions. The process is useful e.g.
XX CC in nucleic acid hybridisation based assays, DNA chip technology and
XX CC biosensor applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 2743
ABL57066
ID ABL57066 standard; DNA; 15 BP.

ABL57066;
22-JUL-2002 (first entry)

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XX DE Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX KM Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base 1 Location/Qualifiers
XX FT /+tag= a
XX FT /mod_base= OTHER
XX FT /note= "Amino-C6 modification"
XX FT modified_base 15
XX FT /+tag= b
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N,
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 12; Page 57; 120pp; English.
XX CC The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
XX CC oligonucleotide that was used in a comparison of hydrazine and amine
XX CC attachment moieties on active ester surfaces in an example from the
XX CC invention. The invention describes an improved process for immobilisation
XX CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX CC RNA and peptides, especially macromolecules containing multiple reactive
XX CC sites, to a substrate surface or other conjugation target. It also
XX CC describes the preparation of oligos containing one or more hydrazides,
XX CC which can be used for conjugation to surface binding moieties, or for
XX CC other conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

```

```

XX OS Synthetic.
XX FH Key
XX FT modified_base 1.15
XX FT /+tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 1
XX FT /+tag= a
XX FT /mod_base= OTHER
XX FT /note= "4-(2-cyanoethyl)(diisopropylamino)
XX FT phosphanyloxyethyl)-benzoic acid methyl ester"
XX FT modified_base 15
XX FT /+tag= c
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N,
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo 033, which was produced in an
XX CC example from the invention. The invention describes an improved process
XX CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX CC multiple reactive sites, to a substrate surface or other conjugation
XX CC target. It also describes the preparation of oligos containing one or
XX CC more hydrazides, which can be used for conjugation to surface binding
XX CC moieties, or for other conjugation reactions. The process is useful e.g.
XX CC in nucleic acid hybridisation based assays, DNA chip technology and
XX CC biosensor applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 2744
ABLS7059
ID ABL57059 standard; DNA; 15 BP.
XX AC ABL57059;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide 033.
XX KW Macromolecule; hydrazide; immobilisation; ss.

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RESULT 2745
ABLS7061
ID ABL57061 standard; DNA; 15 BP.
XX AC ABL57061;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide 037.
XX KW Macromolecule; hydrazide; immobilisation; ss.

```

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-(2',-cyanoethyloxy)
FT (diisopropyl amino)-phosphanyloxy)-propane"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX WO200214558-A2.
XX 21-FEB-2002.
XX 10-AUG-2001; 2001WO-US041663.
XX 11-AUG-2000; 2000WO-US022205.
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N,
XX Havens JR, Onofrey TJ, Greef CH, Wang D,
XX WPI; 2002-404476/43.
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorus containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX Example 3; Page 43; 120pp; English.
XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O37, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15
RESULT 2746
ABLS7056
ID ABL57056 standard; DNA; 15 BP.
XX ABL57056;
XX AC
XX XX
XX 22-JUL-2002 (first entry)
XX Hydrazide phosphoramidite oligonucleotide O31.
XX DE Macromolecule; hydrazide; immobilisation; ss.
XX KW
XX OS
```

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanoehtoxy) (diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX WO200214558-A2.
XX 21-FEB-2002.
XX 10-AUG-2001; 2001WO-US041663.
XX 11-AUG-2000; 2000WO-US022205.
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N,
XX Havens JR, Onofrey TJ, Greef CH, Wang D,
XX WPI; 2002-404476/43.
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorus containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX Example 2; Page 40; 120pp; English.
XX The present sequence is of a trityl deprotected hydrazide phosphoramidite
XX 15-mer, designated oligo O31, which was produced in an example from the
XX invention. The invention describes an improved process for immobilisation
XX of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX RNA and peptides, especially macromolecules containing multiple reactive
XX sites, to a substrate surface or other conjugation target. It also
XX describes the preparation of oligos containing one or more hydrazides,
XX which can be used for conjugation to surface binding moieties, or for
XX other conjugation reactions. The process is useful e.g. in nucleic acid
XX hybridisation based assays, DNA chip technology and biosensor
XX applications
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15
RESULT 2747
ABLS7060
ID ABL57060 standard; DNA; 15 BP.
XX ABL57060;
XX AC
XX XX
XX 22-JUL-2002 (first entry)
XX Hydrazide precursor phosphoramidite oligonucleotide O34.
XX DE Macromolecule; hydrazide; immobilisation; ss.
XX KW
XX OS Synthetic.
```

```

XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
FT phosphanyloxy)methyl)isophthalate"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeier J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O34, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilization of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2748
XX ABR98141
XX ID ABR98141 standard; DNA; 15 BP.
XX
XX ABR98141;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #26.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

```

```

XX 0S Synthetic.
XX
XX PN US6403302-B1.
XX
XX 11-JUN-2002.
XX
XX 16-DEC-1993; 93US-00168920.
XX
XX 17-SEP-1992; 92US-00946976.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX
XX Example 1; Fig 3B; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or repressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2749
XX ABR98184
XX ID ABR98184 standard; DNA; 15 BP.
XX
XX ABR98184;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #48.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;

```

KM oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 OS Synthetic.
 XX US6403302-B1.
 PN 11-JUN-2002.
 PD 16-DEC-1993; 93US-00168920.
 PF 17-SEP-1992; 92US-00946976.
 PR (CALY) CALIFORNIA INST OF TECHNOLOGY.
 PA Derivan PB, Beal PA;
 PI WPI; 2002-536030/57.
 DR A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.
 PS Example 7; Fig 24A; 108pp; English.
 XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation,
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention
 CC XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 1 TTTT TTTT TTTT TTTT 15
 RESULT 2750
 AB237501
 ID AB237501 standard; DNA; 15 BP.
 XX
 AC AB237501;
 XX
 DT 18-FEB-2003 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO:622.
 XX
 KM Library; cleavage; display; diverse family; ss.

OS Synthetic.
 XX
 PN WO200283872-A2.
 XX 24-OCT-2002.
 PD 17-APR-2002; 2002WO-US012405.
 PF 17-APR-2001; 2001US-00837306.
 PR 24-OCT-2001; 2001US-0000516.
 PR 25-OCT-2001; 2001US-00045674.
 XX
 PA (LADN/) LADNER R. C.
 PA (COHE/) COHEN E. H.
 PA (NAST/) NASTRI H. G.
 PA (ROOK/) ROOKEY K. L.
 PA (HOET/) HOET R.
 PA (HOOG/) HOOGENDOORN H R J M.
 XX
 PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
 PI Hoogenboom HRJM;
 DR WPI; 2003-093015/08.
 PT Cleaving single-stranded nucleic acid sequences at a desired location by
 PT contacting the nucleic acid with an single strand oligonucleotide
 PT complementary to a nucleic acid region where cleavage is desired.
 XX
 PS Disclosure, Page 481; 485pp; English.
 XX The present invention describes a method for cleaving single-stranded
 CC nucleic acid sequences at a desired location. Also described: (1) methods
 CC for displaying or expressing a member of a diverse family of peptides,
 CC polypeptides or proteins on the surface of a genetic package and
 CC collectively displaying at least a part of the diversity of the family,
 CC where the displayed or expressed peptide, polypeptide or protein is
 CC encoded at least in part by a nucleic acid that has been cleaved at a
 CC desired location; (2) a method for preparing single-stranded nucleic
 CC acids; (3) a method for preparing a library comprising a collection of
 CC genetic packages that display a member of a diverse family of peptides,
 CC polypeptides or proteins and that collectively display at least a portion
 CC of the family; (4) a vector comprising a DNA sequence encoding an
 CC antibody variable region linked to a version of pIII anchor which does
 CC not mediate infection of phage particles, and wild-type gene III; (5) a
 CC method for producing a population or a library of immunoglobulin genes;
 CC and (6) a library of immunoglobulins that comprise members having at
 CC least one variable domain in which at least one of CDR1 and CDR2 contain
 CC synthetic diversity and CDR3 diversity is captured from B cells. The
 CC method is useful for cleaving single-stranded nucleic acid sequences at a
 CC desired location, which can be subsequently used to produce libraries or
 CC genetic packages that display and/or express a diverse family of
 CC peptides, polypeptides or proteins. AB236912 to AB237510 and AB254464 to
 CC AB254499 represent sequences used in the exemplification of the present
 CC invention
 CC XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 1 TTTT TTTT TTTT TTTT 15
 RESULT 2751
 ABV74142/C
 ID ABV74142 standard; DNA; 15 BP.
 XX
 AC ABV74142;
 XX
 DT 23-JAN-2003 (first entry)

```

XX 5' End of cDNA library clone.
DB
XX G-protein coupled receptor; odourant; receptor; olfaction; array;
XX microarray; anosmia; attractant; aromatic; pesticide; ss.
XX
OS Synthetic.
XX
PN WO200277200-A2.
XX
PD 03-OCT-2002.
XX
PE 26-MAR-2002; 2002WO-US009559.
XX
PR 27-MAR-2001; 2001US-0279168P.
PR 31-JAN-2002; 2002US-0353392P.
PA (INSC-) INSCENT INC.
XX
PI Woods D, Dimitratos S;
XX
DR WPI; 2003-029930/02.
XX
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
PS Disclosure; Fig 5; 83pp; English.
XX
CC The present sequence is that of the 5' end of a cDNA clone isolated from
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC using a method designed to rapidly array and normalize a complex cDNA
CC library obtained from a target species. Clones are arrayed into multi-
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC and a unique 3' sequence, which allows an anchored oligonucleotide in
CC each well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and numerous
CC enough to ensure that every possible cDNA sequence can be bound by an
CC individual, specific oligonucleotide in a single well. The cDNA library
CC is heated to denature the clones into single stranded DNA, and an aliquot
CC is added to every well. The anchored oligonucleotide serves as the 3'
CC primer in PCR, and the common 5' region present in every cDNA clone
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC in each well. The library is now arrayed and normalised. The method was
CC used to identify and isolate clones encoding G-protein coupled receptors,
CC especially odourant receptors, and active effectors involved in the
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that reduce a
CC target animal's sensitivity to odours, for manufacturing compounds or
CC devices that mask odours, or trapping invertebrates with odourants.
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc
XX
SO Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
DB 15 TTTT TTTT TTTT TTTT 1

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ID ABV74141 standard; DNA; 15 BP.
XX
XX ABV74141;
AC
XX 23-JAN-2003 (first entry)
DT
XX
DE Oligonucleotide used in cDNA library array.
XX
XX G-protein coupled receptor; odourant; receptor; olfaction; array;
XX microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /mod_base= OTHER
XX /note= "5' polylinker"
XX
XX WO200277200-A2.
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009559.
XX
XX 27-MAR-2001; 2001US-0279168P.
XX 31-JAN-2002; 2002US-0353392P.
XX
XX (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S;
XX
XX WPI; 2003-029930/02.
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX receptors, useful for isolating odorant binding proteins or pesticide
XX alternatives, by analyzing sequences from a male- and female-specific
XX nucleic acid library.
XX
XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of a poly-T oligonucleotide used in a method
XX designed to rapidly array and normalize a complex cDNA library obtained
XX from a target species. Clones are arrayed into multi-well plates. Each
XX well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
XX capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
XX which allows an anchored oligonucleotide in each well to selectively
XX hybridise only to those cDNA clones with a complementary 5' end. The
XX unique 3' key sequences are designed to give a comprehensive level of
XX degeneracy since they are diverse and numerous enough to ensure that
XX every possible cDNA sequence can be bound by an individual, specific
XX oligonucleotide in a single well. The cDNA library is heated to denature
XX the clones into single stranded DNA, and an aliquot is added to every
XX well. The anchored oligonucleotide serves as the 3' primer in PCR, and
XX the common 5' region present in every cDNA clone serves as the 5' priming
XX site. Denaturing and washing leave anchored cDNA in each well. The
XX library is now arrayed and normalised. The method was used to identify
XX and isolate clones encoding G-protein coupled receptors, especially
XX odourant receptors, and active effectors involved in the olfactory
XX pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
XX or other olfactory or neuronal proteins. The identified receptors and
XX proteins are useful for identifying compounds that reduce a target
XX animal's sensitivity to odours, for manufacturing compounds or devices
XX that mask odours, or trapping invertebrates with odourants.
XX Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
XX with desirable effects on specific species, for the development of pest
XX monitoring systems or non-toxic, species-specific pesticide alternatives,
XX for controlling insect feeding and breeding behaviour, detecting the
XX presence of small air-borne molecules, etc
XX
SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
|||||
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2753

ABV75865
ID ABV75865 standard; DNA, 15 BP.

XX AC ABV75865;

XX DT 05-FEB-2003 (first entry)

XX DE Oligonucleotide T15-Q-CDP13.

XX KM Deprotection; phosphoramidite; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..15

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphoramidite linkage"

FT modified_base 15

FT /*tag= b

FT /mod_base= OTHER

FT /note= "3' Q-CDP13"

XX PN W0200272864-A2.

XX PD 19-SEP-2002.

XX PF 04-MAR-2002; 2002WO-US006739.

XX PR 08-MAR-2001; 2001US-0274309P.

XX PA (PEKE) PE CORP NY.

XX PI Nelson J;

XX DR WPI; 2003-046740/04.

XX PT New oligonucleotide deprotection reagent useful for deprotecting

XX PT oligonucleotide comprises an active methylene compound and an amine

XX PS reagent.

XX PS Example 2; Page 25; 46pp; English.

XX CC The present invention provides a method for deprotection of an
XX CC oligonucleotide. This involves reacting a protected oligonucleotide,
XX CC which is preferably covalently attached to a solid support through a
XX CC linkage, with a deprotection reagent comprising an active methylene
XX CC compound and an amine reagent. The process and reagent minimise side-
XX CC reactions leading to certain impurities that contaminate synthetic
XX CC oligonucleotides. The present sequence is a T15 phosphoramidite
XX CC oligonucleotide having a quencher moiety (Q) and minor groove binder
XX CC (CP13) at the 3' end, which was synthesised in an example of the
XX CC invention. This protected oligonucleotide was treated either with 15%
XX CC ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%
XX CC ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
XX CC deprotection without DEM yielded a complex mixture of products containing
XX CC only 26.5% of the desired product. When DEM was used, 76.8% of the
XX CC desired product was obtained

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
|||||
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2754

ADA14836/c
ID ADA14836 standard; DNA, 15 BP.

XX AC ADA14836;

XX DT 06-NOV-2003 (first entry)

XX DE Hairpin target sequence, #1, used in an example of the invention.

XX KM Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;

XX KM quencherable fluorescing agent; microarray; semiconductor; nanocrystal;

XX KM rhodamine B-labelled dye; detection; gold support; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT misc_binding 1..15

FT /*tag= a

FT /bound_moiety= "Hairpin oligonucleotide #1"

FT /note= "Forms a double-stranded region with the hairpin
oligonucleotide shown in example 2"

XX PN US2003013109-A1.

XX PD 16-JAN-2003.

XX PF 21-JUN-2002; 2002US-00176055.

XX PR 21-JUN-2001; 2001US-0299460P.

XX PA (BAL/) BALINGER C T.

XX PA (LOCA/) LOCASCIO M.

XX PA (LAND/) LANDRY D P.

XX PI Ballinger CT, Locascio M, Landry DP,

XX DR WPI; 2003-596312/56.

XX PT Hairpin sensor useful for detecting a target nucleotide sequence in a

XX PT sample, comprises a hairpin loop assembly including a complementary probe

XX PT and a quencherable fluorescing agent.

XX PS Example 2; Page 11; 16pp; English.

XX CC The invention discloses a hairpin sensor comprising a hairpin loop
XX CC assembly including a complementary probe positioned between a first
XX CC inverse repeat arm and a second inverse repeat arm, and a quencherable
XX CC fluorescing agent joined, directly or indirectly, to the end of the
XX CC second inverse repeat arm of the hairpin loop assembly opposite the
XX CC complementary probe. Also claimed is a microarray comprising the hairpin
XX CC sensor, where the end of the first inverse repeat arm opposite the
XX CC complementary probe is bound, directly or indirectly, to a support, a kit
XX CC for detecting a target nucleotide sequence in a sample comprising the
XX CC hairpin sensor, and a support, and a hairpin sensor system, in which the
XX CC particle is conductive or semi-conductive, including at least one of the
XX CC above hairpin sensor assemblies. The hairpin sensor further comprises a
XX CC functional group joined to the end of the first inverse repeat arm
XX CC opposite the complementary probe, or first spacer opposite the first
XX CC inverse repeat arm, the functional group selected from amino, carboxyl,
XX CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
XX CC between the second inverse repeat arm and the quencherable fluorescing
XX CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
XX CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
XX CC second spacer is positioned between the second inverse repeat arm and the
XX CC quencherable fluorescing agent which comprises a semiconductor nanocrystal
XX CC or rhodamine B-labelled dye. Within the microarray the support is capable

CC	of accepting a charge. At least one hairpin sensor comprises two or more
CC	hairpin sensors. The two or more hairpin sensors include complementary
CC	probes that are the same or different and respective quenchable ..
CC	fluorescing agents that are the same or different. The two or more
CC	hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC	and system are useful for detecting a target nucleotide sequence in a
CC	sample. Further, the method involves identifying the target nucleotide
CC	sequence by the location of the complementary probe to which the target
CC	nucleotide sequence binds. The two or more hairpin sensors include
CC	complementary probes or quenchable fluorescing agents that are
CC	different. The sequence presented is the hairpin oligonucleotide target
CC	sequence, #1, used in an example of the invention.
SQ	Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 15; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 1.3e+03; Mismatches 0; Gaps 0
Matches	15; Conservative 0; Indels 0; Mismatches 0; Gaps 0
Oy	4464 TTTT TTTTTTTTTTTTTT 4478
DB	15 TTTT TTTTTTTTTTTTTT 1
RESULT 2755	
ID	ADB68520
AD	ADB68520 standard; DNA; 15 BP.
AC	ADB68520;
DT	04-DEC-2003 (first entry)
XX	
DE	Single-base mismatch oligonucleotide SEQ ID 10 DNA.
KM	hydroxyproline nucleic acid; HyPNNA; PNA; peptide nucleic acid;
KM	gene expression; respiration; secretion; signalling;
KM	ion-channel activity; cell motility; developmental phenotype;
KM	tumour regression; single-base mismatch; ss;
KW	phosphono-peptide nucleic acid; pPNA.
XX	
OS	Synthetic.
XX	
FN	WO2003068798-A2.
PD	21-AUG-2003.
XX	
PF	07-FEB-2003; 2003WO-US003904.
XX	
PR	09-FEB-2002; 2002US-00072975.
PA	(ACTI-) ACTIVE MOTIF.
P1	Efimov V, Fernandez J, Archdeacon D, Archdeachon J, Choob M;
DR	WP1; 2003-689653/65.
PT	Method of inhibiting expression of genes or RNA transcripts, useful for
PT	therapy and determining effects of genes, by administering oligomers
XX	containing hydroxyproline nucleic acid.
XX	
PS	Example 20; Page 234; 240pp; English.
XX	
CC	The invention relates to a novel method of inhibiting the expression of
CC	one or more genes or RNA transcripts by administering at least one
CC	oligonucleotide analogue that includes at least one hydroxyproline
CC	nucleic acid (HyPNA) monomer to a cell or organism or their extracts. This
CC	oligonucleotide of the invention may be used to monitor properties
CC	including gene expression, respiration, secretion, signalling, ion-
CC	channel activity, cell motility, developmental phenotype and tumour
CC	regression. Furthermore, it may be utilised to determine the effects of
CC	particular genes, as antisense or homologous recombination constructs
CC	e.g. for creating animal models of disease and finally, for increasing
CC	the activity of some enzymes, such as polymerases. The current sequence

CC		is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the invention. This sequence may also comprise a peptide nucleic acid (PNA), a phosphono-PNA (ppna) or a HyDNA.
CC		
CC		
CC		
XX		
SO	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;	
'	Query Match	0.2%; Score 15; DB 1; Length 15;
.	Best Local Similarity	100.0%; Pred. No. 1.3e+03;
Matches	15; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	4464	TTTTTTTTTTTTTTT 4478 1 TTTTTTTTTTTTTT 15
Dd		
	RESULT 2756	
ADClB592		
ID	ADClB592 standard; DNA; 15 BP.	
XX		
AC	ADClB592;	
XX		
XX		
DT	18-DEC-2003 (first entry)	
XX		
DS	Annealing control primer Oligo-dt15 SEQ ID NO:54.	
XX		
KW	annealing control primer; ACP; annealing specificity;	
KM	nucleic acid amplification; hybridisation; DNA fingerprinting;	
KX	genomic DNA; RNA fingerprint; primer; ss.	
OS	Synthetic.	
PN	WO2003050305-A1.	
XX		
PD	19-JUN-2003.	
XX		
Pf	19-SEP-2002; 2002MO-KR001781.	
XX		
PR	08-DEC-2001; 2001MO-KR002133.	
PR	01-MAY-2002; 2002MO-KR000816.	
XX		
PA	(SEEG-) SERGENE INC.	
XX		
XX		
Chun J;		
DR	WPI; 2003-627256/59.	
XX		
PT	Annealing control primer to improve annealing specificity in nucleic acid amplification, has region complementary to target, arbitrary nucleotide sequence, regulator with universal base/non-discriminatory base analog.	
XX		
PS	Example 2; SEQ ID NO 54; 190pp; English.	
XX		
CC	The present invention describes an annealing control primer (ACP) (I) for improving the annealing specificity in nucleic acid amplification. (II) has a 3'-end portion with a nucleotide sequence complementary to a site on a template nucleic acid for hybridisation, a 5'-end portion having a pre-selected arbitrary nucleotide sequence, and a regulator portion between the 3' and 5'-end portions, comprising a universal or non-discriminatory base analogue, where the regulator portion is capable of annealing an annealing portion of the primer in association with the annealing temperature. (I) is useful for improving annealing specificity in nucleic acid amplification. (I) is useful for amplifying a nucleic acid sequence from a DNA or a mixture of nucleic acids, for selectively amplifying a target nucleic acid sequence from a DNA, and for selectively amplifying a target nucleic acid sequence from a mRNA, by reverse transcribing the mRNA and performing an amplification reaction using (I).	
CC	(I) is also useful for detecting DNA complementary to differentially expressed mRNA in two or more nucleic acid samples, by reverse transcribing the mRNA and performing an amplification reaction using (I).	
CC	(I) is also useful for rapidly amplifying a target cDNA fragment comprising a cDNA region corresponding to the 3'-end or 5'-end region of an mRNA, for amplifying a population of full-length double-stranded cDNAs complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs	
CC		

CC complementary to mRNA. (I) is also useful for amplifying more than one
CC target nucleotide sequence simultaneously using more than one pair of
CC primers in the same reaction, where the primers are derived from (1'), for
CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
CC fingerprint of an mRNA sample, identifying conserved homology segments in
CC a multigene family from an mRNA sample, and for identifying conserved
CC homology segments in a multigene family from gDNA. (I) is also useful for
CC identifying a nucleotide variation in a target nucleic acid, and for
CC mutagenesis in a target nucleic acid. The present sequence represents a
CC primer which is used in the exemplification of the present invention.

xx Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
xx

Sequence 15 BP; 0 A; 0 C; 15 T; 0 U; 0 Other;

Query Match	0.2%	Score 15;	DB 1;	Length 15;
Best Local Similarly	100.0%	Pred. No. 1.3e+03;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	4464		4478
Db	1		15

RESULT 2757
AAK5055
ID AAK5055 standard; DNA; 16 BP.

AC AAX55055;

DT 05-JUL-1999 . (first entry)

C/EBP-beta antisense oligonucleotide fragment.

KM Antisense oligonucleotide; multiple target; antisense treatment;
KM impaired respiration; inflammation; lung disease;
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM acute asthma; allergy; asthma; impaired respiration;
KM respiratory distress syndrome; pain; cystic fibrosis;
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KM prostate cancer; ss.

OS Synthetic.

PN WO9913886-A1.

PD 25-MAR-1999.

PF 17-SEP-1998; 98WO-US019419.

PR 17-SEP-1997; 97US-0059160P.

XX

XX

XX

XX

PT VASOCONSTRICTION.

PS Disclosure; Page 70; 120pp; English.

CC The specification describes antisense oligonucleotides (AA528694-555271).
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target gene, gene intralocus
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AA552272-74. These multiple target oligonucleotides

OY 4470 TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT G 15

RESULT 2759
 AAX18366
 ID AAX18366 standard; DNA; 16 BP.
 XX
 AC AAX18366;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE RT-PCR primer of the invention SEQ ID 7.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 FN JP11032765-A.
 XX
 PD 09-FEB-1999.
 XX
 PE 18-JUL-1997; 97JP-00208312.
 XX
 PR 18-JUL-1997; 97JP-00208312.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 DR WPI; 1999-183822/16.
 XX
 PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 XX
 PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

XX
 SQ Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
 OY Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4470 TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT G 15

RESULT 2760
 AAX34502
 ID AAX34502 standard; DNA; 16 BP.
 XX
 AC AAX34502;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2191.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorochiote; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyrostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PE 03-AUG-1999; 99NO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI NycE JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 539; 1343pp; English.

CC The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cyrostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, CC impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, CC impeded respiration, respiratory distress syndrome, pain, cystic CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, CC carcinomas, and cancers which may metastasise to the lungs, including CC breast and prostate cancer. The reduction of the adenosine content of the CC ONs reduces side effects. The A-containing ONs break down with the CC release of deoxyadenosine which activates adenosine receptors causing CC bronchoconstriction and inflammation. AAX32313 to AAX35312 represent the CC nucleotide sequences given in the sequence listing from the present CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ CC from the previously named sequences. SEQ ID NO:11 to 1660 (AAX32323 to CC AAX33922) are specifically claimed ONs from the present invention. N.B. CC Sequences given in the disclosure of the present invention do not match CC up with their corresponding SEQ ID NO: sequences given in the sequence CC listing

XX
 SQ Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;
 OY Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 GCGGCGGCGGCGGCGG 82
 DB 2 GCGGCGGCGGCGGCGG 16

RESULT 2761
 AAF20624
 ID AAF20624 standard; DNA; 16 BP.
 XX
 AC AAF20624;
 XX

DT 14-MAR-2001 (first entry)
 XX Human C/EBP polynucleotide fragment #2191.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 KM
 XX Homo sapiens.
 OS
 XX
 PN W0200062736-A2.
 PD
 PD 26-OCT-2000.
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI NYCE JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 PT
 PS Claim 14; Page 264; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF19434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 CC
 SO Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGGGGCGGCGGCG 82
 DB 2 GCGGGGCGGCGGCG 16
 RESULT 2762
 ID ABL57075/c
 ABLS7075 standard; DNA, 16 BP.
 XX
 AC ABL57075;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Molecular beacon target sequence.
 KM
 KM Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT msc_binding 1..16
 FT /*tag= a
 FT /bound_molec= "Molecular beacon"
 FT /note= "forms double-stranded region with bases 5-21 of
 sequence in ABL57069"
 XX
 PN W0200218951-A2.
 XX
 XX 07-MAR-2002.
 PD
 PD 29-AUG-2001; 2001WO-US041941.
 PF
 XX 29-AUG-2000; 2000US-0228728P.
 PR 30-MAR-2001; 2001US-0280350P.
 PR
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 PA
 XX
 PI Dubertret B, Calame M, Libhaber A;
 XX
 XX WPI; 2002-404569/43.
 DR
 XX
 XX Sensitive detecting proximity changes in a system that utilizes an
 PT intersecting fluorophore and quencher, for high sensitivity applications,
 PT involves utilizing a metal surface as quencher.
 PT
 PS Example 3; Page 30; 62pp; English.
 XX
 XX The present sequence is that of a perfectly matched target sequence for a
 CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
 CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
 CC a nanoparticle. In the native state, the probe forms a hairpin
 CC conformation with hybridised termini. The proximity of the fluorophore
 CC and quencher (gold nanoparticle) in the molecular beacon results in
 CC little or no detectable fluorescence. Upon hybridisation of the central
 CC complementary stretch of the probe to a target sequence, such as the
 CC present sequence, the hairpin undergoes a conformational change resulting
 CC in an increase in fluorescence, the extent of which is proportional to
 CC the amount of target sequence present. Single mismatches can be detected.
 CC The invention relates generally to the use of metal surface quenchers
 CC such as particles or films for high sensitivity applications in, for
 CC example, detection and diagnostic systems
 CC
 SO Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 DB 16 TTTT TTTT TTTT TTTT 2

RESULT 2763
AB296318 standard; DNA, 16 BP.
XX AC AB296318;
XX DT 17-OCT-2003 (first entry)
XX DS Human C/EBP antisense fragment no.2178.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX KW antiasmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002MO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIDEMIS PHARM INC.
XX PI Nye JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahbuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 11560; 872bp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 68 GCGGGGGGCGGGCGG 82
DB 2 GCGGGGGGCGGGCGG 16

RESULT 2764
AAD57845/C
ID AAD57845 standard; DNA, 16 BP.
XX AC AAD57845;
XX DT 20-NOV-2003 (first entry)
XX DS Target oligonucleotide #2 used in nonlinear optical technique.
XX KW Nonlinear optical technique; screening; ss.
XX OS Unidentified.
XX PN WO2003064991-A2.
XX PD 07-AUG-2003.
XX PF 17-JUL-2002; 2002MO-US022681.
XX PR 17-JUL-2001; 2001US-0306040P.
XX PR 23-OCT-2001; 2001US-0347821P.
XX PR 06-FEB-2002; 2002US-0354668P.
XX PA (SALA/) SALAFSKY J S.
XX PI Salafsky JS;
XX DR WPI; 2003-646172/61.
XX PT Screening candidate binding partner(s) for binding to test molecule by
XX PT applying external force field to sample in homogeneous phase, the
XX PT illuminating sample with light beam(s) at fundamental frequencies, and
XX PT measuring physical properties.
XX PS Disclosure; Fig 20-B; 146bp; English.
XX CC The present invention relates to a method for detecting interactions
XX CC between biological components using a nonlinear optical technique. The
XX CC invention is used for screening candidate binding partner(s) for binding
XX CC to test molecule. It can also be used to detect changes in orientation or
XX CC conformation of the probe and/or target. The present sequence is a target
XX CC oligonucleotide used in nonlinear optical technique
XX CC
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTTTTTTTTTTTTTT 4478
DB 16 TTTTTTTTTTTTTTTT 2
RESULT 2765
ADB68508
ID ADB68508 standard; DNA, 16 BP.
XX AC ADB68508;
XX DT 04-DEC-2003 (first entry)
XX DS PNA-HyPNA hybridisation oligomer.
XX KW hydroxyproline nucleic acid; HyPNA; PNA; peptide nucleic acid;
XX KW gene expression; respiration; secretion; signalling;
XX KW ion-channel activity; cell motility; developmental phenotype;
XX KW tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
XX KW phosphono-peptide nucleic acid; pPNA.
XX OS Synthetic.

```

XX Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /mod base= OTHER
FT /note= "OTHER = P (Phosphono PNA monomer with phenyl
PT group attached to terminal phosphate"
XX
XX WO2003068798-A2.
XX
XX 21-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003904.
XX
XX 09-FEB-2002; 2002US-00072975.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX WPI; 2003-689653/65.
XX
XX Method of inhibiting expression of genes or RNA transcripts, useful for
XX therapy and determining effects of genes, by administering oligomers
XX containing hydroxyproline nucleic acid.
XX
XX Example 17; Page 148; 240pp; English.
XX
XX The invention relates to a novel method of inhibiting the expression of
XX one or more genes or RNA transcripts by administering at least one
XX oligonucleotide analogue that includes at least one hydroxyproline
XX nucleic acid (HYPNA) monomer to a cell or organism or their extracts. The
XX oligonucleotides of the invention may be used to monitor properties
XX including gene expression, respiration, secretion, signalling, ion-
XX channel activity, cell motility, developmental phenotype and tumour
XX regression. Furthermore, they may be utilised to determine the effects of
XX particular genes, as antisense or homologous recombination constructs
XX e.g. for creating animal models of disease and finally, for increasing
XX the activity of some enzymes, such as polymerases. The current sequence
XX is that of the PNA-HYPNA hybridisation oligomer of the invention. This
XX sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
XX (SerNA) components.
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2766
XX AAX69797
XX ID AAX69797 standard; RNA; 17 BP.
XX
XX AAX69797;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme subsequence #1092.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX

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XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1). Kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 13.3%; Pred. No. 1.5e+03;
XX Matches 2; Conservative 13; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4462 ACTTTT TTTT TTTT TTTT 4476
XX 3 ACUUUUUUUUUUUUU 17
XX
XX RESULT 2767
XX AAX69802
XX ID AAX69802 standard; RNA; 17 BP.
XX
XX AAX69802;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme subsequence #1097.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX

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PI Pavco P, Mcswaygen J, Stinchcomb D, Escobedo U;
XX
XX WPI, 1997-259017/23.
DR
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
PS Claim 4; Page 79, 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), Kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;
QY
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 0.0%; Pred. NO. 1.5e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0
QY 4464 TTTTYYYYTTTTTT 4478
DB 1 UUUUUUUUUUUUUU 15
*****
RESULT 2768
AAV37934
ID AAV37934 standard; cDNA; 17 BP.
AC
XX AAV37934;
DT 05-OCT-1998 (first entry)
XX
DE Primer of the specification.
KM Leukocyte; Iga nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS Synthetic.
PN MO9824815-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-JP004469.
PP
XX 05-DEC-1996; 96JP-00325752.
PR
XX (KTOM ) KIOWA HAKKO KOGYO KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;
PI Nomura N, Nagase T, Sawada S, Takei M;
XX
DR WPI, 1998-333259/29.
XX
XX Protein from leukocytes and DNA encoding it - useful as reagents for
PT diagnosing and treating Iga nephropathy.
PS Example 2; Page 33; 41pp; Japanese.
XX
XX PCR primers AAV37933-39 are used in the course of the invention. The
CC specification describes a novel protein isolated from leukocytes of
CC patients with Iga nephropathy. Oligonucleotides based on the DNA sequence
CC encoding this protein are useful as reagents for diagnosing and treating
XX Iga nephropathy
XX

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```

SQ      Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
      Query Match          0.2%; Score 15; DB 1; Length 17;
      Best Local Similarity 100.0%; Pred. No. 1.5e+03;
      Matches 15; Conservative 0; Mismatches 0; Indels 0;
QY      4464 TTTT TTTT TTTT TTTT TTTT 4478
      |||||
      2 TTTT TTTT TTTT TTTT 16
DB
      RESULT 2769
      ID AAV49503
      AAV49503 standard; cDNA to mRNA; 17 BP.
      AC AAV49503;
      XX
      XX
      DT 18-NOV-1998 (first entry)
      DE Human eosinophil cell activator HVC002 primer #1.
      KW Eosinophil cell activator; treatment; diagnosis; malignant tumour;
      KW parasitic infection; allergic inflammation; eosinophilic pneumonia;
      KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
      XX
      XX Synthetic.
      OS Homo sapiens.
      XX
      XX MO9824817-A1.
      PN
      XX 11-JUN-1998.
      PD
      XX
      XX 05-DEC-1997; 97WO-JP004470.
      PF
      XX
      XX 05-DEC-1996; 96JP-00325762.
      PR
      XX
      XX (KTOW ) KTOWA HAKKO KOGYO KK.
      PA
      XX Yoshisue H, Satto A, Nakagawa S, Kuga T, Shinkai A, Koike M;
      XX Nishii T;
      XX WPT, 1998-333261/29.
      DR
      XX
      XX DNA and encoded protein which activates eosinophil cells - for treatment
      PT of cancer, parasite infection, autoimmune disease and allergic
      PT inflammation.
      XX
      XX Example 1; Page 64; 92pp; Japanese.
      XX
      XX AAV49503-V49507 are primers used in the isolation of a human eosinophil
      CC cell activator. This protein and antibodies generated from the protein
      CC can be used for treatment and diagnosis of malignant tumours, parasitic
      CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset
      CC eosinophilia, and autoimmune disease. DNA can be used for diagnosis, and
      CC the antisense DNA in gene therapy of these disorders. The protein can be
      CC used for screening of potential agonists or antagonists of its activity
      XX
      SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
      Query Match          0.2%; Score 15; DB 1; Length 17;
      Best Local Similarity 100.0%; Pred. No. 1.5e+03;
      Matches 15; Conservative 0; Mismatches 0; Indels 0;
QY      4464 TTTT TTTT TTTT TTTT TTTT 4478
      |||||
      2 TTTT TTTT TTTT TTTT 16
DB
      RESULT 2770
      ID AAX18370
      AAX18370 standard; DNA; 17 BP.
      AC AAX18370;
      XX

```

```

XX
DT 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 11.
DE
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JP11032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
XX PS Disclosure; Page 11; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma; in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
XX SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX |||||
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX Db
XX
XX RESULT 2771
XX AAA30179
XX ID AAA30179 standard; DNA; 17 BP.
XX
XX AC AAA30179;
XX
XX DT 16-AUG-2000 (first entry)
XX
XX DE PCR primer GT15A used in pollenosis associated gene identification.
XX
XX KM Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200020575-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 06-OCT-1999; 99WO-JP005506.
XX
XX PR 06-OCT-1998; 98JP-00284610.
XX
XX

```

```

PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kaehiwaraba T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
XX DR WPI; 2000-317712/27.
XX
XX PT Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
XX PS Example 6; Page 38; 44pp; Japanese.
XX
XX This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX |||||
XX 2 TTTT TTTT TTTT TTTT 16
XX
XX Db
XX
XX RESULT 2772
XX AAA30180
XX ID AAA30180 standard; DNA; 17 BP.
XX
XX AC AAA30180;
XX
XX DT 16-AUG-2000 (first entry)
XX
XX DE PCR primer GT15C used in pollenosis associated gene identification.
XX
XX KM Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200020575-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 06-OCT-1999; 99WO-JP005506.
XX
XX PR 06-OCT-1998; 98JP-00284610.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kaehiwaraba T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
XX DR WPI; 2000-317712/27.
XX
XX PT Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
XX PS Example 6; Page 38; 44pp; Japanese.
XX
XX This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis

```

CC associated protein, diagnosing pollenosis and screening candidate
 CC compounds for treating pollenosis. The gene can be used in diagnosing
 CC pollenosis, particularly cedar pollenosis, and screening candidate
 CC compounds for pollenosis treatment

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

2 TTTT TTTT TTTT TTTT 16

RESULT 2773

AAZ82722

ID AAZ82722 standard; DNA; 17 BP.

AC AAZ82722;

DT 10-NOV-2000 (first entry)

DE Human IGA nephropathy-associated cDNA primer #63.

XX IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 KW human; primer; ss.

XX Homo sapiens.

XX WO9963085-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-JP002855.

XX 02-JUN-1998; 98JP-00152603.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;

PI Sawada S, Takei M, Shibata K, Furiya A;

DR WPI; 2000-097328/08.

XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.

XX Claim 3; Page 170; 180pp; Japanese.

CC This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy
 CC incorporating the antisense sequences; the treatment of IGA nephropathy
 CC using the antisense sequences; for mRNA inhibition; proteins associated
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
 CC antibodies recognizing these proteins; the production of the proteins by
 CC culture of host cells transformed with DNA encoding them; diagnostic
 CC reagents for IGA nephropathy containing the antibodies; and compositions
 CC for the treatment of IGA nephropathy which contain the antibodies. The
 CC products of the invention can be used for the diagnosis and treatment of
 CC IGA nephropathy. This sequence represents a primer used in the isolation
 CC and identification of the human IGA nephropathy-associated proteins
 CC described in the method of the invention

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

db 2 TTTT TTTT TTTT TTTT 16

RESULT 2774

AAZ82720

ID AAZ82720 standard; DNA; 17 BP.

AC AAZ82720;

DT 10-NOV-2000 (first entry)

DE Human IGA nephropathy-associated cDNA primer #61.

XX IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 KW human; primer; ss.

XX Homo sapiens.

XX WO9963085-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-JP002855.

XX 02-JUN-1998; 98JP-00152603.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;

PI Sawada S, Takei M, Shibata K, Furiya A;

DR WPI; 2000-097328/08.

XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.

XX Claim 3; Page 169; 180pp; Japanese.

CC This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy
 CC incorporating the antisense sequences; the treatment of IGA nephropathy
 CC using the antisense sequences; for mRNA inhibition; proteins associated
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
 CC antibodies recognizing these proteins; the production of the proteins by
 CC culture of host cells transformed with DNA encoding them; diagnostic
 CC reagents for IGA nephropathy containing the antibodies; and compositions
 CC for the treatment of IGA nephropathy which contain the antibodies. The
 CC products of the invention can be used for the diagnosis and treatment of
 CC IGA nephropathy. This sequence represents a primer used in the isolation
 CC and identification of the human IGA nephropathy-associated proteins
 CC described in the method of the invention

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

2 TTTT TTTT TTTT TTTT 16

RESULT 2775

AAZ89372

ID AAZ89372 standard; DNA; 17 BP.

AC AAZ89372;

DT 15-JUN-2000 (first entry)


```

DE RNA detecting primer #2.
XX Amplification; detection; gene expression; primer; ss.
XX Unidentified.
XX DE19840731-A1.
XX PN
XX PD
XX 09-MAR-2000.
XX PF
XX 07-SEP-1998; 98DE-01040731.
XX PR
XX 07-SEP-1998; 98DE-01040731.
XX PA
XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX DR
XX WPI; 2000-257789/23.
XX
PT Analysis of RNA samples, useful for detection of differential gene
PT expression uses two differently labeled primers.
XX
XX PS
XX Disclosure; Page 10; 10pp; German.
XX
CC This invention describes a novel method for analysis of an RNA sample
CC which comprises amplifying cDNA with first and second differentially labeled
CC primers and analysis of the amplified labeled cDNA. The method is useful
CC for analyzing differential gene expression, for identifying and/or
CC characterizing pharmacological activities or for identifying target
CC genes. The use of different primer combinations allow more cDNAs to be
CC amplified. The method also provides a more detailed analysis than prior
CC art methods. This sequence represents a primer used to illustrate the
CC method of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
QY
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

```

RESULT 2776

AA236739
ID AA236739 standard; DNA; 17 BP.

XX
AC AA236739;

XX
DT 13-MAR-2000 (first entry)

XX
DE Anchored oligo(dT) primer ATISA used for modified differential display.

XX
KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer; disease;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

XX
OS Synthetic.

XX
PN WO9955913-A2.

XX
PD 04-NOV-1999.

XX
PF 27-APR-1999; 99WO-US009119.

XX
PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.

```

PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
XX PI
XX McCelland M, Welsh J, Trenkle T;
XX DR
XX WPI; 2000-086388/07.
XX
XX PT
XX Measuring expression of low abundance reduced complexity target nucleic
XX acid molecules.
XX
XX PS
XX Example 3; Page 91, 187pp; English.
XX
CC AA236739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC practically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify disease
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery
XX
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
QY
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16

```

RESULT 2777

AAC64202
ID AAC64202 standard; DNA; 17 BP.

XX
AC AAC64202;

XX
DT 21-FEB-2001 (first entry)

XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.

XX
KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.

XX
OS Synthetic.

XX
PN WO200065046-A1.

XX
PD 02-NOV-2000.

XX
PF 26-APR-2000; 2000WO-JP002730.

XX
PR 27-APR-1999; 99JP-00120489.

XX
PA (GENO-) GENOX RES INC.

XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687339/67.

XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.

XX Example 6; Page 69; 80pp; Japanese.

PS The invention relates to the human pollinosis-associated gene 373 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates also relates

CC to the protein encoded by pollinosis gene 373; expression constructs and

CC host cells comprising pollinosis-associated gene 373 nucleic acids;

CC pollinosis-associated gene 373 primers and probes; antibodies against the

CC protein encoded by the gene; methods of detection of pollinosis-

CC associated gene 373 nucleic acids; and a method of diagnosis of allergic

CC diseases via the detection of pollinosis-associated gene 373 nucleic

CC acids. The invention additionally encompasses methods of screening drug

CC candidates for the treatment of allergic disease by measuring the

CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated

CC T-cells in the presence of a test compound relative to a control.

CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic

CC diseases and in the screening of drug candidates for the treatment of

CC such diseases. The present sequence represents a PCR primer used in the

CC isolation of human pollinosis-associated gene 373 cDNA

CC

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478

Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2778

AAC64203

ID AAC64203 standard; DNA; 17 BP.

XX AAC64203;

AC

XX 21-FEB-2001 (first entry)

DT

XX PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.

DE

XX Human; pollinosis-associated gene 373; IGE; immunoglobulin E;

KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;

KW drug screening; allergic disease; PCR primer; ss.

XX

OS Synthetic.

XX

FN WO200065046-A1.

PN

XX 02-NOV-2000.

PD

XX 26-APR-2000; 2000WO-JP002730.

PE

XX 27-APR-1999; 99JP-00120489.

PR

XX (GENO-) GENOX RES INC.

PA

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX

DR WPI; 2000-687339/67.

XX

PT Pollinosis-associated gene 373 undergoing significantly low expression in

PT subjects with high cedar pollen-specific immunoglobulin E levels, useful

PT in diagnosis of allergic diseases and screening drug candidates.

XX

XX Example 6; Page 70; 80pp; Japanese.

PS The invention relates to the human pollinosis-associated gene 373 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates also relates

CC to the protein encoded by pollinosis gene 373; expression constructs and

CC host cells comprising pollinosis-associated gene 373 nucleic acids;

CC pollinosis-associated gene 373 primers and probes; antibodies against the

CC protein encoded by the gene; methods of detection of pollinosis-

CC associated gene 373 nucleic acids; and a method of diagnosis of allergic

CC diseases via the detection of pollinosis-associated gene 373 nucleic

CC acids. The invention additionally encompasses methods of screening drug

CC candidates for the treatment of allergic disease by measuring the

CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated

CC T-cells in the presence of a test compound relative to a control.

CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic

CC diseases and in the screening of drug candidates for the treatment of

CC such diseases. The present sequence represents a PCR primer used in the

CC isolation of human pollinosis-associated gene 373 cDNA

CC

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478

Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2779

AAC64181

ID AAC64181 standard; DNA; 17 BP.

XX AAC64181;

AC

XX 21-FEB-2001 (first entry)

DT

XX PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.

DE

XX Human; pollinosis-associated gene 419; FAF-1 homologue;

KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;

KW T-cell; reduced expression; detection; diagnosis; drug screening;

KW allergic disease; PCR primer; ss.

XX

OS Synthetic.

XX

FN WO200065045-A1.

PN

XX 02-NOV-2000.

PD

XX 26-APR-2000; 2000WO-JP002729.

PE

XX 27-APR-1999; 99JP-00120490.

PR

XX (GENO-) GENOX RES INC.

PA

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX

DR WPI; 2000-687338/67.

XX

PT Pollinosis-associated gene 419 undergoing significantly low expression in

PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis

PT of allergic diseases and screening drug candidates.

XX

XX Example 6; Page 49; 77pp; Japanese.

PS The invention relates to the human pollinosis-associated gene 419 which

CC exhibits reduced expression in the T-cells of individuals with high cedar

CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from

CC T-cells from individuals allergic to cedar pollen using the differential

CC display method. Pollinosis-associated gene 419 has homology with the gene

CC encoding human Fas-associated factor-1 (FAF-1). The invention also

CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
|||||
2 TTTT TTTT TTTT TTTT 16
Db
RESULT 2780
AAC64182
ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
XX Human; pollinosis-associated gene 419; PAF-1 homologue;
KM Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KM T-cell; reduced expression; detection; diagnosis; drug screening;
KM allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200065045-A1.
PN
XX 02-NOV-2000.
PD
XX 26-APR-2000; 2000WO-JP002729.
PF
XX 27-APR-1999; 99JP-00120490.
PR
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687338/67.
DR
XX Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;

CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
|||||
2 TTTT TTTT TTTT TTTT 16
Db
RESULT 2781
AAC64171
ID AAC64171 standard; DNA; 17 BP.
XX
AC AAC64171;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
XX
XX Human; pollinosis-associated gene 513; IGE; immunoglobulin E;
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KM drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200065049-A1.
PN
XX 02-NOV-2000.
PD
XX 26-APR-2000; 2000WO-JP002733.
PF
XX 27-APR-1999; 99JP-00120491.
PR
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687342/67.
DR
XX Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 513 cDNA
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2782
 AAC64172
 ID AAC64172 standard; DNA; 17 BP.

AC AAC64172;
 XX
 DT 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.

XX Human; pollinosis-associated gene 513; IGE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KM drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

PN WO20065049-A1.

XX 02-NOV-2000.

PF 26-APR-2000; 2000WO-JP002733.

PR 27-APR-1999; 99JP-00120491.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 P1 Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687342/67.

DR WPI; 2000-687342/67.
 XX
 PT Pollinosis-associated gene 513 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.

XX Example 6; Page 38; 46pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 513 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 513 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 513 nucleic acids; and methods of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 513
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 513 cDNA

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2783
 AAC64161
 ID AAC64161 standard; DNA; 17 BP.

AC AAC64161;
 XX
 DT 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.

XX Human; pollinosis-associated gene 581; IGE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KM drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

PN WO20065048-A1.

XX 02-NOV-2000.

PF 26-APR-2000; 2000WO-JP002732.

PR 27-APR-1999; 99JP-00120492.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 P1 Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687341/67.

DR WPI; 2000-687341/67.
 XX
 PT Pollenosis-associated gene 581 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.

XX Example 6; Page 39; 69pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 581 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods
 CC to the protein encoded by pollinosis-associated gene 581; to expression
 CC constructs and host cells comprising pollinosis-associated gene 581
 CC nucleic acids; pollinosis-associated gene 581 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 581 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 581 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 581 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 581 cDNA

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

```

RESULT 2784
AAC64162
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IGE; immunoglobulin E;
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000MO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Ohida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16
XX
RESULT 2785
AAC64213
ID AAC64213 standard; DNA; 17 BP.
XX
AC AAC64213;
XX

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XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IGE; immunoglobulin E;
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000MO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Ohida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 41; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16
XX
RESULT 2786
AAC64214
ID AAC64214 standard; DNA; 17 BP.
XX
AC AAC64214;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IGE; immunoglobulin E;
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX

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OS Synthetic.
XX
XX WO200065051-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002735.
XX
XX 27-APR-1999; 99JP-00120493.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687344/67.
XX
XX Pollinosis-associated gene 627 undergoing significantly low expression in
XX subjects with high cedar pollen-specific IgE levels, useful in diagnosis
XX of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 42; 51pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 627 which
XX exhibits significantly reduced expression in the T-cells of individuals
XX with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX was isolated from T-cells from individuals allergic to cedar pollen using
XX the differential display method. The invention also relates to methods of
XX detection of pollinosis-associated gene 627 nucleic acids; a method of
XX diagnosis of allergic diseases via the detection of pollinosis-associated
XX gene 627 nucleic acids; and a method of screening drug candidates for the
XX treatment of allergic disease by measuring the expression of pollinosis-
XX associated gene 627 in pollen antigen-stimulated T-cells in the presence
XX of a test compound relative to a control. Pollinosis-associated gene 627
XX is useful in the diagnosis of allergic diseases and in the screening of
XX drug candidates for the treatment of such diseases. The present sequence
XX represents a PCR primer used in the isolation of human pollinosis-
XX associated gene 627 cDNA
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16
RESULT 2787
AAC64231
ID AAC64231 standard; DNA; 17 BP.
XX
XX AAC64231;
AC
XX 21-FEB-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
DE
XX
XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;
XX immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
XX detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200065050-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002734.
XX
XX 27-APR-1999; 99JP-00120494.
XX
XX (GENO-) GENOX RES INC.

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XX
XX (GENO-) GENOX RES INC.
XX (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX Yokoi A;
XX WPI; 2000-687343/67.
XX
XX Pollinosis-associated gene 795 undergoing significantly low expression in
XX subjects with high cedar pollen-specific IgE levels, useful in diagnosis
XX of allergic diseases and screening drug candidates.
XX
XX Page 45; Example 6; 73pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 795 which
XX exhibits significantly reduced expression in the T-cells of individuals
XX with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX was isolated from T-cells from individuals allergic to cedar pollen using
XX the differential display method. Pollinosis-associated gene 795 has
XX homology with the human vimentin gene. The invention also relates also
XX relates to the protein encoded by pollinosis gene 795; to expression
XX constructs and host cells comprising pollinosis-associated gene 795
XX nucleic acids; pollinosis-associated gene 795 primers and probes;
XX antibodies against the protein encoded by the gene; methods of detection
XX of pollinosis-associated gene 795 nucleic acids; and a method of
XX diagnosis of allergic diseases via the detection of pollinosis-associated
XX gene 795 nucleic acids. The invention additionally encompasses methods of
XX screening drug candidates for the treatment of allergic diseases by
XX measuring the expression of pollinosis-associated gene 795 in pollen
XX antigen-stimulated T-cells in the presence of a test compound relative to
XX a control. Pollinosis-associated gene 795 is useful in the diagnosis of
XX allergic diseases and in the screening of drug candidates for the
XX treatment of such diseases. The present sequence represents a PCR primer
XX used in the isolation of human pollinosis-associated gene 795 cDNA
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16
RESULT 2788
AAC64230
ID AAC64230 standard; DNA; 17 BP.
XX
XX AAC64230;
AC
XX 21-FEB-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
DE
XX
XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;
XX immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
XX detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200065050-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002734.
XX
XX 27-APR-1999; 99JP-00120494.
XX
XX (GENO-) GENOX RES INC.

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PA (EISA) EISAI CO LTD.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX WPI; 2000-667343/67.
DR
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16
RESULT 2789
AAC92292
ID AAC92292 standard; DNA; 17 BP.
XX
AC AAC92292;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200073439-A1.
XX PD 07-DEC-2000.
XX PF 18-MAY-2000; 2000WO-JP003191;
XX PR 27-MAY-1999; 99JP-00148784.
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX WPI; 2001-061528/07.
XX
DR
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 43; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16
RESULT 2790
AAC92293
ID AAC92293 standard; DNA; 17 BP.
XX
AC AAC92293;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200073439-A1.
XX PD 07-DEC-2000.
XX PF 18-MAY-2000; 2000WO-JP003191.
XX PR 27-MAY-1999; 99JP-00148784.
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX WPI; 2001-061528/07.
XX
DR
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 44; 61pp; Japanese.
XX

CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
CC
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
QY Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16
RESULT 2791
AAC91720
ID AAC91720 standard; DNA; 17 BP.
AC AAC91720;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
QY Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16
RESULT 2792
AAC91719
ID AAC91719 standard; DNA; 17 BP.
AC AAC91719;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-associated gene 787 cDNA
 CC associated gene 787 cDNA
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 |||||
 DB 2 TTTT TTTT TTTT TTTT 16
 RESULT 2793
 AAC82875 AAC82875 standard; DNA; 17 BP.
 XX AAC82875;
 AC AAC82875;
 XX 20-MAR-2001 (first entry)
 DT Human pollinosis-associated gene 441 primer #2.
 XX
 DE Human pollinosis-associated gene 441; allergy; T cell;
 XX
 KM Pollinosis; pollinosis-associated gene 441; allergy; T cell;
 KW pollen scattering; antigen; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073435-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003190.
 XX
 PR 27-MAY-1999; 99JP-00148783.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2001-061526/07.
 XX
 PT Pollinosis-associated gene 441 which undergoes lower expression in
 PT subjects after pollen scattering; useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 35; 42pp; Japanese.
 XX
 CC This invention describes a novel nucleic acid molecule comprising a
 CC sequence (I) which undergoes significantly low expression in subjects
 CC after pollen scattering, and is useful in diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 |||||
 DB 2 TTTT TTTT TTTT TTTT 16
 RESULT 2794
 AAC82874 AAC82874 standard; DNA; 17 BP.
 XX AAC82874;
 AC AAC82874;

XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Human pollinosis-associated gene 441 primer #1.
 XX
 KM Pollinosis; pollinosis-associated gene 441; allergy; T cell;
 KW pollen scattering; antigen; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073435-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003190.
 XX
 PR 27-MAY-1999; 99JP-00148783.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2001-061526/07.
 XX
 PT Pollinosis-associated gene 441 which undergoes lower expression in
 PT subjects after pollen scattering; useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 35; 42pp; Japanese.
 XX
 CC This invention describes a novel nucleic acid molecule comprising a
 CC sequence (I) which undergoes significantly low expression in subjects
 CC after pollen scattering, and is useful in diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 |||||
 DB 2 TTTT TTTT TTTT TTTT 16
 RESULT 2795
 AAH47127
 ID AAH47127 standard; DNA; 17 BP.
 XX
 AC AAH47127;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of primer GT15C.
 XX
 KM B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200165259-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 23-FEB-2001; 2001WO-JP001372.
 XX
 PR 02-MAR-2000; 2000JP-00061832.
 XX
 PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saio H;
 XX WPI; 2001-557789/62.
 DR WPI; 2001-557789/62.
 XX
 PT Diagnosis of allergies including atopic dermatitis.
 XX
 PS Example 6; Page 66; 83pp; Japanese.
 XX
 CC The invention provides a method of diagnosis of allergies that involves:
 CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
 CC in T-cells; and comparing them with the level of expression in healthy T-
 CC cells. The method is useful for diagnosing allergies, particularly atopic
 CC dermatitis. The present sequence represents a PCR primer used for
 CC analysis of the expression of the above genes
 CC
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 DB 2 TTTT TTTT TTTT TTTT 16
 RESULT 2796
 AAH47126
 ID AAH47126 standard; DNA; 17 BP.
 XX
 AC AAH47126;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of primer GT15A.
 XX
 KM B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
 KM PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200165259-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 23-FEB-2001; 2001WO-JP001372.
 XX
 PR 02-MAR-2000; 2000JP-00061832.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX
 PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saio H;
 XX
 DR WPI; 2001-557789/62.
 XX
 PT Diagnosis of allergies including atopic dermatitis.
 XX
 PS Example 6; Page 65; 83pp; Japanese.
 XX
 CC The invention provides a method of diagnosis of allergies that involves:
 CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
 CC in T-cells; and comparing them with the level of expression in healthy T-
 CC cells. The method is useful for diagnosing allergies, particularly atopic
 CC dermatitis. The present sequence represents a PCR primer used for
 CC analysis of the expression of the above genes
 CC
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4478
 DB 2 TTTT TTTT TTTT TTTT 16
 RESULT 2797
 ABN01547/C
 ID ABN01547 standard; DNA; 17 BP.
 XX
 AC ABN01547;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1539.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Yi Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or a specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 1539; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognize hGDMLP-
 CC 1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionization, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart

CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2474 TCCAGGGCACCGCC 2488
Db 15 TCCAGGGCACCGCC 1
RESULT 2798
ABN01546/c
ID ABN01546 standard; DNA; 17 BP.
XX
AC ABN01546;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1538.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 1538; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2474 TCCAGGGCACCGCC 2488
Db 16 TCCAGGGCACCGCC 2
RESULT 2799
ABN01545/c
ID ABN01545 standard; DNA; 17 BP.
XX
AC ABN01545;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1537.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX

PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
PS Disclosure; SEQ ID NO 1537; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2474 TCCAGGCGACCGCC 2488
DB 17 TCCAGGCGACCGCC 3
XX
RESULT 2800
ABK49634
ID ABK49634 standard; DNA; 17 BP.
XX
AC ABK49634;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G,
PI Takahashi E;
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing

PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
XX Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprising determining the expression level of a gene containing the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTTTTTTTTTTTTT 4478
DB 2 TTTTTTTTTTTTTTT 16
XX
RESULT 2801
ABK49635
ID ABK49635 standard; DNA; 17 BP.
XX
AC ABK49635;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G,
PI Takahashi E;
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate

PT compounds for remedies.
 XX
 PS Example 1; Page 56; 72pp; Japanese.
 XX
 CC The invention relates to a method for examining allergic diseases
 CC comprises determining the expression level of a gene containing, the
 CC human cDNA appearing as ABK43633 which has homology with
 CC acetyltransferases in the eosinophils of a patient and comparing the
 CC expression level with that in the eosinophils of a healthy individual
 CC (i.e. differential display). Also included are methods of screening for
 CC candidate compounds which affect the expression level of the gene or the
 CC activity of the protein encoded by the gene (including related proteins
 CC and mutants), the use of probes based on the gene sequence in the
 CC examination of allergic diseases, the use of reporter constructs in the
 CC screening of candidate compounds, a vector containing a the transcription
 CC -controlling region of the gene, cells transformed with the vector, an
 CC antibody against the protein and a model animal for allergic diseases
 CC which is a transgenic non-human vertebrate with lowering of expression
 CC intensity of the gene in eosinophils. The method is examining allergic
 CC diseases particularly atopic dermatitis which is also applicable in
 CC screening candidate compounds for remedies. Such method can be performed
 CC in high throughput, at low cost. The present sequence is a differential
 CC display PCR primer for the cDNA encoding the human acetyltransferase-like
 CC protein 20-90-05
 CC
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16
 RESULT 2802
 ABL59038
 ID ABL59038 standard; DNA; 17 BP.
 XX
 AC ABL59038;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Nucleotide sequence of PCR primer GT15A.
 XX
 KM Human; allergosis; eosinophil; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002095500-A.
 XX
 PD 02-APR-2002.
 XX
 PF 25-SEP-2000; 2000JP-00291316.
 XX
 PR 25-SEP-2000; 2000JP-00291316.
 XX
 PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
 XX
 DR WPI; 2002-439993/47.
 XX
 PT Examining allergosis, involves measuring the expression levels of a
 PT specific gene, and comparing it to the levels in the eosinophils of a
 PT healthy control.
 XX
 PS Example 1; Page 17; 20pp; Japanese.
 XX
 CC The specification describes a method for examining allergosis. The method
 CC comprises measuring the expression level of the gene given in ABL59037,
 CC and comparing it with the expression level of the gene in the eosinophils
 CC of a healthy person. The method is used for the examination of

CC allergosis. The present sequence represents a PCR primer, which is used
 CC in the course of the invention
 CC
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16
 RESULT 2803
 ABL59039
 ID ABL59039 standard; DNA; 17 BP.
 XX
 AC ABL59039;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Nucleotide sequence of PCR primer GT15C.
 XX
 KM Human; allergosis; eosinophil; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002095500-A.
 XX
 PD 02-APR-2002.
 XX
 PF 25-SEP-2000; 2000JP-00291316.
 XX
 PR 25-SEP-2000; 2000JP-00291316.
 XX
 PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
 XX
 DR WPI; 2002-439993/47.
 XX
 PT Examining allergosis, involves measuring the expression levels of a
 PT specific gene, and comparing it to the levels in the eosinophils of a
 PT healthy control.
 XX
 PS Example 1; Page 17; 20pp; Japanese.
 XX
 CC The specification describes a method for examining allergosis. The method
 CC comprises measuring the expression level of the gene given in ABL59037,
 CC and comparing it with the expression level of the gene in the eosinophils
 CC of a healthy person. The method is used for the examination of
 CC allergosis. The present sequence represents a PCR primer, which is used
 CC in the course of the invention
 CC
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16
 RESULT 2804
 ABL59829
 ID ABL59829 standard; DNA; 17 BP.
 XX
 AC ABL59829;
 XX
 DT 15-AUG-2002 (first entry)
 XX

DE	Human allergic disease related PCR primer SEQ ID NO: 18.
XX	
KW	Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW	primer; ss.
XX	
OS	Homo sapiens.
PN	WO200233069-A1.
PD	
PP	25-APR-2002.
XX	
PF	28-SEP-2001; 2001WO-JP008574.
XX	
PR	13-OCT-2000; 2000JP-00314093.
XX	
PA	(GENO-) GENOX RES INC.
XX	(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PI	Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagaau T, Saito H,
XX	
DR	WPI; 2002-372311/40.
PT	
PT	Method for examining allergic diseases by differential display of
PT	seventeen genes showing different expression particularly significant
PT	increase in eosinophils in patients with mild atopic dermatitis, also
PT	applicable in screening compounds.
PS	
XX	Example 1; Page 109; 165pp; Japanese.
CC	
CC	The present invention relates to a method for examining allergic diseases
CC	which involves determining the expression level of a gene, having one of
CC	the 17 nucleotide sequences shown in ABN9812-ABN9828, in the
CC	eosinophils in a patient and comparing the expression level with that in
CC	the eosinophils of a healthy individual. The method can be used to
CC	examine allergic diseases, particularly atopic dermatitis, and its early
CC	diagnosis, which is also applicable in screening candidate compounds for
CC	remedies. The present sequence is a PCR primer described in the
CC	exemplification of the invention
SO	
	Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
	Query Match 0.2%; Score 15; DB 1; Length 17;
	Best Local Similarity 100.0%; Pred. No. 1.5e+03;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTT TTTTTTTTTTTT 4478 DB 2 TTTT TTTTTTTTTT 16
	RESULT 2805
ID	ABN9830 standard; DNA; 17 BP.
AC	ABN9830;
XX	
DT	15-AUG-2002 (first entry)
XX	
DE	Human allergic disease related PCR primer SEQ ID NO: 19.
XX	
KW	Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW	primer; ss.
XX	
OS	Homo sapiens.
PN	WO200233069-A1.
PD	
PP	25-APR-2002.
XX	
PF	28-SEP-2001; 2001WO-JP008574.
XX	
PR	13-OCT-2000; 2000JP-00314093.
XX	

```

PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI, 2002-372311/40.
XX
XX
XX Example 1, Page 109, 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX which involves determining the expression level of a gene, having one of
XX the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
XX eosinophils in a patient and comparing the expression level with that in
XX the eosinophils of a healthy individual. The method can be used to
XX examine allergic diseases, particularly atopic dermatitis, and its early
XX diagnosis, which is also applicable in screening candidate compounds for
XX remedies. The present sequence is a PCR primer described in the
XX exemplification of the invention
XX
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTTTT 4478
XX |||||||
XX 2 TTTTTTTTTTTTTTTT 16
XX
XX RESULT 2806
XX AAL49948
XX ID AAL49948 standard; DNA; 17 BP.
XX AC AAL49948;
XX
XX 10-DEC-2002 (first entry)
XX DT
XX DE Human B153 expression in allergic disease related PCR primer G715A.
XX
XX Human; allergy; B153; differential expression; anti-allergic; asthma;
XX KW antiaesthetic; anti-inflammatory; atopic skin inflammation; PCR; primer;
XX 88.
XX
XX OS
XX OS Unidentified.
XX
XX WO200250269-A1.
XX PN
XX PD 27-JUN-2002.
XX
XX PF 21-DEC-2001; 2001WO-JP011286.
XX
XX PR 21-DEC-2000; 2000JP-00389476.
XX
XX (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI, 2002-713252/77.
XX DR
XX
XX Examination of allergic diseases comprises detecting gene B153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.
XX
XX Example 6; Page 81; 102pp; Japanese.
XX
XX The present invention relates to a method of examining allergic diseases

```

CC which comprises comparing the expression level of gene B153 in allergy
 CC patients with the expression level in healthy subjects. The method is
 CC useful for the treatment, prevention, diagnosis and study of allergic
 CC diseases including atopic skin inflammation and asthma. The present
 CC sequence is a PCR primer described in the exemplification of the
 CC invention

XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478
 2 TTTT TTTT TTTT TTTT TTTT 16

Db

RESULT 2807
 AAL49949
 ID AAL49949 standard; DNA; 17 BP.
 XX
 AC AAL49949;
 XX
 DT 10-DEC-2002 (first entry)
 DE Human B153 expression in allergic disease related PCR primer GT15C.
 XX
 KM Human; allergy; B153; differential expression; antiallergic; asthma;
 KM antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
 KM ss.
 XX
 OS Unidentified.
 XX
 PN WO200250269-A1;
 XX
 PD 27-JUN-2002.
 XX
 PF 21-DEC-2001; 2001WO-JP011286.
 XX
 PR 21-DEC-2000; 2000JP-00389476.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX
 PI Matsunoto Y, Imai Y, Oshida T, Sugita Y, Nagaau T, Tsujimoto G;
 XX
 DR WPI; 2002-713252/77.
 XX
 PT Examination of allergic diseases comprises detecting gene B153 over-
 PT expressed in T cells of allergy patients for diagnosis treatment and
 PT investigation of atopic skin inflammation and asthma.
 XX
 PS Example 6; Page 82; 102pp; Japanese.
 XX
 CC The present invention relates to a method of examining allergic diseases
 CC which comprises comparing the expression level of gene B153 in allergy
 CC patients with the expression level in healthy subjects. The method is
 CC useful for the treatment, prevention, diagnosis and study of allergic
 CC diseases including atopic skin inflammation and asthma. The present
 CC sequence is a PCR primer described in the exemplification of the
 CC invention

XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478
 2 TTTT TTTT TTTT TTTT TTTT 16

Db

RESULT 2808
 AAL47234
 ID AAL47234 standard; DNA; 17 BP.
 XX
 AC AAL47234;
 XX
 DT 22-AUG-2002 (first entry)
 DE Allergic disease examination method related anchor primer SEQ ID NO: 2.
 XX
 KM Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KM atopic dermatitis; human; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200233122-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-JP008937.
 XX
 PR 13-OCT-2000; 2000JP-00314093.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (RISA) RISA CO LTD.
 XX
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagaau T, Saito H;
 PI Takahashi E;
 XX
 DR WPI; 2002-372313/40.
 XX
 PT Method for examining allergic diseases by differential display of
 PT intersectin 2 gene showing different expression particularly significant
 PT increase in eosinophils in patients.
 XX
 PS Example 1; Page 52; 90pp; Japanese.
 XX
 CC The present invention relates to a method for examining allergic diseases
 CC with intersectin 2 gene or a gene with equivalent function of intersectin
 CC 2 as an indicator gene, which comprises determining the expression level
 CC of the gene in the eosinophils in a patient, and comparing the expression
 CC level with that in the eosinophils of a healthy individual. The method is
 CC also applicable in screening allergic diseases, particularly atopic dermatitis, which is
 CC present sequence is an anchor primer described in the exemplification of
 CC the invention

XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478
 2 TTTT TTTT TTTT TTTT TTTT 16

Db

RESULT 2809
 AAL47235
 ID AAL47235 standard; DNA; 17 BP.
 XX
 AC AAL47235;
 XX
 DT 22-AUG-2002 (first entry)
 DE Allergic disease examination method related anchor primer SEQ ID NO: 3.
 XX
 KM Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KM atopic dermatitis; human; PCR; primer; ss.
 XX

```

OS Unidentified.
PN WO200233122-A1.
PD 25-APR-2002.
PF 11-OCT-2001; 2001WO-JP008937.
PR 13-OCT-2000; 2000JP-00314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA ) EISAI CO LTD.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagaau T, Saito H;
XX Takahashi E;
XX WPI, 2002-372313/40.
XX
XX Method for examining allergic diseases by differential display of
XX intersectin 2 gene showing different expression particularly significant
XX increase in eosinophils in patients.
XX
XX Example 1; Page 53; 90pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX with intersectin 2 gene or a gene with equivalent function of intersectin
XX 2 as an indicator gene, which comprises determining the expression level
XX of the gene in the eosinophils in a patient, and comparing the expression
XX level with that in the eosinophils of a healthy individual. The method is
XX for examining allergic diseases, particularly atopic dermatitis, which is
XX also applicable in screening candidate compounds for remedies. The
XX present sequence is an anchor primer described in the exemplification of
XX the invention
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Silarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16

```

PA	(SYNTE) SYNTAX USA LLC.
PA	(THOM/) THOMPSON J.
PX	
PI	Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX	Grupe A;
DR	WFI; 2002-217145/27.
XX	
PT	Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
PS	Claim 4; Page 134; 152pp; English.
XX	
CC	The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
CC	
XX	Sequence 17 BP; 2 A; 3 C; 9 G; 0 T; 3 U; 0 Other;
SQ	
Query Match	0.2%; Score 15; DB 1; Length 17;
Best Local Similarity	86.7%; Pred. No. 1.5e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
OY	5017 GGCGCTGTGGAGGAG 5031 : DB 2 GGCGCTUGGAGAG 16
RESULT 2811	
ID	ABKS7744
XX	ABKS7744 standard; RNA; 17 BP.
AC	ABKS7744;
XX	
DT	02-JUL-2002 (first entry)
XX	
DE	Human CLCA1 gene enzymatic nucleic acid #2115.
XX	
KM	Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.
KW	
XX	Homo sapiens.
OS	
XX	MOZ00211674-A2.
PN	
XX	14-FEB-2002.
PD	
XX	09-AUG-2001; 2001WO-US024970.
PF	
XX	09-AUG-2000; 2000US-0224383P.
PR	
XX	(RIBO-) RIBOZYME PHARM INC.
PA	(SYNT) SYNTAX USA LLC.
PA	(THOM/) THOMPSON J.
XX	

PI Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX WPI; 2002-217145/27.
XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 135; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 1.5e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 5017 GGGCTCTGGAGAG 5031
Db 1 GGGCTCTGGAGAG 15
RESULT 2812
ABK49757
ID ABK49757 standard; DNA; 17 BP.
XX
AC ABK49757;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15c.
XX
KM Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KM allergic disease; antiallergic; dermatological; GT15c.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients.

XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15c PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
Db 2 TTTT TTTT TTTT TTTT 16
RESULT 2813
ABK49756
ID ABK49756 standard; DNA; 17 BP.
XX
AC ABK49756;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15a.
XX
KM Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KM allergic disease; antiallergic; dermatological; GT15a.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients.
XX
PS Example 1; Page 54; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen

CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the G15a PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16

RESULT 2814
ACC52645
ID ACC52645 standard; DNA; 17 BP.

XX
AC ACC52645;
XX
DT 27-JUN-2003 (first entry)

XX Human tumour suppressor sequence #1412.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX tumour regression; apoptosis; virus resistance; diagnosis;
XX cellular degeneration.

XX Homo sapiens.

XX FR2826373-A1.

XX 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Tuijnder M, Teleman A, Amson R;

XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,
XX apoptosis or virus resistance are useful to diagnose and treat viral
XX disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 366; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
XX with tumour suppression or regression, apoptosis or virus resistance. The
XX invention relates to these sequences or sequences having at least 80%
XX identity to them, and polypeptides encoded by the sequences or
XX polypeptides having 80% identity to the polypeptide sequences. The
XX invention is used to diagnose or treat viral disease or disease
XX characterized by development of tumour cells or cellular degeneration

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2395 ATCCAGCTGGAGC 2409
DB 2 ATCCAGCTGGAGC 16

RESULT 2815
ABX79793

ID ABX79793 standard; cDNA; 17 BP.

XX ABX79793;

XX 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #118.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

XX US6472154-B1.

XX 29-OCT-2002.

XX 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for
XX understanding or treating genetic disease, comprises detecting tandem
XX repeats in a target coding sequence and scoring the repeats for
XX polymorphic probability.

XX Example; Col 483; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
XX repeat within a coding sequence (expressed sequence tag, EST), which
XX comprises detecting tandem repeats in a target coding sequence, scoring
XX the repeats for polymorphic probability and generating a dataset
XX correlating the repeats with polymorphic probability to identify a
XX candidate polymorphic repeat. The computational methods (polymorphic
XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX useful for identifying and detecting candidate polymorphic repeats in
XX human genes, which can be used to understand, treat or eliminate genetic
XX diseases, predispositions or adverse drug-treatment reactions. Examples
XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX the polymorphic repeats identified for a search of human ESTs

XX Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2816

ID ABT36431/c

XX ABT36431 standard; DNA; 17 BP.

XX ABT36431;

XX 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID NO 2068.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW anticense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrentia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
OS Homo sapiens.
XX WO2003025175-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002MO-IB004208.
XX 17-SEP-2001; 2001FR-00011978.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX PA
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX PS Disclosure; Page 274; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optional
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acid, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrentia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6294 CTGGCCTTCAGGAT 6308
DB 16 CTGGCCTTCAGGAT 2
XX
RESULT 2817
ADB04274
ID ADB04274 standard; DNA; 17 BP.
XX
AC ADB04274;
XX 20-NOV-2003 (first entry)
XX Human MD27 scanning oligonucleotide SEQ ID 5260.
XX

KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX EP1281758-A2.
XX PN
XX PD 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX PF
XX 02-AUG-2001; 2001US-00922181.
XX PR
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5260; 103pp; English.
XX
XX CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4470 TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT G 15
XX
RESULT 2818
ADC84469
ID ADC84469 standard; DNA; 17 BP.
XX
AC ADC84469;
XX 01-JAN-2004 (first entry)
XX
XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
XX Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX JP2003159071-A.
XX PN
XX PD 03-JUN-2003.
XX

XX 22-NOV-2001; 2001JP-00358366.
 PF 22-NOV-2001; 2001JP-00358366.
 PR 22-NOV-2001; 2001JP-00358366.
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA WPI; 2003-818676/77.
 DR
 XX New naturally derived DNA specifically expressed during blastogenesis of
 PT a plant, useful for producing a transformed plant and for compulsive
 PT expression of a protein.
 XX
 PS Example 3; SEQ ID NO 2; 43pp; Japanese.
 CC The invention relates to naturally derived DNA specifically expressed
 CC during plant blastogenesis. The DNA of the invention is useful for
 CC producing a transformed plant. Methods of the invention are also useful
 CC for compulsive expression of this DNA. Methods of the invention are
 CC useful for plant tissue specific expression of genes. Also, the growth
 CC stage of a plant can be controlled specifically. The current sequence
 CC represents a PCR primer for amplifying a plant blastogenesis specific
 CC gene of the invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT 4478
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2819
 ADC84468
 ID ADC84468 standard; DNA; 17 BP.
 AC
 XX ADC84468;
 AC
 XX 01-JAN-2004 (first entry)
 DT
 XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
 DE
 XX Plant blastogenesis; transformation; gene expression; tissue specific;
 KM PCR; primer; ss.
 KM
 XX Synthetic.
 OS
 XX JP2003159071-A.
 PN
 XX 03-JUN-2003.
 PD
 XX 22-NOV-2001; 2001JP-00358366.
 PF
 XX 22-NOV-2001; 2001JP-00358366.
 PR
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA WPI; 2003-818676/77.
 DR
 XX New naturally derived DNA specifically expressed during blastogenesis of
 PT a plant, useful for producing a transformed plant and for compulsive
 PT expression of a protein.
 XX
 PS Example 3; SEQ ID NO 1; 43pp; Japanese.
 CC The invention relates to naturally derived DNA specifically expressed
 CC during plant blastogenesis. The DNA of the invention is useful for
 CC producing a transformed plant. Methods of the invention are also useful
 CC for compulsive expression of this DNA. Methods of the invention are
 CC useful for plant tissue specific expression of genes. Also, the growth

CC stage of a plant can be controlled specifically. The current sequence
 CC represents a PCR primer for amplifying a plant blastogenesis specific
 CC gene of the invention.
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT 4478
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2820
 ADE77745
 ID ADE77745 standard; DNA; 17 BP.
 AC
 XX ADE77745;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX DNA oligo (SeqID 5) related to the human B1799 gene.
 DE
 XX ss; allergic disease; B1799; anti-allergic; anti-inflammatory;
 KM dermatological; gene therapy; atopic dermatitis.
 KM
 XX Unidentified.
 OS
 XX WO2003083139-A1.
 PN
 XX 09-OCT-2003.
 PD
 XX 25-FEB-2003; 2003WO-JP002047.
 PF
 XX 03-APR-2002; 2002JP-00100908.
 PR
 XX (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN AGENCY NATION.
 PA
 XX Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
 PI WPI; 2003-804076/75.
 DR
 XX Examining allergic diseases, such as atopic dermatitis, comprises
 DT comparing the expression levels of gene B1799 in T cells in a patient and
 XX a healthy individual.
 XX
 PS Example 1; SEQ ID NO 5; 87pp; Japanese.
 CC This invention relates to a novel method for screening and examining
 CC allergic diseases by the use of B1799 as the indicator gene.
 CC Specifically, it comprises determining the expression level of this
 CC indicator gene in a biological sample obtained from the patient, and
 CC identifying differential expression (increased expression of B1799) in
 CC comparison to that observed in a healthy individual. The present
 CC invention describes the B1799 protein as anti-allergic, anti-inflammatory
 CC and dermatological. As such, through the use of gene therapy, this method
 CC can be used to treat allergic diseases particularly atopic dermatitis.
 CC Furthermore, it is useful for determining a diagnosis that is convenient
 CC and non-invasive, and is also applicable in high throughput screening to
 CC identify candidate compounds for additional remedies. This
 CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
 CC B1799 gene of the invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4464 TTTT TTTT TTTT TTTT 4478

Db |||||
 2 TTTTTTTTTTTTTT 16

RESULT 2821
ID AAV54175 standard; cDNA; 18 BP.
XX
AC AAV54175;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 12.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KM immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 51; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478
 |||||
 2 TTTTTTTTTTTTTT 16

Db

RESULT 2822
ID AAV54173 standard; cDNA; 18 BP.
XX
AC AAV54173;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 10.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KM immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX

PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 50; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478
 |||||
 2 TTTTTTTTTTTTTT 16

Db

RESULT 2823
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KM immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

SO Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2824

AAV54166 standard; cDNA; 18 BP.

AAV54166;

21-DEC-1998 (first entry)

Nucleotide sequence PCR primer 3.

PCR; primer; amplification; apoptosis; antibody; inhibition; ss;

immunohistological staining.

Synthetic.

WO9839437-A1.

11-SEP-1998.

05-MAR-1998; 98WO-JP000905.

05-MAR-1997; 97JP-00050302.

(KYOW) KYOWA HAKKO KOGYO KK.

Sakaki Y;

WPI; 1998-495844/42.

Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 treating diseases associated with apoptosis.

Example 1; Page 48; 70pp; Japanese.

This is the nucleotide sequence of a PCR primer used in the method of the
 invention, involving the use of novel apoptosis-related DNAs and
 proteins. The inventions can be used as diagnostic reagents for apoptosis
 e.g. (monoclonal) antibodies for the protein, as a reagent in
 immunohistological staining, as apoptosis inhibitors. It can also be used
 for treatment of apoptosis-related diseases

Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2825

AAZ90649 standard; DNA; 18 BP.

AAZ90649;

13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #10.

DE Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

OS Homo sapiens.

JP2000037190-A.

08-FEB-2000.

23-JUL-1998; 98JP-00225228.

23-JUL-1998; 98JP-00225228.

(NISR) JAPAN TOBACCO INC.

WPI; 2000-306578/27.

A physiologically active protein specifically derived from mammal tissue.

Example 2; Page 18; 50pp; Japanese.

The invention relates to identification of genes and proteins of adipose
 tissue relating to obesity, particularly complications of visceral
 obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
 and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 represent PCR primers amplifying the human adipose tissue genes

Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2826

AAZ90648 standard; DNA; 18 BP.

AAZ90648;

13-JUN-2000 (first entry)

Human adipose tissue gene amplifying primer #9.

Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

OS Homo sapiens.

JP2000037190-A.

08-FEB-2000.

23-JUL-1998; 98JP-00225228.

23-JUL-1998; 98JP-00225228.

(NISR) JAPAN TOBACCO INC.

WPI; 2000-306578/27.

A physiologically active protein specifically derived from mammal tissue.

Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 1 A; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2827
 AA290646
 ID AA290646 standard; DNA; 18 BP.

XX AA290646;
 AC
 XX 13-JUN-2000 (first entry)
 DT
 XX
 DE Human adipose tissue gene amplifying primer #7.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KM arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.
 OS
 XX JP2000037190-A.

PD 08-FEB-2000.

PF 23-JUL-1998; 98JP-00225228.

PR 23-JUL-1998; 98JP-00225228.

XX (NISR) JAPAN TOBACCO INC.

DR WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.
 PT
 XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX

SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2828
 AA290651
 ID AA290651 standard; DNA; 18 BP.

XX AA290651;
 AC

XX 13-JUN-2000 (first entry)
 DT

XX Human adipose tissue gene amplifying primer #12.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KM arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.
 OS

XX JP2000037190-A.

PD 08-FEB-2000.

PF 23-JUL-1998; 98JP-00225228.

PR 23-JUL-1998; 98JP-00225228.

XX (NISR) JAPAN TOBACCO INC.

DR WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.
 PT
 XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX

SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2829
 AAA58385/c
 ID AAA58385 standard; DNA; 18 BP.

XX AAA58385;
 AC

XX 01-NOV-2000 (first entry)
 DT

XX Polynucleotide # 1 used in a biomolecule detection system.

XX Nanocrystal; biomolecule detection; nonisotopic detection system; ss.

XX Synthetic.
 OS

XX WO200028088-A1.

PD 18-MAY-2000.

PF 10-NOV-1999; 99WO-US026612.

PR 10-NOV-1998; 98US-0107828P.

PR 09-NOV-1999; 99US-00437076.

XX (BIOC-) BIOCRYSTAL LTD.

XX Barbera-Guillem E, Nelson MB, Castro S;

XX
DR WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to
PT amplify the fluorescent signal.
XX
PS Example 3; Page 68; 72pp; English.
XX
CC The present invention relates to functionalised nanocrystals for use in
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such
CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Adenine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Thymine bases (AA58386)
XX
SQ Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
DB 18 TTTT TTTT TTTT TTTT 4
XX
RESULT 2830
AA58386
ID AA58386 standard; DNA; 18 BP.
XX
AC AA58386;
XX
DT 01-NOV-2000 (first entry)
XX
DE Polynucleotide # 2 used in a biomolecule detection system.
XX
KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS Synthetic.
XX
PN WO200028088-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1998; 98US-0107828P.
XX
PR 09-NOV-1999; 99US-00437076.
XX
PA (BIOC-) BIOCRYSTAL LTD.
XX
PI Barbera-Guillem E, Nelson MB, Castro S;
XX
DR WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to,
PT amplify the fluorescent signal.
XX
PS Example 3; Page 69; 72pp; English.
XX
CC The present invention relates to functionalised nanocrystals for use in
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such

CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Thymine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Adenine bases (AA58385)
XX
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT 4478
DB 4 TTTT TTTT TTTT TTTT 18
XX
RESULT 2831
AAF2668
ID AAF2668 standard; DNA; 18 BP.
XX
AC AAF2668;
XX
DT 02-APR-2001 (first entry)
XX
DE Human Smad7 phosphorothioate antisense oligonucleotide SEQ ID NO:11.
XX
KW Human; Smad7; antisense oligonucleotide; phosphorothioate; inhibition;
KW antiinflammatory; cytostatic; infection; inflammation; tumour formation;
KW ss.
XX
OS Homo sapiens.
XX
PN Key Location/Qualifiers
XX
FT modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
PN US6159697-A.
XX
PD 12-DEC-2000.
XX
PF 09-JAN-2000; 2000US-00487444.
XX
PR 09-JAN-2000; 2000US-00487444.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowbert LM;
XX
DR WPI; 2001-070108/08.
XX
PT Antisense compound capable of inhibiting the expression of human Smad7,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
XX
PS Claim 1; Col 40; 33pp; English.
XX
CC The present invention describes an antisense compound (I) of up to 30
CC nucleobases in length capable of inhibiting the expression of human
CC Smad7. (I) has antiinflammatory and cytostatic, and is a modulator of
CC Smad7 expression. (I) can be useful for inhibiting the expression of
CC human Smad7 in human cells or tissues, in vitro. (I) is commonly used as
CC a research reagent and in diagnostics for example, to elucidate the
CC function of particular genes. (I) is also useful for distinguishing
CC between functions of various members of a biological pathway and for
CC research use. (I) is also utilised for diagnostics, therapeutics,
CC prophylaxis and in kits. (I) is also useful prophylactically, e.g. to
CC prevent or delay infection, inflammation or tumour formation. AAF2667 to
CC AAF26706 represent human Smad7 antisense oligonucleotides from the
CC present invention

XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7413 CAGCAGCAGCAGCAG 7427
 |||||
 DB 4 CAGCAGCAGCAGCAG 18
 RESULT 2832
 AAS17036/C
 ID AAS17036 standard; DNA; 18 BP.
 XX AAS17036;
 AC AAS17036;
 DT 27-FEB-2002 (first entry)
 DE Human G-alpha2 reverse PCR primer.
 XX Luciferase; ss; PCR primer; protein-protein interaction;
 KM transcriptional activation protein DNA binding domain; TAP; luciferase;
 KW cancer; human immunodeficiency virus infection; antiviral;
 KM modified yeast cell; human; G-alpha2; RGS-Z.
 XX Homo sapiens.
 OS WO200181548-A1.
 PN 01-NOV-2001.
 PD 23-APR-2001; 2001WO-US013006.
 PE 24-APR-2000; 2000US-00556390.
 PR (AMHP) AMERICAN HOME PROD CORP.
 PA Young KH, Gao J;
 PI WPI; 2002-049273/06.
 DR New yeast cell, useful for determining protein-protein interactions,
 PT expresses heterologous fusion proteins comprising peptides of peptide
 PT binding pair joined to transcriptional activation protein DNA binding
 domain.
 XX Example 6; Page 53; 119pp; English.
 XX The invention relates to a yeast cell comprising nucleotide sequences
 CC encoding first and second heterologous fusion proteins comprising first
 CC and second peptides (P1, P2) of a peptide binding pair joined to a
 CC transcriptional activation protein (TAP) DNA binding domain or TAP
 CC transcriptional activation domain, respectively, and a luciferase gene
 CC activated by positive transcriptional control of TAP reconstructed by
 CC binding of P1 and P2. The cell is useful for detecting the interaction of
 CC a first peptide and a second peptide of a peptide binding pair which
 CC involves culturing the cell, incubating a test sample with the yeast cell
 CC under conditions suitable to detect the selected phenotype and detecting
 CC the level of expression of the luciferase gene. The cell is also useful
 CC for determining whether a test sample interacts with a first or second
 CC peptide of a peptide binding pair. The yeast cell comprises a nucleotide
 CC The new modified yeast cells are useful in the study and discovery of
 CC peptide mimics, including ligand mimics and receptor mimics. The cell may
 CC be used for monitoring the binding of peptides by peptide binding pair
 CC which bind through extracellular interaction, and for studying numerous
 CC mammalian ligand/receptor interactions, e.g., hormone/receptor
 CC interactions. The cells are also useful in the detection of the ability
 CC of the test sample to affect the binding of a peptide binding pair for
 CC example ligand-receptor interaction. The screening methods can be used
 CC for identifying compounds interacting with any peptide binding pair and
 CC to discover novel compounds that disrupt that interaction, e.g., protein

CC kinases implicated in cancers can be inserted into the yeast system to
 CC screen for compounds that block the kinase-target interaction and thus
 CC may serve as unique cancer therapeutics; viral coat proteins such as
 CC human immunodeficiency virus glycoprotein and corresponding cell surface
 CC proteins such as CD4 can be inserted into the cell system to screen for
 CC compounds that disrupt this interaction and may serve as antiviral
 CC agents. The present sequence is a PCR primer used to isolate a cDNA
 CC encoding human G-alpha2. G-alpha2 is expressed in yeast cells in a
 CC construct which uses the luciferase gene as a marker for the interaction
 CC between G-alpha2 and a coexpressed RGS-Z
 XX
 SQ Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 2994 ATGTCCCGCCACCCCT 3008
 |||||
 DB 17 ATGTCCCGCCACCCCT 3
 RESULT 2833
 AAA83021/C
 ID AAA83021 standard; DNA; 19 BP.
 XX AAA83021;
 AC AAA83021;
 DT 04-DEC-2000 (first entry)
 DE cdK6 ribozyme binding site #81.
 XX
 KM Ribozyme; hairpin; hammerhead; gene therapy; vasotrophic; restenosis; ss.
 OS Mammalia.
 OS WO200032765-A2.
 PN 08-JUN-2000.
 PD 06-DEC-1999; 99WO-US028772.
 PE 04-DEC-1998; 98US-0110954P.
 PR (IMMU-) IMMUSOL INC.
 PA Tritz R, Welch PJ, Barber JR, Robbins JM;
 PI WPI; 2000-412314/35.
 DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX Disclosure; Page 55; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 5 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 15; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1678 TTCTGCAATATGCA 1692
 |||||

DB 19 TTGCAAAATATGCA 5

RESULT 2834
AAH58183/c
ID AAH58183 standard; DNA; 19 BP.

XX
AC AAH58183;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:607.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiapoptotic; dermatological; antiseborrheic; antidiabetic; vitruide;
KW antisticking; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.

XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.

XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX
PS Example 1; Page 116; 408pp; English.

XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiseborrheic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,
CC ophthalmological, vulnery, keratolytic and vitruide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention

XX
SQ Sequence 19 BP; 5 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

XX
Query Match 0.2%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1678 TTGCAAAATATGCA 1692
DB 19 TTGCAAAATATGCA 5

RESULT 2835
AAQ13458/c
ID AAQ13458 standard; DNA; 20 BP.

XX
AC AAQ13458;
XX
DT 25-MAR-2003 (revised)
XX
DT 05-NOV-1991 (first entry)
XX
DE Probe to mutant codon 201 (AAA) of G-protein Gi(alpha)1 subunit.
XX
KW Gi(alpha)1-201; point mutation; oncogenesis; PCR; tumour;
KW adenylate cyclase activity inhibition; ss.

XX
OS Synthetic.
XX
FN WO9112343-A.
XX
PD 22-AUG-1991.
XX
PF 07-FEB-1990; 90US-00477260.
XX
PR 07-FEB-1990; 90US-00477260.
XX
PA (CERTU) CERTUS CORP.
XX
PI McCormick FP, Lyons JF;
XX
DR WPI; 1991-267154/36.

XX
PT Method for detection of point mutation(s) in nucleic acid segments -
PT where segments encode GTP binding protein or sub-unit and method involves
PT amplification followed by sequence-specific probe hybridisation.

XX
PS Claim 18; Page 65; 69pp; English.

XX
CC This probe corresponds to a mutant sequence around codon 201 (AGA = Arg).
CC This codon is a potentially oncogenic site and a group of mutant probes
CC were synthesised based on single point mutations at codon 201. After PCR
CC amplification of nucleic acid samples using specific primer pairs, these
CC probes can be used to detect Gi(alpha)1 mutations associated with
CC oncogenesis. See AAQ13431-Q13542. (Updated on 25-MAR-2003 to correct PI
CC field.)

XX
SQ Sequence 20 BP; 10 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

XX
Query Match 0.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7204 GTTTCACCTTACGTT 7218
DB 19 GTTTCACCTTACGTT 5

XX
RESULT 2836
AAT73291
ID AAT73291 standard; DNA; 20 BP.

XX
AC AAT73291;
XX
DT 12-DEC-1997 (first entry)
XX
DE Primer 1 for pUC19 DNA amplification.
XX
KW primer; PCR; polymerase chain reaction; sequencing; walking;
KW complementary extension reaction; low redundancy; universal primer; ss.

OS Synthetic.
 XX EP767240-A2.
 XX 09-APR-1997.
 PD
 XX 17-SEP-1996; 96EP-00114907.
 PF
 XX 18-SEP-1995; 95JP-00238141.
 PR 30-JAN-1996; 96JP-00013634.
 XX
 PA (HITA) HITACHI LTD.
 XX
 PI Kambara H, Okano K;
 DR WPI; 1997-205424/19.
 XX
 PT Efficient sequencing of long DNA by fragment walking - with simultaneous
 PT sequencing of restriction enzyme fragment and adjacent region of intact
 PT DNA, avoids the need for cloning and requires fewer primers.
 XX
 PS Example 1; Page 11; 50pp; English.
 CC A method for DNA analysis based on a complementary extension reaction
 CC using a DNA polymerase, comprises a combination of fragment walking and
 CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
 CC restriction enzyme and the targeted DNA sequence can be determined
 CC directly from the digested DNA fragments. By exploring the overlapping
 CC sequence of the determined base sequence, the overall base sequence of a
 CC lengthy DNA can be determined with low redundancy without cloning or
 CC subcloning. In addition, the method can be done with commercially
 CC available universal primers or with fewer primers than required in
 CC existing methods. AAT73291-92 are primers used in determination of the
 CC pUC19 sequence. Primer extension was carried out using 16 primers
 CC AAT73293
 CC
 SO Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4470 TTTTTTTTTTTTG 4484
 Db 1 TTTTTTTTTTTTG 15
 RESULT 2837
 AAT73292
 ID AAT73292 standard; DNA; 20 BP.
 XX
 AC AAT73292;
 XX
 DT 12-DEC-1997 (first entry)
 XX
 DE Primer 2 for pUC19 DNA amplification.
 XX
 KW primer; PCR; polymerase chain reaction; sequencing; walking;
 KW complementary extension reaction; low redundancy; universal primer; ss.
 XX
 OS Synthetic.
 XX EP767240-A2.
 FN
 XX 09-APR-1997.
 PD
 XX 17-SEP-1996; 96EP-00114907.
 PF
 XX 18-SEP-1995; 95JP-00238141.
 PR 30-JAN-1996; 96JP-00013634.
 XX
 PA (HITA) HITACHI LTD.
 XX

PI Kambara H, Okano K;
 XX
 DR WPI; 1997-205424/19.
 XX
 PT Efficient sequencing of long DNA by fragment walking - with simultaneous
 PT sequencing of restriction enzyme fragment and adjacent region of intact
 PT DNA, avoids the need for cloning and requires fewer primers.
 XX
 PS Example 1; Page 11; 50pp; English.
 CC A method for DNA analysis based on a complementary extension reaction
 CC using a DNA polymerase, comprises a combination of fragment walking and
 CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
 CC restriction enzyme and the targeted DNA sequence can be determined
 CC directly from the digested DNA fragments. By exploring the overlapping
 CC sequence of the determined base sequence, the overall base sequence of a
 CC lengthy DNA can be determined with low redundancy without cloning or
 CC subcloning. In addition, the method can be done with commercially
 CC available universal primers or with fewer primers than required in
 CC existing methods. AAT73291-92 are primers used in determination of the
 CC pUC19 sequence. Primer extension was carried out using 16 primers
 CC AAT73293
 CC
 SO Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4470 TTTTTTTTTTTTG 4484
 Db 1 TTTTTTTTTTTTG 15
 RESULT 2838
 AAA72163
 ID AAA72163 standard; DNA; 20 BP.
 XX
 AC AAA72163;
 XX
 DT 15-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody heavy chain primer, SEQ ID NO.93.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
 KW humanised antibody; complementarity determining region; CDR; human Fas;
 KW Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenias;
 KW hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-00278301.
 XX
 PR 30-SEP-1998; 98JP-00276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality in
 PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
 PT antibody.
 XX
 PS Example 15; Page 49; 139p; Japanese.

PA (SANTY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI; 2000-256930/23.
 DR
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX
 PS Example reference 15; Page 137; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-aneitic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephroprotective, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC primer used in the construction of a humanised anti-Fas antibody HFE7A
 CC designed heavy chain which is used in the method described in the
 CC invention
 CC
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7181 GGTGGGCATGTGTGA 7195
 Db |||||||
 5 GGTGGGCATGTGTGA 19
 RESULT 2841
 ABL48723
 ID ABL48723 standard; DNA; 20 BP.
 AC ABL48723;
 XX
 XX 30-APR-2002 (first entry)
 DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 61.
 XX
 KW Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
 KW autoimmune disease; allergy; atopy; PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX JP2001342149-A.
 PN
 XX 11-DEC-2001.
 PD
 XX 28-MAR-2001; 2001JP-00093243.
 PF

XX
 XX 29-MAR-2000; 2000JP-00091144.
 PR
 XX (SANTY) SANKYO CO LTD.
 PA
 XX
 XX WPI; 2002-145114/19.
 DR
 XX
 PT Drug for preventing or treating e.g. autoimmune disease or allergy,
 PT comprises humanized anti-Fas antibody.
 XX
 PS Example 14 (preparatory); Page 32; 154pp; Japanese.
 XX
 CC The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in the Fas/Fas ligand system containing, as the
 CC active component, an antibody having a light chain subunit and a heavy
 CC chain subunit and an activity of combining specifically with mammalian
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is
 CC used for preventing and treating autoimmune diseases, allergy, atopy and
 CC others. The present sequence is that of a PCR primer useful in the
 CC construction of anti-Fas antibodies of the invention
 CC
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7181 GGTGGGCATGTGTGA 7195
 Db |||||||
 5 GGTGGGCATGTGTGA 19
 RESULT 2842
 ABQ74807
 ID ABQ74807 standard; DNA; 20 BP.
 AC ABQ74807;
 XX
 XX 24-OCT-2002 (first entry)
 DE Human TNFR2 antisense oligonucleotide SEQ ID NO:57.
 XX
 KW Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
 KW phosphorothioate; 2'-O-methoxyethyl; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl nucleotides"
 FT 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl nucleotides"
 FT
 FT US6410324-B1.
 FN
 XX 25-JUN-2002.
 XX
 XX 27-APR-2001; 2001US-00844634.
 PF
 XX 27-APR-2001; 2001US-00844634.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Watt AT;
 PI

XX DR WPI; 2002-606814/65.
XX PT New compounds antisense to nucleic acid encoding human or mouse tumor
PT necrosis factor receptor 2 are useful to treat disease associated with
PT mouse tumor necrosis factor receptor 2 expression.
XX PS Claim 3; Col 47, 69pp; English.
XX CC The present invention describes compounds of 8-30 nucleobases antisense
CC to a nucleic acid encoding human or mouse tumor necrosis factor receptor
CC 2 (TNFR2). Also described is a method for inhibiting expression of human
CC or mouse TNFR2 comprising contacting cells or tissues in vitro with one
CC of the claimed compounds. The antisense compounds are used to treat a
CC disease or condition associated with expression of TNFR2. The present
CC sequence represents a human TNFR2 antisense chimeric phosphorothioate
CC oligonucleotide, which is given in the present invention
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1765 GTCATCCGCGCAGG 1779
Db 1 GTCATCCGCGCAGG 15
RESULT 2843
ABL45980
ID ABL45980 standard; DNA; 20 BP.
XX AC ABL45980;
XX DT 26-APR-2002 (first entry)
XX DB Humanised anti-Fas antibody related PCR primer SEQ ID NO 18.
XX KM Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KM light chain subunit; apoptosis; immunosuppressive; antiallergic;
KM autoimmune disease; allergy; atopic; PCR primer; ss.
XX OS Synthetic.
XX PN JP2001342148-A.
XX PD 11-DEC-2001.
XX PF 28-MAR-2001; 2001JP-00093106.
XX PR 29-MAR-2000; 2000JP-00090918.
XX PS (SANYO) SANKYO CO LTD.
XX DR WPI; 2002-145113/19.
XX PT Drug containing humanised anti-Fas antibody, used for preventing and
PT treating autoimmune diseases, allergy, and atopy.
XX PS Example 4 (Preparatory); Page 23; 194pp; Japanese.
XX CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC fully defined in the specification and having an activity of combining
CC specifically with mammalian Fas and an activity of inducing apoptosis in
CC a cell expressing Fas. The agent has immunosuppressive and antiallergic
CC activity and is used for preventing and treating autoimmune diseases,
CC allergy, atopy and others. The present sequence is that of a PCR primer,
CC useful to the invention

XX SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
XX PT Query Match 0.2%; Score 15; DB 1; Length 20;
PT Best Local Similarity 100.0%; Pred. No. 1.9e+03;
PT Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 7181 GGTGGCATGTGTGA 7195
Db 5 GGTGGCATGTGTGA 19
RESULT 2844
ABZ85436
ID ABZ85436 standard; DNA; 20 BP.
XX AC ABZ85436;
XX DT 17-OCT-2003 (first entry)
XX DB Human oligonucleotide sequence.
XX KM Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PS (EPIC-) EPIGENESIS PHARM INC.
XX PI NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX PS Claim 15; SEQ ID NO 678; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4470 TTTT TTTT TTTT TTTT G 4484
Db 1 TTTT TTTT TTTT TTTT G 15

RESULT 2845
AB291658/c
ID AB291658 standard; DNA; 20 BP.
AC AB291658;
XX
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiaesthetic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahbuddin S,
XX
XX WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

Disclosure; SEQ ID NO 6900; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of ubiquinone
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT T 4478
Db 20 TTTT TTTT TTTT TTTT T 6

RESULT 2846
ADA66464
ID ADA66464 standard; DNA; 20 BP.
XX
XX ADA66464;
XX
XX 20-NOV-2003 (first entry)
XX
XX
DE Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 23.
XX
XX Cytostatic; antirheumatic; antiarthritic; gynecological;
KM antiarteriosclerotic; transforming growth factor beta-3; TGF beta-3;
KM hyperproliferative disorder; cancers; atherosclerosis;
KM rheumatoid arthritis; preeclampsia; fibrosis; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX
XX WO2003008544-A2.
XX
XX 30-JAN-2003.
XX
XX 12-JUL-2002; 2002WO-US022423.
XX
XX 14-JUL-2001; 2001US-00906158.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freiler SM;
XX
XX WPI; 2003-229569/22.

Novel antisense compound which is targeted to nucleic acid encoding
transforming growth factor beta-3, and inhibits expression of TGF-beta 3,
useful for treating a condition associated with TGF-beta 3, e.g. cancer.

Claim 3; Page 87; 154pp; English.

The present invention relates to antisense oligonucleotides (ADA66459-
CC ADA66609), which inhibit transforming growth factor (TGF) beta-3
CC expression, which inhibit transforming growth factor (TGF) beta-3
CC of TGF-beta3 in cells or tissues, and for treating an animal having a
CC disease condition associated with TGF-beta3, e.g. a hyperproliferative
CC disorder such as cancers of lung, liver, colon, oesophagus, pancreas,
CC breast, skin or haematopoietic, atherosclerosis, rheumatoid arthritis,
CC preeclampsia and fibrosis.

Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
QY 4464 TTTT TTTT TTTT TTTT T 4478
Db 20 TTTT TTTT TTTT TTTT T 6

Query Match 0.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4290 TTGCAAGTGCATCTT 4304
 |||||
 DB 2 TTGCAAGTGCATCTT 16

RESULT 2847
 ABZ80969
 ID ABZ80969 standard; DNA; 20 BP.
 XX
 AC ABZ80969;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Herpes virus infection diagnostic primer III.
 XX
 KW Primer; PCR; diagnosis; ss.
 XX
 OS Human herpesvirus.
 XX
 PN RU2192473-C1.
 PD 10-NOV-2002.
 XX
 PF 26-JUN-2001; 2001RU-00117331.
 XX
 PR 26-JUN-2001; 2001RU-00117331.
 XX
 PA (ASMO=) AS USSR MOLECULAR GENETICS INST.
 XX
 PI Demkin VV, Kruglova AI, Nikolaeva NP;
 XX
 DR WPI; 2003-146311/14.
 XX
 PT Method of diagnosis of herpes virus infection.
 XX
 PS Claim 1; Page 5; 6pp; Russian.
 XX

CC The invention relates to a method of diagnosing herpes virus infections
 CC by two-stage polymerase chain reaction (PCR) carried out using two
 CC external primers I (ABZ80967) and II (ABZ80968) on the first stage and
 CC two internal primers I and III (this sequence) on the second stage. The
 CC method ensures determination of four types of herpes viruses in a single
 CC sample simultaneously. The method is useful in medicine, especially in
 CC immunobiology, virology and molecular biochemistry
 CC
 SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 GTGTCCCGTAGAGT 416
 |||||
 DB 5 GTGTCCCGTAGAGT 19

RESULT 2848
 ABZ80971
 ID ABZ80971 standard; DNA; 20 BP.
 XX
 AC ABZ80971;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Alternative Herpes virus infection diagnostic primer III.
 XX
 KW Primer; PCR; diagnosis; ss.
 XX
 OS Human herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT modified_base 2
 FT /*tag= a

FT /mod base= i
 FT /note= "inosine"
 XX
 PN RU2192473-C1.
 PD 10-NOV-2002.
 XX
 PF 26-JUN-2001; 2001RU-00117331.
 XX
 PR 26-JUN-2001; 2001RU-00117331.
 XX
 PA (ASMO=) AS USSR MOLECULAR GENETICS INST.
 XX
 PI Demkin VV, Kruglova AI, Nikolaeva NP;
 XX
 DR WPI; 2003-146311/14.
 XX
 PT Method of diagnosis of herpes virus infection.
 XX
 PS Disclosure; Page 3; 6pp; Russian.
 XX

CC The invention relates to a method of diagnosing herpes virus infections
 CC by two-stage polymerase chain reaction (PCR) carried out using two
 CC external primers I (ABZ80967) and II (ABZ80968) on the first stage and
 CC two internal primers I and III (ABZ80969) on the second stage. The method
 CC ensures determination of four types of herpes viruses in a single sample
 CC simultaneously. The method is useful in medicine, especially in
 CC immunobiology, virology and molecular biochemistry. This sequence
 CC represents an alternative version of primer III with an inosine residue
 CC replacing at thymidine at position 2
 CC
 SQ Sequence 20 BP; 3 A; 6 C; 6 G; 4 T; 0 U; 1 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 GTGTCCCGTAGAGT 416
 |||||
 DB 5 GTGTCCCGTAGAGT 19

RESULT 2849
 ABZ59521
 ID ABZ59521 standard; DNA; 20 BP.
 XX
 AC ABZ59521;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE Mouse src-c chimeric phosphorothioate oligonucleotide SEQ ID NO:142.
 XX
 KW Mouse; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
 KW antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
 KW antisense oligonucleotide; aberrant bone remodeling; breast cancer;
 KW hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
 KW ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
 KW Kaposi's sarcoma; infection; inflammation; tumour formation;
 KW phosphorothioate; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
 FT 16..20
 FT modified_base


```

FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl gapmer (2'-MOE wing) "
XX
XX      WO200295053-A2.
XX
XX      28-NOV-2002.
XX
XX      16-MAY-2002; 2002WO-US015684.
XX
XX      18-MAY-2001; 2001US-00860473.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett FC, Watt AT;
XX
XX      WPI; 2003-120806/11.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding src-c,
XX      useful for diagnosing, treating or preventing diseases associated with
XX      the expression of src-c, e.g. cancer or inflammation, and in research
XX      applications.
XX
XX      Example 16; Page 92; 137pp; English.
XX
XX      The present invention describes a compound (I) that is 8-50 nucleobases
XX      in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
XX      coding region, intron region, exon region, stop codon, intron:exon
XX      junction, exon:exon junction, or 5' mRNA variant of src-c, and which
XX      specifically hybridizes with and inhibits the expression of src-c. (1)
XX      have cytotoxic, antiinflammatory, osteopathic and antibacterial
XX      activities, and can be used in antisense therapy and in vaccines. The
XX      antisense compounds (I) can be used for modulating the expression of src-
XX      c and for treating diseases or conditions associated with expression of
XX      src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
XX      particularly cancer, such as breast cancer, pancreatic cancer, lung
XX      cancer, ovarian cancer, esophageal cancer, neuroblastoma, retinoblastoma
XX      or Kaposi's sarcoma. (1) are also useful for diagnosis, therapeutics,
XX      prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
XX      formation, as research reagents and kits, and in distinguishing between
XX      functions of various members of a biological pathway. The present
XX      sequence represents a mouse src-c antisense chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention
XX
XX      Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      30 GAGCTGCTGCAGGCT 44
XX      |||||
XX      6 GAGCTGCTGCAGGCT 20
XX
XX      RESULT 2850
XX      ID      ADA08088 standard; DNA; 20 BP.
XX
XX      ADA08088;
XX
XX      06-NOV-2003 (first entry)
XX
XX      Human PFM5 cDNA RT-PCR primer.
XX
XX      Human; PR Family Member 5; PFM5; PFM PR domain; PFM zinc finger domain;
XX      PFM ZF domain; modulation of cell growth; cancer;
XX      cell degeneration disease; Alzheimer's disease; Parkinson's disease;
XX      insulin-dependent diabetes mellitus; IDDM; neuroprotective;
XX      antiparkinsonian; antidiabetic; cytostatic; RT-PCR;
XX      reverse transcriptase-PCR; primer; ss.
XX
XX      Homo sapiens.
XX

```

```

XX      US6586579-B1.
XX
XX      01-JUL-2003.
XX
XX      03-SEP-1999; 99US-00389956.
XX
XX      03-SEP-1999; 99US-00389956.
XX
XX      (BURN-) BURHAM INST.
XX
XX      Huang S;
XX
XX      WPI; 2003-669568/63.
XX
XX      New PR Family Member 2 oligonucleotide, useful for preparing a
XX      composition for modulating cell growth for treating cancer or diseases of
XX      cell degeneration, e.g., Alzheimer's disease or insulin-dependent
XX      diabetes mellitus.
XX
XX      Example 5; Col 32; 95pp; English.
XX
XX      The present invention relates to the isolation of human and mouse PR
XX      Family Member (PFM) proteins, and the polynucleotide sequences encoding
XX      them. Also disclosed are PFM PR and PFM zinc finger (ZF) domains, and the
XX      polynucleotide sequences encoding them. The invention also discloses PFM
XX      oligonucleotide sequences and methods for detecting a PFM polynucleotide sequence
XX      in a sample. The PFM polypeptide and polynucleotide sequences are useful
XX      for preparing a composition for modulating cell growth for treating
XX      cancer or diseases of cell degeneration, e.g. as Alzheimer's disease,
XX      Parkinson's disease or insulin-dependent diabetes mellitus (IDDM). The
XX      present sequence represents a primer used in the examples of the present
XX      invention.
XX
XX      Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      4647 GGAATTCCTCTTTG 4661
XX      |||||
XX      6 GGAATTCCTCTTTG 20
XX
XX      RESULT 2851
XX      AA226500/c
XX      ID      AA226500 standard; DNA; 21 BP.
XX
XX      AA226500;
XX
XX      30-NOV-1999 (first entry)
XX
XX      Human polymorphic region 689.
XX
XX      Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX      cell viability; loss of heterozygosity; precancerous condition; ASI;
XX      allele specific inhibitor; somatic cell; diagnosis; prevention;
XX      atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX      dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX      graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX      Homo sapiens.
XX
XX      WO9841648-A2.
XX
XX      24-SEP-1998.
XX
XX      19-MAR-1998; 98MO-US005419.
XX
XX      20-MAR-1997; 97US-0041057P.
XX
XX      (VARI-) VARIAGENICS INC.
XX

```

XX Housman D, Ledley FD, Stanton VP;
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC preneoplastic condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AA25812-226825 represent
CC human polymorphic sites described in the method of the invention
SQ
SQ Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4470 TTTT TTTT TTTT TTTT G 4484
|||
Db 21 TTTT TTTT TTTT TTTT G 7

RESULT 2852
AA26584/c
ID AA26584 standard; DNA; 21 BP.
XX
XX AA26584;
AC
XX
XX 30-NOV-1999 (first entry)
DT
XX
XX Human polymorphic region 773.
DE

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX
XX W09841648-A2.
PN
XX
XX 24-SEP-1998.
PD
XX
XX 19-MAR-1998; 98WO-US005419.
PE
XX
XX 20-MAR-1997; 97US-0041057P.
PR
XX
XX (VARI-) VARIAGENICS INC.
PA
XX
XX Housman D, Ledley FD, Stanton VP;
PI
XX
XX WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC preneoplastic condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AA25812-226825 represent
CC human polymorphic sites described in the method of the invention
SQ
SQ Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT T 4478
|||
Db 21 TTTT TTTT TTTT TTTT T 7

RESULT 2853
AA274799/c
ID AA274799 standard; DNA; 21 BP.
XX
XX AA274799;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:9155.
DE

XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX W09954500-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB000822.
PE
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX
XX 23-NOV-1998; 98US-0109732P.
PR
XX
XX (GEST) GENSET.
PA
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX
XX WPI; 2000-013267/01.
DR
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
PT
XX

PS Claim 8; Page 2182; 2745pp; English.

XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses; they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

XX
SQ Sequence 21 BP; 6 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5151 GGGAGGGAGGCTTC 5165
DB 21 GGGAGGGAGGCTTC 7

RESULT 2854
AAC73128/c
ID AAC73128 standard; DNA; 21 BP.

XX
AC AAC73128;
DT 02-FEB-2001 (first entry)
XX

DE SNP flanking sequence #15 used in multiplexing PCR/SBE assay.

XX
KM Oligonucleotide array; genotyping; single base extension reaction; SBE;
KM polymorphic locus; single nucleotide polymorphism; ss.
XX

OS Unidentified.
XX
FN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 49; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one such polymorphic locus

CC used in the present invention. The amplified nucleic acid product is then
CC used as a template in a SBE reaction with an extension primer. The SBE
CC reaction products are used to form the oligonucleotide array. Note: This
CC sequence includes a SNP represented by the degenerate codon in the
CC sequence

XX
SQ Sequence 21 BP; 4 A; 11 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 GGGAGCTGGCGGCGCG 77
DB 20 GGGAGCTGGCGGCGCG 4

RESULT 2855
AAQ30432/c
ID AAQ30432 standard; DNA; 23 BP.

XX
AC AAQ30432;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
XX
KM Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KM malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
FH Key
FH Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT misc_feature 11..12
FT /*tag= d
FT /note= "o-xyloso dimer synthon linkage"
FT 12..23
FT /*tag= c
FT /label= inverted polarity_region
FT /note= "see comments"
FT modified_base 23
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
XX
PN WO9209705-A1.
XX
PD 11-JUN-1992.
XX
PE 25-NOV-1991; 91WO-US008811.
XX
PR 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00686544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.

XX Claim 12; Page 71; 77pp; English.

XX The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a putine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC interleukin 6 gene untranslated sequence contg. a putine rich sequence
 CC concd. on one strand of the duplex. The oligomer, and others like it are
 CC useful in diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
 CC tumours and inflammation. The triplex helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3' positions of xylose sugars linked via the o-
 CC xylene ring). Two nucleotides are coupled through a xylene residue to
 CC form the dimer synthon. This additional modifications may render the
 CC oligomer stable to nuclease activity. The oligomer is able to inhibit
 CC gene expression, as verified by in vitro systems. See also AAQ025452-25501
 CC and AAQ030226-448. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4019 GAAAAAAGAGAAAAACAAATG 4041
 DB 23 GAAAAAAGAAAAAAG 1

RESULT 2856
 AAQ03762
 ID AAQ03762 standard; DNA; 23 BP.

XX AAQ03762;
 XX 25-MAR-2003 (revised)
 XX 09-AUG-1990 (first entry)

XX Tissue plasminogen activator analogue oligonucleotide.
 XX Tissue plasminogen activator; tPA analogues; fibrinolytic therapy; ss.
 XX Synthetic.
 XX DE3831714-A.
 XX 22-MAR-1990.
 XX 17-SEP-1988; 88DB-03831714.
 XX 17-SEP-1988; 88DE-03831714.
 XX (BADT) BASF AG.
 XX Bach A, Schmidt M, Scrube KH, Baldinger V, Schwarz M;
 XX WPI; 1990-100100/14.

XX New tissue plasminogen activator analogues - are polypeptide(s) with tPA
 XX sequence contg. arginine-glycine-aspartic acid tripeptide units.
 XX Example 3.6; Page 5; 17pp; German.

XX Sequence containing this oligonucleotide encodes tPA-like polypeptides
 CC displaying the amino acid sequence of tPA in which 1-6 tripeptides are
 CC replaced by thr tripeptide RGD (-Arg-Gly-Asp). The produced polypeptides
 CC have plasminogen activator activity and can be used in fibrinolytic
 CC therapy, eg after cardiac infarct. They have increased blood clot
 CC specificity, longer half life, reduced inhibitor binding and/or greater
 CC proteolytic activity. See also AAQ03754-Q03771 and DR 3830734. (Updated

CC on 25-MAR-2003 to correct PD field.)

XX Sequence 23 BP; 1 A; 13 C; 5 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3524 GACCCGTCTTCTTCGCGCCGC 3546
 DB 1 GATGCCGTCTTCTTCGCGCCGC 23

RESULT 2857
 AAQ21598/c
 ID AAQ21598 standard; DNA; 23 BP.

XX AAQ21598;
 XX 27-AUG-2003 (revised)
 XX 25-MAR-2003 (revised)
 XX 16-MAY-1992 (first entry)

XX Infectious bovine rhinotracheitis virus primer oligo Ed48.
 XX Herpes virus-based viral vector; foot and mouth disease; epitope;
 XX vaccine; ss.
 XX Bovine herpesvirus 1.
 XX Foot-and-mouth disease virus.
 XX virus.
 XX EP471457-A.
 XX 19-FEB-1992.
 XX 22-JUL-1991; 91EP-00306646.
 XX 24-JUL-1990; 90US-00556593.
 XX (NOVA-) NOVAGEN INC.
 XX (BLIL) LILLY & CO ELI.
 XX Dimarchi RD, Kit S, Little SP, Gale C, Kit M;
 XX WPI; 1992-058515/08.

XX Vaccine for foot and mouth disease and Herpes virus - comprising a Herpes
 XX virus-based viral vector which expresses a foot and mouth disease virus
 XX epitope.
 XX Example; Page 63; 72pp; English.

XX An oligonucleotide cloning/expression cassette was synthesised for
 CC insertion into the NcoI site of the IBRV gIII gene-contg. plasmid
 CC pIA(GIII):30 dl. Hind III/HpaI (see AAQ21591). The cassette was designed
 CC to provide cloning sites, optimal translation start signals for the
 CC bovine growth hormone (bGH) signal sequence, the RMDV epitope sequence
 CC and restriction nuclease sites to permit unidirectional nuclease digestion
 CC into the IBRV gene. The resulting plasmid was then transformed with a bGH
 CC -FMV sequence and subjected to exonuclease II digestion to remove
 CC sequences encoding the 39 N-terminal amino acids from the IBRV gIII
 CC gene. The final plasmid obtained has the sequences for bGH-FMV which can
 CC be expressed from the IBRV gIII promoter. When the PstI to MluI region of
 CC AAQ21592 is transferred into the pIA(GIII):30 dl HindIII/HpaI oligo
 CC 171/172 cassette, the bGH-FMV sequence will be in the same reading frame
 CC as the gIII protein. (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 23 BP; 4 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7234 CCTCTCAAGTCCAGCATGATGG 7256

DB 23 CCTCTCAAGTGGGACGAGGG 1

RESULT 2858

AAQ23949

ID AAQ23949 standard; DNA; 23 BP.

XX AAQ23949;

DT 27-OCT-1992 (first entry)

DE Degenerate PCR primer DG129 based on thermostable polymerase conserved sequence.

KW Thermophilicity; polymerase chain reaction; Tsf Pol I;

KM Thermophilic africanus; thermophilic bacteria; ss.

XX Synthetic.

PN WO9206202-A.

PD 16-APR-1992.

PF 26-SEP-1991; 91WO-US007076.

PR 28-SEP-1990; 90US-00590490.

PA (CETU) CETUS CORP.

PI Gelfand DH, Lawyer FC, Abramson RD, Greenfield L, Reichert FL;

DR WPI; 1992-150887/18.

PT Thermostable DNA polymerase from Thermophilic africanus - prepd. by purification from cells or by expression of Tsf polymerase gene in host cells.

PS Example 2; Page 38; 80pp; English.

CC Chromosomal DNA from Thermophilic africanus (Tsf) was PCR-amplified with

CC degenerate primers corresponding to the amino acid sequences of conserved

CC regions of known thermostable polymerases. DG129 is one example of a

CC degenerate primer. See AAQ23917 for full-length Tsf Pol I coding sequence

SO Sequence 23 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 4 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 2.2e+03;

Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4687 GATCTGGTATGATGAGCCATG 4706

DB 4 GATCTGGTATGATGAGCCATG 23

RESULT 2859

AAAT40331/c

ID AAAT40331 standard; DNA; 23 BP.

XX AAAT40331;

DT 06-DEC-1996 (first entry)

DE DNA cleavage substrate for generation of improved ribozymes.

KW Wild type; self-splicing group I intron; large ribosomal RNA precursor;

KM Tetrahymena thermophila; catalysis; enzymatic RNA; food product;

XX anti-viral agent; mutation; personal care product; cleaning agent; ss.

OS Synthetic.

PN WO9531551-A1.

PD 23-NOV-1995.

PF 26-APR-1995; 95WO-US005141.

PR 13-MAY-1994; 94US-00242402.

PA 01-JUL-1994; 94US-00270180.

PA (SCRI) SCRIPPS RES INST.

PI Joyce GF;

DR WPI; 1996-010936/01.

PT Enzymatic RNA molecules having one or more point mutation(s) - improve the enzymatic performance of the molecules.

PS Example 1; Page 111; 209pp; English.

CC The sequences given in AAAT40331-32 represent sequences that were as

CC substrate molecules in experiments for selection of improved catalytic

CC activity of ribozymes. The evolution experiment spanned 10 successive

CC generations and catalytic activity was deduced after each generation. The

CC self-splicing group I intron of the invention is based on the large

CC ribosomal RNA precursor from Tetrahymena thermophila. The biological

CC function of this molecule is to catalyze its own excision from precursor

CC RNA to produce mature RNA. The Tetrahymena wild type sequence was used

CC in the design of the enzymatic RNA molecules of the invention. A number

CC of mutations are listed in the specification which improve the enzymatic

CC properties of this molecule, e.g. G444A, G191U, U190A and A314G. The

CC modified enzymatic molecules may be used as medical or pharmaceutical

CC agents for use in anti-viral agents, food products, personal care

CC products or cleaning agents

SO Sequence 23 BP; 12 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;

Best Local Similarity 78.3%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6683 TATTTTATTTATTTATGAGGCC 6705

DB 23 TTTTATTTATTTATTTATGAGGCC 1

RESULT 2860

AAAT40328/c

ID AAAT40328 standard; DNA; 23 BP.

XX AAAT40328;

DT 05-DEC-1996 (first entry)

DE Group I intron substrate.

KW Wild type; self-splicing group I intron; large ribosomal RNA precursor;

KM Tetrahymena thermophila; catalysis; enzymatic RNA; food product;

XX anti-viral agent; mutation; personal care product; cleaning agent; ss.

PA (SCRI) SCRIPPS RES INST.
 XX Joyce GF;
 PS WPI; 1996-010936/01.
 XX Enzymatic RNA molecules having one or more point mutation(s) - improve
 PT the enzymatic performance of the molecules.
 XX Example 1; Page 97; 209pp; English.
 PS The sequences given in AAT37491-30 represent sequences that were used to
 CC optimise DNA cleavage activity of the enzymatic RNA molecule of the
 CC invention. The 3' portion of the substrate was transferred to the 3'
 CC terminal G of the ribozyme and amplification was performed. The product
 CC of the reaction was a molecule which contained the 3' portion of the
 CC substrate attached to the 3' end of the ribozyme. Selection occurred when
 CC a primer was hybridised across the ligation junction and used to initiate
 CC cDNA synthesis. The primer does not bind to unreacted starting materials
 CC and thus led to selective amplification of the catalytically active
 CC RNA's. The self-splicing group I intron of the invention is based on the
 CC large ribosomal RNA precursor from *Tetrahymena thermophila*. The
 CC biological function of this molecule is to catalyse its own excision from
 CC precursor RNA to produce mature rRNA. The *Tetrahymena* wild type sequence
 CC was used in the design of the enzymatic RNA molecules of the invention. A
 CC number of mutations are listed in the specification which improve the
 CC enzymatic properties of this molecule, e.g. G44A, G191U, U190A and
 CC A314G. The modified enzymatic molecules may be used as medical or
 CC pharmaceutical agents for use in anti-viral agents, food products,
 CC personal care products or cleaning agents
 XX Sequence 23 BP; 12 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 6683 TATTTTATTTATATATGCGGCC 6705
 DB 23 TTTATTTATTTATTTAGAGGCC 1
 RESULT 2861
 AAT37491
 ID AAT37491 standard; DNA; 23 BP.
 XX
 AC AAT37491;
 XX
 DT 19-FEB-1997 (first entry)
 XX
 DE Intron-5 primer for RPPS transcript RT-PCR analysis.
 XX
 KW Primer; Intron-5; Arabidopsis; RPP5; disease-resistance; RT-PCR;
 KW reverse transcription; nested polymerase chain reaction; downy mildew;
 KW *Peronospora parasitica*; transgenic plant; crop improvement; ss.
 XX
 OS Synthetic.
 XX
 PN WO9631608-A1.
 XX
 PD 10-OCT-1996.
 XX
 PF 09-APR-1996; 96WO-GB000849.
 XX
 PR 07-APR-1995; 95GB-00007232.
 XX
 PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
 XX
 PI Jones JDG, Parker J, Coleman M, Daniels MJ, Szabo V;
 XX WPI; 1996-465029/46.
 DR
 XX Isolated Arabidopsis pathogen resistance gene RPP5 - for prodn. of

PT transgenic plants esp. resistant to downy mildew fungus.
 XX
 PS Disclosure; Page 33; 59pp; English.
 XX
 CC This primer may be used with primers AAT37483-90 and AAT37492 in RT-PCR
 CC analysis of a gene (AAT37476) encoding Arabidopsis RPP5 protein, which
 CC confers disease-resistance against the downy mildew fungus (*Peronospora*
 CC *parasitica*). First strand cDNA synthesis from seedling leaf mRNA and PCR
 CC amplification have been performed using intron flanking primers. Primers
 CC AAT37489-90 are used in the first amplification in a nested PCR strategy
 CC for identification of intron-5, and this primer and primer AAT37492 are
 CC used in the second amplification. Cloned PCR products have been sequenced
 CC using vector-specific and insert-specific primers, to identify introns
 CC and exons. Primers corresponding to conserved regions in the protein may
 CC be used to identify other resistance genes in plants. The RPP5 gene may
 CC be expressed in a transgenic plant to confer disease-resistance
 XX
 SQ Sequence 23 BP; 5 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 21 TCGCAGTGGAGCTGCTGCAAGC 43
 DB 1 TCTCAATGTGAGCGGCTGCAAGC 23
 RESULT 2862
 AAT76031
 ID AAT76031 standard; DNA; 23 BP.
 XX
 AC AAT76031;
 XX
 DT 11-SEP-1997 (first entry)
 XX
 DE Human A1 adenosine receptor antisense oligonucleotide.
 XX
 KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640162-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US009306.
 XX
 PR 07-JUN-1995; 95US-00474497.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW, Metzger WJ;
 XX WPI; 1997-051871/05.
 DR
 XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.
 XX
 PS Example 5; Page 23; 71pp; English.
 XX
 CC A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the human A1 adenosine receptor. The method can be used to treat
 CC airway diseases such as cystic fibrosis, asthma, chronic obstructive
 CC pulmonary disease, bronchitis and other airway diseases characterised by
 CC an inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-

CC reactive airways
XX
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5699 TTGGCTTCCTTTCTCTCTCTC 5721
DB 1 TTTCCTTCCTTCCTCTCTCTC 23
RESULT 2863
AAV37972/c
ID AAV37972 standard; DNA; 23 BP.
XX
AC AAV37972;
XX
DT 11-SEP-1998 (first entry)
XX
DE ECEPO section 2 construction oligonucleotide 9 for human EPO.
XX
KM Human; erythropoietin; EPO; bone marrow; reticulocyte; red blood cell;
KM expression; CHO; chinese hamster ovary cell; diagnosis; blood disorder;
KM ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN A0688723-B.
XX
PD 19-FEB-1998.
XX
PF 02-DEC-1997; 97AU-00046867.
XX
PR 02-DEC-1997; 97AU-00046867.
XX
PA (KIRI) KIRIN AMGEN INC.
XX
PI Lin F;
XX
DR WPI; 1998-261957/24.
XX
PT Recombinant human erythropoietin - potentially useful for diagnosis and
PT treatment of blood disorders.
XX
PS Example 11; Page 64; 100pp; English.
XX
CC The present sequence represents a construction oligonucleotide for ECEPO
CC section 2 as part of the assembly of human erythropoietin (EPO), used in
CC an example from the present invention. The present invention describes
CC recombinant human EPO which causes bone marrow cells to increase
CC production of reticulocytes or red blood cells, where the polypeptide is
CC the product of expression in CHO (Chinese hamster ovary) cells of an
CC exogenous DNA sequence encoding human EPO. EPO is potentially useful in
CC the diagnosis and treatment of blood disorders characterised by low or
CC defective red blood cell production
XX
SQ Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 7124 TTCTGTGACACAGTCCAGCCT 7146
DB 23 TGCTGGCCACGACGTACAGCCT 1
RESULT 2864
AAV09049/c
ID AAV09049 standard; DNA; 23 BP.

XX
AC AAV09049;
XX
DT 25-JUN-1998 (first entry)
XX
DE Substrate for tetrahymena ribozyme L-21.
XX
KM Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase;
KM protease; antiviral agent; gene regulator; immunogenic virus; vaccine;
KM mutation detection; ss.
XX
OS Synthetic.
OS Tetrahymena sp.
XX
PN M09802583-A1.
XX
PD 22-JAN-1998.
XX
PF 16-JUL-1997; 97MO-US012394.
XX
PR 17-JUL-1996; 96US-00682423.
XX
PA (SCRI) SCRIPPS RBS INST.
XX
PI Joyce GF;
XX
DR WPI; 1998-110627/10.
XX
PT Catalytic RNA for site-specific cleavage of nucleic acid or hydrolysis of
PT amide bonds - and ribozyme amidase intermediates, useful e.g. as
PT peptidase(s), antiviral agents and gene regulators.
XX
PS Example 1; Page 120; 215pp; English.
XX
CC This sequence is a substrate for a wild type tetrahymena ribozyme L-21
CC form. The ribozyme sequence is an example of a catalytic RNA (I) of the
CC invention, which catalyses site-specific cleavage of nucleic acid under
CC physiological conditions includes a sequence derived from a group I
CC intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide
CC ends are useful as peptidases and proteases, e.g. in wound debridement,
CC clot dissolution, in detergents or as a meat tenderiser. (I) cleave
CC single- and (partly) double-stranded nucleic acids in vitro or in vivo,
CC and are potentially useful as antiviral agents and gene regulators; also
CC to generate defective but still immunogenic viruses (for vaccines);
CC diagnostically to detect mutations in nucleic acid or to identify nucleic
CC acid binding agents; to modulate/terminate reactions initiated by DNA
CC primers; to generate truncated transcripts from DNA; to modulate
CC therapeutic/diagnostic processes using antisense sequences; in DNA
CC fingerprinting and for vector construction. (I) and (II) are produced by
CC in vitro evolution processes that provide better catalytic performance;
CC broader active temperature and pH ranges; new enzymatic activities or
CC specificities; altered recognition sites or co-factor requirement
XX
SQ Sequence 23 BP; 12 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 6683 TATTTTATTTATATGGGCC 6705
DB 23 TTATTTATTTATTTAGAGGCC 1
RESULT 2865
AAT99526
ID AAT99526 standard; DNA; 23 BP.
XX
AC AAT99526;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human ST receptor PCR primer.

```

XX ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KW metastasis; diagnosis; human; PCR; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX MO9742506-A1.
XX 13-NOV-1997.
XX 02-MAY-1997; 97WO-US007467.
XX 03-MAY-1996; 96US-0016564P.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Waldman SA, Carrithers SL;
PI WPI; 1998-008454/01.
XX Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
XX
XX Claim 14; Page 54; 62pp; English.
XX Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AAW37371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99528 and AAT99527. Claimed in
CC vitro methods for determining whether or not (i) a tumour cell is a
CC metastasised colorectal cancer cell, or (ii) an individual has
CC colorectal cancer cell comprise the steps of examining a sample of
CC colorectal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunosassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AAT97229)
XX
XX Sequence 23 BP; 8 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3199 AGTAGGGGCTTGAGAAAGTGGG 3221
Db 1 AATGAGGGGCTGGAATAGTAGAG 23

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PF 19-SEP-1997; 97JP-00271927.
XX 19-SEP-1997; 97JP-00271927.
XX (SHIS ) SHISEIDO CO LTD.
XX WPI; 1999-281045/24.
XX
XX Immortalised human hair papilla cells used for evaluation of hair growth
PT agent - are prepared by transformation of human hair papilla cells with
PT gene with deleted replication initiation point.
XX
XX Example 2; Page 7; 23pp; Japanese.
XX
XX The specification describes the preparation of immortalized human hair
CC papilla cells (HPC). The method comprises transformation of HPC with an
CC SV40 viral Large T-antigen gene with deleted replication initiation
CC point. The immortalized HPC can be used in a screening method for a hair
CC growth agent, by culture of immortalized HPC in the presence of a
CC substance to be tested and observation of the growth of the immortalized
CC HPC. HPC is also used in development of hair growth stimulating agents.
CC The present sequence represents a PCR primer, which is used in the course
CC of the invention
XX
XX Sequence 23 BP; 5 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 374 ACTACGAGCTGGAGCATGACCG 396
Db 1 ACTACCTGCTGGGCATCAAGCG 23

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RESULT 2866
AAK34877
ID AAK34877 standard; DNA; 23 BP.
XX
XX AAK34877;
XX
XX 28-JUN-1999 (first entry)
XX
XX PCR primer used to amplify FGFA.
XX
XX Immortalised human hair papilla cell; HPC; screening; hair growth;
KW SV40 viral Large T-antigen gene; deleted replication initiation point;
KW hair growth stimulating agent; PCR primer; ss.
XX
XX Synthetic.
OS
XX JP11089565-A.
XX
XX 06-APR-1999.
XX
XX

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RESULT 2867
AAK53824
ID AAK53824 standard; DNA; 23 BP.
XX
XX AAK53824;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX Synthetic.
OS
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX

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PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction.
 PS Disclosure, Page 42, 120pp; English.
 XX The specification describes antisense oligonucleotides (AA52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the junction between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AA55272-74. These multiple target oligonucleotides
 CC (specifically AA55180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 23 BP, 0 A, 8 C, 1 G, 14 T, 0 U, 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5699 TTTCCTTCCTTCCTTCCTTCCTC 5721
 DB 1 TTTCCTTCCTTCCTTCCTTCCTTC 23
 RESULT 2868
 AAX18455/C
 ID AAX18455 standard; DNA, 23 BP.
 XX
 AC AAX18455;
 XX
 DT 12-MAY-1999 (first entry)
 XX
 DE Primer for DNA encoding orphan homologue GPR12.
 XX
 KM Agonist identification; orphan receptor; constitutively active OR;
 KM Graves' disease; thyroid adenoma; hypertension; cardiomyopathy;
 KM schizophrenia; Kaposi's sarcoma; fibroblast growth factor receptor;
 KM adenylylate cyclase constitutive activator; thyrotropin receptor;
 KM thyrotropin stimulating hormone; beta-adrenergic receptor; PCR primer;
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX
 PN WO9846995-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 14-APR-1998; 98WO-US007496.
 XX
 PR 14-APR-1997; 97US-00839449.
 XX
 XX (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 XX
 PI Behan DP, Chalmers DT;
 XX
 DR WPI; 1999-105468/09.
 XX
 PT Identifying agonists of orphan receptors from their effect on the

PT constitutively active receptor - particularly therapeutically active
 PT inverse agonists at G protein coupled receptors, without requiring
 PT knowledge of endogenous ligand or receptor function.
 XX
 XX Example 4; Page 72; 114pp; English.
 XX
 PS This sequence is a primer for DNA encoding the orphan receptor homologue
 CC GPR3. The invention relates to a method for the identification of
 CC candidate compounds as agonists, including inverse or partial, of an
 CC orphan receptor (OR), which comprises: (i) applying test compound to
 CC constitutively active OR; and (ii) measuring its effect on OR. The method
 CC is particularly used to identify inverse agonists of G protein-coupled
 CC OR, i.e. potential therapeutic agents for treating conditions in which
 CC constitutively active OR are implicated (e.g. Graves' disease, thyroid
 CC adenoma, hypertension, cardiomyopathy, schizophrenia, major depression,
 CC Kaposi's sarcoma and many others tabulated). It is based on
 CC identification of agents that reduce receptor activation, rather than
 CC compounds that antagonise the normal ligand. Once identified, (inverse)
 CC agonists can be used to study OR function. The method does not require
 CC knowledge of the endogenous receptor ligand or receptor function, and
 CC identifies directly compounds that inhibit the activated receptor, i.e.
 CC able to block both ligand-dependent and -independent activation, rather
 CC than only the ligand-dependent process, as is the case with compounds
 CC identified by ligand-dependent assays. It should accelerate drug
 CC discovery at a wide range of OR and since activated receptors have a
 CC greater response to the agents, potential drugs are more likely to be
 CC detected
 XX
 SQ Sequence 23 BP, 6 A, 4 C, 8 G, 5 T, 0 U, 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1669 CAACCTGTGTTTCGCAATATGC 1691
 DB 23 CACCCTATGTCCTGCTAATAGGC 1
 RESULT 2869
 AAX00055
 ID AAX00055 standard; DNA, 23 BP.
 XX
 AC AAX00055;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Human Y chromosome-specific sequence DY21 PCR primer Y21.
 XX
 XX Human Y chromosome; DY21; urine; detection; amplification; diagnosis;
 KM hybridisation; kidney barrier; foetal sex; maternal; inherited disease;
 KM cancer; pathogenic infection; paternity testing; PCR primer; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX
 PN WO9854364-A1.
 XX
 PD 03-DEC-1998.
 XX
 PF 29-MAY-1998; 98WO-US010965.
 XX
 PR 30-MAY-1997; 97US-0048170P.
 PR 03-JUN-1997; 97US-0048381P.
 XX
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA
 PI Lichtenstein AV, Melkonian HS, Umanaky SR;
 XX
 DR WPI; 1999-070223/06.
 XX
 XX Analysis of DNA present in urine that has crossed the kidney barrier -
 PT useful in the determination of foetal sex, and in the diagnosis of

PT inherited disease, cancer and pathogenic infections.
XX
PS Claim 44; Page 34; 72pp; English.
CC
CC A method has been developed for the analysis of a fragment of foetal DNA
CC that has crossed the placental and kidney barriers. The method comprises
CC assaying for presence of foetal DNA in a urine sample from a pregnant
CC subject. Also described are: (1) detecting any target nucleic acid
CC sequences in a urine sample; (2) diagnosis for male foetal DNA in
CC maternal urine; and (3) general method for detecting Y chromosome-
CC specific nucleic acids using the primers given in AA00055 to AA00058.
CC The methods are used: (i) to determine the sex of a foetus (by detecting
CC Y-specific fragments); (ii) for diagnosing or monitoring diseases,
CC particularly cancer and infections, also pre-natal diagnosis of inherited
CC diseases and predisposition to disease; or (iii) to establish paternity.
CC Analysis of urinary DNA is non-invasive and provides early indication of
CC foetal sex or disease
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 5692 CCACGTTTGCCTTCCTTC 5714
DB 1 CCATTCTTGCATTCGTTTC 23
RESULT 2870
AAA33267
ID AAA33267 standard; DNA; 23 BP.
XX
AC AAA33267;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:956.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
FN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Claim 18; Page 385; 1343pp; English.
CC
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ON reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:1 to 1680 (AAA32323 to
CC AAA33892) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 5699 TTGCGCTTCTTTCCTTCCTTC 5721
DB 1 TTTTCTTCTTCTTCTCTCTTC 23
RESULT 2871
AAA64522/C
ID AAA64522 standard; DNA; 23 BP.
XX
AC AAA64522;
XX
DT 02-JAN-2001 (first entry)
XX
DE PCR primer IncuBR used to amplify exon 1 of human FEZ1 gene.
XX
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
KW tumour proliferation; tubulin; microtubule; protein BPI-gamma;
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
KW tumorigenesis; tumour survival; metastasis; PCR primer; ss.
XX
OS Homo sapiens.
XX
FN WO2000050565-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004950.
XX
PR 25-FEB-1999; 99US-0121537P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Ishii H;
XX
DR WPI; 2000-558396/51.
XX
PT New polynucleotide homologous with a portion of one strand of the human
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
PT cancer.
XX
PS Example 1; Page 45; 255pp; English.
XX

PCR primers AAA64521-22 were used to amplify a fragment of the human FEZ1 gene. FEZ1 is a tumour suppressor gene located at chromosome location 8p22. Decreased or no expression of FEZ1 is detected in a variety of cancer cells. Expression of FEZ1 inhibits tumor growth and proliferation. FEZ1 also interacts with tubulin, with microtubules, and with protein ERF-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are useful for inducing cells to proliferate. Compounds which modulate FEZ1 association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FEZ1 binding and phosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis

Sequence 23 BP; 4 A; 10 C; 2 G; 7 T; 0 U; 0 Other:

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 199 GCACGGGTATGATGATGAGC 221
23 GCACGGGTATGATGATGAGC 1

RESULT 2872
AAZ50566/C
ID AAZ50566 standard; DNA; 23 BP.

AAZ50566;
20-JUN-2000 (first entry)

PCR primer-2 to amplify human GPR12 DNA.

G protein-coupled orphan receptor; GPCR; agonist; G protein;
GPCR fusion protein; inverse agonist; drug; treatment; PCR primer; GPR12;
G protein-coupled receptor; human; ss.

Homo sapiens.
WO200006597-A2.

10-FEB-2000.
30-JUL-1999; 99WO-US017425.

31-JUL-1998; 98US-0094879P.
30-OCT-1998; 98US-0106300P.
04-DEC-1998; 98US-0110906P.
26-FEB-1999; 99US-0121851P.

(AREN-) ARENA PHARM INC.

Behan DP, Chalmers DT, Liaw C, Lan I, Lowitz K, Chen R;
WPI; 2000-195260/17.

Identification of a compound useful as a therapeutic agent, comprises identifying a compound against constitutively activated G protein-coupled orphan receptors.

Example 7; Page 34; 123pp; English.

The patent discloses a method of identifying agonists and inverse or partial agonists to the endogenous, constitutively activated G protein-coupled orphan receptors (GPCRs), by contacting them with a GPCR fusion protein comprising a GPCR and a G protein. Determining expression of

GPCRs in tissue samples can be used to identify related diseases. Inverse agonists to these receptors can be used as drugs for treating GPCR-related diseases. The present sequence is a PCR primer used to amplify a 220 bp fragment of human GPR12 (G protein-coupled receptor) DNA, to examine tissue samples for expression of these receptors

Sequence 23 BP; 6 A; 4 C; 8 G; 5 T; 0 U; 0 Other:

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1669 CAACCTGTTCGCAATATGC 1691
23 CAACCTGTTCGCAATATGC 1

RESULT 2873
AAA03669
ID AAA03669 standard; DNA; 23 BP.

AAA03669;
19-MAY-2000 (first entry)

Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:953.

Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
adenosine A2a receptor; adenosine A2b receptor; adenosine A3 receptor;
phosphodiesterase; cardiopulmonary failure; renal failure; ischaemia;
endotoxin release; ARDS; acute respiratory distress syndrome;
cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
supraventricular tachycardia; allergic rhinitis; acute inflammation;
chronic obstructive pulmonary disease; ss.

Homo sapiens.
Synthetic.
WO9963938-A2.

16-DEC-1999.
08-JUN-1999; 99WO-US012775.

08-JUN-1998; 98US-0086501P.
09-JUN-1998; 98US-00093972.
09-JUN-1998; 98US-0086577P.

(EPIC-) EPIGENESIS PHARM INC.

Nyce JW, Hill JL;
WPI; 2000-116433/10.

Novel composition for treating or preventing e.g. cardiopulmonary and renal injury.

Claim 17; Page 38; 252pp; English.

The present invention describes a pharmaceutical composition, comprising at least one agent (I) that prevents, alleviates and/or inhibits adenosine-mediated cardiopulmonary and/or renal damage and/or failure. (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide (Ib), containing less than 15% adenosine (A), that is antisense to target genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3' ends or segments between coding and non-coding sequences), or to all segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and has A1, A2b or A3 agonist activity or A2a antagonist activity (or at least no agonist activity at this receptor). (I) may be a mixture of (Ia) and (Ib), and optionally also contains one or more surfactants. The compositions are used to prevent, alleviate and/or treat adenosine receptor-mediated cardiac, lung and/or renal damage or failure (particularly where associated with ischaemia, toxin release and/or

CC compound having inverse agonist activity, partial agonist activity or
 CC agonist activity to a constitutively active orphan receptor (OR). The
 CC method comprises determining the efficacy of the compound by contacting
 CC it with the OR. A compound identified by the above method having inverse
 CC agonist activity to OR is useful for the treatment of diseases
 CC characterised by constitutive activation of the receptor e.g. Graves'
 CC disease, male precocious puberty, Jansen's disease, retinitis pigmentosa,
 CC hyperparathyroidism, neuropsychiatric diseases, schizophrenia, major
 CC depression, and cancerous growth in Kaposi's sarcoma. The method can
 CC identify (i) directly without prior knowledge or use of receptor ligands
 CC and is useful for accelerating drug discovery at a broad range of OR.
 CC The present sequence represents a reverse transcriptase PCR primer for
 CC the human orphan receptor GPR12, which is used in an example from the
 CC present invention

XX Sequence 23 BP; 6 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

XX
 SQ Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03; Mismatches 0; Gaps 0;
 Matches 18; Conservative 0; Indels 5;

QY 1669 CAACCTGTTCTGCAAAATATGC 1691
 23 CACCCTGTTCTGCTAATAGGC 1

RESULT 2876
 AAD19181/c
 ID AAD19181 standard; DNA; 23 BP.
 XX
 AC AAD19181;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human GPCR12 cDNA expression analysis determining probe Ag1223.
 XX
 XX Human; G-protein coupled receptor 12; GPCR12; cardiomyopathy; vaccine;
 KM atherosclerosis; diabetes; cardiant; cytosolic; cancer; obesity; pain;
 KM diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM immune disorder; haematopoietic disorders; retinal disorder; HIV;
 KM human immunodeficiency virus; adenocarcinoma; bulimia; asthma; ulcer;
 KM angina pectoris; hypotension; hypertension; Crohn's disease; anxiety;
 KM multiple sclerosis; schizophrenia; dementia; mental retardation;
 KM gene therapy; osteoporosis; urinary retention; probe; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "FAM-labelled adenosine"
 FT modified_base 23
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "TAMRA-labelled thymidine"
 FT
 XX WO200181378-A2.
 PN
 XX
 PD 01-NOV-2001.
 XX
 XX 27-APR-2001; 2001WO-US013660.
 PF
 XX 27-APR-2000; 2000US-0199947P.
 PR 27-APR-2000; 2000US-0199960P.
 PR 14-AUG-2000; 2000US-0275226P.
 PR 18-DEC-2000; 2000US-0256399P.
 PR 18-DEC-2000; 2000US-0256524P.
 PR 22-DEC-2000; 2000US-0258159P.
 PR 28-DEC-2000; 2000US-0258511P.
 PR 28-DEC-2000; 2000US-0258828P.
 PR 04-JAN-2001; 2001US-0259659P.

PR 13-MAR-2001; 2001US-00275226.
 XX
 XX (CURA-) CURAGEN CORP.
 PA Padigaru M, Mishra V, Spyrek KA, Grosse WM, Szekeres ES;
 PI Alsbrook JP, Burgess CE, Caeman SJ, Lepley DM, Gangoli EA;
 PI Macdougall JR, Sathison G;
 XX
 DR WPI; 2001-611739/70.
 XX
 XX G-protein coupled receptor polypeptides and NAs useful for
 PT preventing, diagnosing and treating cardiomyopathy, atherosclerosis,
 PT cancers and diabetes.
 XX
 PS Example 1G; Page 198; 242pp; English.

XX
 XX The present DNA sequence is a probe which is used for determining the
 CC expression analysis of human G-protein coupled receptor-12 (GPCR-12)
 CC cDNA. GPCR protein and DNA may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate GPCR expression,
 CC obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain,
 CC atherosclerosis, neurodegenerative disorders (Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease); bulimia, immune disorder,
 CC haematopoietic disorders, disorders related to cell signal processing and
 CC metabolic pathway modulation, retinal disorder (photoreception),
 CC bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm
 CC adenocarcinoma); angina pectoris, hypotension, hypertension, asthma,
 CC Crohn's disease, multiple sclerosis, ulcers, neurological disorders
 CC (dementia, mental retardation, schizophrenia, anxiety); acute heart
 CC failure, osteoporosis, myocardial infarction and urinary retention

XX
 XX Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

XX
 SQ Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0;

QY 267 GCAGGTGTTCCAGGC 281
 17 GCAGGTGTTCCAGGC 3

Db 17 GCAGGTGTTCCAGGC 3

RESULT 2877
 AAD19184/c
 ID AAD19184 standard; DNA; 23 BP.
 XX
 AC AAD19184;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human GPCR12 cDNA expression analysis determining probe Ag1609.
 XX
 XX Human; G-protein coupled receptor 12; GPCR12; cardiomyopathy; vaccine;
 KM atherosclerosis; diabetes; cardiant; cytosolic; cancer; obesity; pain;
 KM diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM immune disorder; haematopoietic disorders; retinal disorder; HIV;
 KM human immunodeficiency virus; adenocarcinoma; bulimia; asthma; ulcer;
 KM angina pectoris; hypotension; hypertension; Crohn's disease; anxiety;
 KM multiple sclerosis; schizophrenia; dementia; mental retardation;
 KM gene therapy; osteoporosis; urinary retention; probe; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "FAM-labelled adenosine"
 FT modified_base 23
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "TAMRA-labelled thymidine"
 FT

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XX      WO200181378-A2.
PN      01-NOV-2001.
XX      27-APR-2001; 2001WO-US013680.
XX      27-APR-2000; 2000US-0199947P.
XX      27-APR-2000; 2000US-0199960P.
XX      14-AUG-2000; 2000US-0275226P.
XX      18-DEC-2000; 2000US-0256399P.
XX      18-DEC-2000; 2000US-0256524P.
XX      22-DEC-2000; 2000US-0258159P.
XX      28-DEC-2000; 2000US-0258511P.
XX      28-DEC-2000; 2000US-0258828P.
XX      04-JAN-2001; 2001US-0259659P.
XX      13-MAR-2001; 2001US-00275226.
XX      (CURA-) CURAGEN CORP.
XX      Padigaru M, Mishra V, Spytek KA, Grosse WM, Szekeres ES;
XX      Alsobrook JP, Burgess CE, Casman SJ, Lepley DM, Gangolli EA;
XX      Macdonald JR, Smithson G;
XX      WPI; 2001-611739/70.
XX      G-Protein coupled receptor polypeptides and NAs useful for
XX      preventing, diagnosing and treating cardiomyopathy, atherosclerosis,
XX      cancers and diabetes.
XX      Example 1G; Page 198; 242pp; English.
XX      The present DNA sequence is a probe which is used for determining the
XX      expression analysis of human G-protein coupled receptor-12 (GPCR-12)
XX      cDNA. GPCR protein and DNA may be used in the prevention, diagnosis and
XX      treatment of diseases associated with inappropriate GPCR expression,
XX      obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain,
XX      atherosclerosis, neurodegenerative disorders (Alzheimer's disease,
XX      Parkinson's disease, Huntington's disease), bulimia, immune disorder,
XX      haematopoietic disorders, disorders related to cell signal processing and
XX      metabolic pathway modulation, retinal disorder (photoreception),
XX      bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm
XX      adenocarcinoma); angina pectoris, hypotension, hypertension, asthma,
XX      Crohn's disease, multiple sclerosis, ulcers, neurological disorders
XX      (dementia, mental retardation, schizophrenia, anxiety); acute heart
XX      failure, osteoporosis, myocardial infarction and urinary retention
XX      Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX      Query Match      0.2%; Score 15; DB 1; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      267 GCAGGTGTCAGGC 281
DB      17 GCAGGTGTCAGGC 3

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XX      inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX      Homo sapiens.
XX      WO200129262-A2.
XX      26-APR-2001.
XX      13-OCT-2000; 2000WO-US028436.
XX      15-OCT-1999; 99US-0160096P.
XX      (ORCH-) ORCHID BIOSCIENCES INC.
XX      Picoult-Newburg L, Pohl M;
XX      WPI; 2001-290930/30.
XX      New genotyping oligonucleotide, useful for detecting the presence,
XX      absence or identity of single polynucleotide polymorphism in a nucleic
XX      acid sample.
XX      Claim 1; Page 66; 83pp; English.
XX      Sequences AAH37205 - AAH4094 represent PCR primers, single nucleotide
XX      primer extension (SNPE) primers, and the sequences of regions flanking
XX      sites of single nucleotide polymorphisms SNPs. The present invention
XX      includes kits for determining the presence or absence of a SNP, using the
XX      oligonucleotides of the invention. The PCR primers are used to amplify a
XX      SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX      The oligonucleotides are useful for genotyping a nucleic acid sample by
XX      performing a single-nucleotide primer extension reaction. The
XX      oligonucleotides are useful for determining the presence, absence or
XX      identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX      assess by association analysis the genotype of an individual or group of
XX      individuals, having a pathological phenotypic trait suspected of being
XX      caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX      agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
XX      dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX      osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX      traits also include symptoms of or susceptibility to multifactorial
XX      disease of which a component is or may be genetic such as autoimmune
XX      diseases, including, rheumatoid arthritis, multiple sclerosis,
XX      inflammation, cancer, nervous system diseases and infection by pathogenic
XX      microorganism. The method is also useful in forensic investigations and
XX      paternity analysis. The present sequence represents a PCR primer specific
XX      for a human SNP containing DNA sequence
XX      Sequence 23 BP; 15 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
XX      Query Match      0.2%; Score 15; DB 1; Length 23;
XX      Best Local Similarity 78.3%; Pred. No. 2.2e+03;
XX      Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      3926 GCGTTCTTTCTCCCTTGATGCT 3948
DB      23 GCGTTTCTCTCTTTGCTTGT 1

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RESULT 2878
AAH40410/C
ID      AAH40410 standard; DNA; 23 BP.
XX      AAH40410;
XX      14-AUG-2001 (first entry)
XX      SNP specific lower PCR primer SEQ ID 3206.
XX      Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX      SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX      Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX      polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX      acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

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RESULT 2879
AAF32064/C
ID      AAF32064 standard; DNA; 23 BP.
XX      AAF32064;
XX      10-APR-2001 (first entry)
XX      eIF-5A PCR primer #5.
XX      eIF-5A; eukaryotic initiation factor 5A; senescence inhibition;
XX      PCR primer; ss.
XX      Unidentified.

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XX MO200102592-A2.
 XX 11-JAN-2001.
 XX 06-JUL-2000; 2000MO-US018364.
 XX 06-JUL-1999; 99US-00348675.
 PR 19-JUN-2000; 2000US-00597771.
 XX (SENE-) SENESCO INC.
 XX Thompson JE, Wang T, Lu DL;
 XX WPI; 2001-061978/07.
 XX
 XX Tomato, Arabidopsis and carnation cDNA clones encoding senescence-induced
 PT deoxyhypusine synthase and eif-5a, useful for inhibiting senescence in a
 PT plant when introduced in reverse orientation into the genome of the
 PT plant.
 XX
 PS Claim 21; Page 51; 135pp; English.
 XX
 CC The present sequence is a PCR primer used to isolate the coding sequences
 CC for Arabidopsis, carnation and tomato eukaryotic initiation factor 5A
 CC (eif-5A; see AAF2055, AAF2056 and AAF2057). The eif-5A coding
 CC sequence, when introduced into a plant cell in reverse orientation,
 CC inhibits expression of the endogenous eif-5A gene. The eif-5A coding
 CC sequences are useful for altering age-related senescence and/or
 CC environmental stress-related senescence, for inhibiting seed aging and
 CC for increasing seed yield in a plant. In addition, the inhibition of
 CC senescence in a plant results in increased resistance of the plant to
 CC environmental stress-induced and/or pathogen-induced senescence,
 CC increased plant biomass, delayed fruit softening and spoilage
 XX
 SQ Sequence 23 BP; 12 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3912 CATTTCCTCTGCTTCTTT 3934
 Db |||||
 23 CCTTCTCTCTGATTTCTT 1
 RESULT 2880
 AAF27080
 ID AAF27080 standard; DNA; 23 BP.
 XX
 AC AAF27080;
 XX
 DT 06-APR-2001 (first entry)
 XX
 DE Human MEK1 real-time quantitative PCR primer, SEQ ID NO:2.
 XX
 KW Human MEK1; mitogen-activated protein kinase kinase kinase 1;
 KW MEK kinase 1; MAP/ERK kinase 1; pro-apoptotic;
 KW apoptosis signal regulation; programmed cell death;
 KW serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
 KW Jun N-terminal kinase/stress-activated protein kinase; Bcl-2 substrate;
 KW NF-kappa-B-mediated transcription regulation; expression inhibition;
 KW antisense therapy; hyperproliferative disorder; cancer; inflammation;
 KW quantitative real-time PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6168950-B1.
 XX
 PD 02-JAN-2001.
 XX
 PF 23-JUL-1999; 99US-00359756.
 XX

PR 23-JUL-1999; 99US-00359756.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Cowseert LM, Gaarde W, Ward DT;
 PT WPI; 2001-122264/13.
 XX
 DR New antisense compound targeting nucleic acid encoding human mitogen-
 PT activated protein kinase kinase 1 (MEK1), useful for treating diseases
 PT or conditions associated with MEK1 expression, or preventing
 PT inflammation or tumor formation.
 XX
 PS Example 14; Col 39; 35pp; English.
 XX
 CC Sequences AAF27080-AAF27081 represent human MEK1 PCR primers used in
 CC quantitative real-time PCR with probe AAF27082 in an exemplification of
 CC the present invention. The invention relates to antisense
 CC oligonucleotides targeted to the human MEK1 gene, which inhibit its
 CC expression. A series of oligonucleotides (AAF27086-AAF27125) were
 CC designed to target different regions of the human MEK1 RNA, and were
 CC analysed for their effect on MEK1 mRNA levels by quantitative real-time
 CC PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as a
 CC control. MEK1 (also known as mitogen-activated protein kinase kinase
 CC kinase 1, MEK kinase 1 and MAP/ERK kinase 1) is a dual-specific
 CC serine/threonine kinase which mediates cellular responses to mitogenic
 CC stimuli, being involved in JNK/SAPK (Jun N-terminal kinase/stress-
 CC activated protein kinase) MAP kinase cascades. MEK1 regulates signalling
 CC events associated with apoptosis (programmed cell death) and NF-kappa-B,
 CC both of which have been associated with the development of
 CC hyperproliferative disorders such as cancer. Specifically, MEK1 lies
 CC directly downstream of Bcl-2 in an apoptotic signalling cascade, and
 CC plays a critical role in the control of NF-kappa-B-mediated transcription
 CC at multiple points in the apoptotic cascade. The oligonucleotides of the
 CC invention are useful for diagnosis, prevention and treatment of
 CC conditions associated with MEK1 expression, such as inflammation, and
 CC cancer and other hyperproliferative disorders
 XX
 SQ Sequence 23 BP; 9 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4878 GCAACTCACAAGGTTGCA 4900
 Db |||||
 1 GAACTCTCAAGGTTGCA 23
 RESULT 2881
 ABK52683
 ID ABK52683 standard; DNA; 23 BP.
 XX
 AC ABK52683;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human GPCR promoting insulin secretion, 5' RACE primer #1.
 XX
 KW Human; ss; G protein coupled receptor; GPCR; insulin secretion; primer;
 KW diabetes; antidiabetic; pancreatic beta cell; PCR;
 KW intracellular cAMP concentration.
 XX
 OS Homo sapiens.
 XX
 PN WO200244362-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 30-NOV-2001; 2001WO-JP010472.
 XX
 PF 01-DEC-2000; 2000JP-00367349.
 PR 10-AUG-2001; 2001JP-00243841.
 XX

XX (YAMA) YAMANOUCHI PHARM CO LTD.
 XX PA
 XX PI Ohishi T, Takasaki J, Matsumoto M, Saito T, Kamohara M, Soga T,
 XX PI Yoshida S, Ueda Y;
 XX DR WPI; 2002-463740/49.
 XX PT Drug screening using a polypeptide which promotes pancreatic beta cell
 PT insulin secretion and intracellular cyclic adenosine monophosphate
 PT concentration for identification of antidiabetic agents.
 XX PS
 XX Claim 1; Page 62; 73pp; Japanese.
 CC The invention relates to screening for potential diabetes treatment
 CC agents using G-protein coupled receptor (GPCR) polypeptide which promotes
 CC insulin secretion by pancreas beta-cells under high glucose levels, and
 CC increases intracellular cyclic adenosine monophosphate (cAMP
 CC concentration. Also included are (1) screening method of cells
 CC transformed by a vector containing a gene encoding the GPCR polypeptide;
 CC (2) antidiabetic agents identified by the screening method; (3) drug
 CC compositions containing these compounds; and (4) treatment of diabetes
 CC using these drug compositions. The present sequence is a 5' RACE (rapid
 CC amplification of cDNA ends) PCR primer used to isolate the human cDNA
 CC encoding the GPCR
 XX SO
 XX Sequence 23 BP; 4 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 2215 GGGGTGCTGAAGCCAGCTACC 2237
 Db 1 GGCGCTGTGATGCGAAGTACC 23
 RESULT 2882
 ABK8382/c
 ID ABK8382 standard; DNA; 23 BP.
 XX AC
 XX ABK8382;
 XX DT 07-OCT-2002 (first entry)
 XX DE Tomato senescence-induced eIF-5A cDNA PCR primer.
 XX KM Tomato; ss; PCR; deoxyhypusine synthase; DHS; senescence; eIF-5A; primer;
 KM eukaryotic initiation factor 5A; plant; cell death; disease resistance;
 KM antisense; blossom end rot; environmental stress; pathogen resistance;
 KM shelf-life; perishable fruit; flower; vegetable.
 XX OS
 XX Lycopersicon sp.
 XX PN WO200244392-A2.
 XX PD 06-JUN-2002.
 XX PF 29-NOV-2001; 2001WO-US044505.
 XX PR 29-NOV-2000; 2000US-00725019.
 XX PA (SENE-) SENESCO TECHNOLOGIES INC.
 XX PI Thompson JE, Wang T, Lu DL;
 XX DR WPI; 2002-557545/59.
 XX PT Increasing resistance to physiological disease in plant, by integrating
 PT gene or its fragment encoding senescence-induced deoxyhypusine synthase
 PT or eIF5A in antisense orientation into plant genome and growing the
 XX plant.

PS Example 9; Page 44; 114pp; English.
 XX CC
 CC The invention relates to increasing resistance to physiological disease
 CC in a plant, involving integrating into the plant genome a vector having
 CC antisense sequences complementary to corresponding portion of one strand
 CC of DNA encoding endogenous senescence-induced eIF-5A (eukaryotic
 CC initiation factor 5A) gene or 3' end of endogenous senescence-induced
 CC deoxyhypusine synthase (DHS), a portion of RNA sequence encoded by eIF-5A
 CC gene or DHS gene, and growing the plant. Also included is a plant or its
 CC progeny, where the plant is derived from a cell having inhibited or
 CC reduced expression of senescence-induced DHS, senescence-induced eIF-5A,
 CC or both, where the cell is produced by the method of the invention. The
 CC method is useful for increasing resistance to physiological disease such
 CC as blossom end rot in a plant. The method results in delayed onset of
 CC senescence and improved resistance to environmental stress and pathogens,
 CC thus extending the plant shelf-life and/or growth period. The method
 CC delays deterioration and spoilage of perishable fruits, flowers,
 CC vegetables, and plants, increases the shelf-life of perishable fruits,
 CC flowers, vegetables, and plants, and renders their tissues more stress-
 CC tolerant and pathogen resistant. The present sequence is a PCR primer
 CC used to isolate their full length the tomato senescence-induced eIF-5A
 CC cDNA
 XX SO
 XX Sequence 23 BP; 12 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 3912 CATTTTCACCTTGCTGCTTT 3934
 Db 23 CTTTCTCTCTAGGATCTTT 1
 RESULT 2883
 ABK95525/c
 ID ABK95525 standard; DNA; 23 BP.
 XX AC
 XX ABK95525;
 XX DT 24-SEP-2002 (first entry)
 XX DE Novel G-protein coupled receptor probe #14.
 XX KM G protein coupled receptor; GPCR; olfactory receptor;
 KM cell signal processing disorder; metabolic pathway modulation;
 KM cardiomyopathy; atherosclerosis; diabetes; developmental disease;
 KM immune disease; taste disorder; scent detectability disorder; obesity;
 KM Burkitt's lymphoma; corticosteroid-induced disease; infectious disease; pain;
 KM signal transduction pathway disorder; metabolic pathway disorder;
 KM retinal disease; metabolic disorder; cancer; Parkinson's disease;
 KM acute heart failure; urinary retention; osteoporosis; Crohn's disease;
 KM ulcer; allergy; neurological disorder; genetic disorder; transplantation;
 KM fertility; pancreatitis; Hyperthyroidism; Endometriosis;
 KM forensic biology; transgenic animal; probe; ss.
 XX OS
 XX Synthetic.
 XX PN WO200240539-A2.
 XX PD 23-MAY-2002.
 XX PF 16-OCT-2001; 2001WO-US032256.
 XX PR 16-OCT-2000; 2000US-0240704P.
 PR 26-OCT-2000; 2000US-0243497P.
 PR 31-OCT-2000; 2000US-0244542P.
 PR 03-NOV-2000; 2000US-0245484P.
 PR 12-DEC-2000; 2000US-0255017P.
 PR 17-JAN-2001; 2001US-0262159P.
 PR 22-JAN-2001; 2001US-0263216P.
 PR 22-JAN-2001; 2001US-0263340P.
 PR 25-JAN-2001; 2001US-0264118P.


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PR 12-FEB-2001; 2001US-0268225P.
PR 15-FEB-2001; 2001US-0269031P.
PR 27-JUL-2001; 2001US-0308203P.
XX
XX
XX (CURA-) CURAGEN CORP.
PI Kikuda R, Spyrek KA, Casman SJ, Zernusen BD, Li L, Tchernev VT;
PI Colman SD, Ballinger RA, Padigaru M, Wolenc AR, Shenoy SG;
PI Edinger SR, Gerlach V, Gangoll EA, MacDougall JR, Smithson G;
PI Payman JA, Stone DJ, Gunther E, Ellerman K, Grose WM, Alsobrook JP;
PI Lepley DM, Burgess CE;
XX
XX WPI; 2002-500205/53.
XX
XX
XX Novel G protein coupled receptor especially olfactory receptor
PT polypeptides and nucleic acids for diagnosing and treating
PT atherosclerosis, cardiomyopathy and diabetes.
XX
XX
XX Example 2; Page 223; 309pp; English.
XX
XX The invention describes an isolated G protein coupled receptor X (GPCR1-
CC 12) polypeptide, especially an olfactory receptor. GPCR polypeptides are
CC useful for identifying an agent that binds to the polypeptide and for
CC identifying a candidate substance or ligand molecules interacting with an
CC olfactory receptor polypeptide. The polypeptide, (I) and (II) are also
CC useful for treating diseases and disorders related to cell signal
CC processing and metabolic pathway modulation e.g. cardiomyopathy,
CC atherosclerosis and diabetes, and developmental diseases, immune
CC diseases, taste and scent detectability disorders, Burkitt's lymphoma,
CC corticosteroid disease, signal transduction pathway disorders,
CC metabolic pathway disorders, retinal diseases, metabolic disorders,
CC obesity, infectious disease, pain, cancer, Parkinson's disease, acute
CC heart failure, urinary retention, osteoporosis, Crohn's disease, ulcers,
CC allergies, neurological disorders, genetic disorders, transplantation,
CC fertility, Pancreatitis, Hyperthyroidism and Endometriosis. GPCR
CC sequences are also useful for identifying a cell or tissue type in a
CC biological sample, to amplify DNA sequences from very small biological
CC samples such as tissues e.g. hair or skin or body fluids in forensic
CC biology. Cells comprising (I) are useful for producing non-human
CC transgenic animals for studying the function and/or activity of GPCR
CC protein and for identifying and/or evaluating modulators of GPCR protein
CC activity. This sequence represents a probe used to detect DNA encoding a
CC novel G-protein coupled receptor produced from real time quantitative (RTQ)
CC -PCR
XX
XX Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 267 GCAGGTGTCACGC 281
DB 17 GCAGGTGTCACGC 3

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RESULT 2884
AAD32230/c
ID AAD32230 standard; DNA; 23 BP.
XX
XX AAD32230;
XX
XX 18-JUN-2002 (first entry)
XX
XX RASSF1A gene amplifying reverse unmethylated PCR primer.
XX
XX Nested polymerase chain reaction; gene inactivation; cancer; lung; head;
XX neck; leukaemia; colorectal; prostate; bladder; immunological modulation;
XX antisense treatment; alkylating treatment; aberrant methylation; primer;
XX gene therapy; PCR; ss.
XX
XX Unidentified.
XX

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PN WO200218649-A1.
XX
XX 07-MAR-2002.
XX
XX 24-AUG-2001; 2001WO-US026452.
XX
XX 25-AUG-2000; 2000US-0228057P.
XX
XX (LOVE-) LOVEBLAZE RESPIRATORY RES INST.
XX
XX Belinsky SA, Palmsano WA;
XX
XX WPI; 2002-269531/31.
XX
XX
XX Nested, two-stage polymerase chain reaction for amplifying gene in cancer
PT e.g. of lung, comprises expanding copies of gene by amplification method
PT and using the product in a second amplification to detect gene
PT inactivation.
XX
XX
XX Example 2; Page 21; 55pp; English.
XX
XX The invention relates to a nested, two-stage polymerase chain reaction
CC (PCR) for amplifying a gene that is altered in a particular cancer. The
CC method comprises expanding copies of a gene by amplification method and
CC using the product in a second methylation-specific amplification to
CC detect gene inactivation. The method is useful for amplifying the gene
CC that may be altered in a particular cancer (preferably lung cancer, other
CC cancers which include head and neck, leukaemia, colorectal, prostate and
CC bladder) thereby permitting cancer detection and monitoring by detecting
CC gene inactivation in biological fluid such as sputum and blood. The
CC method finds application in the area of chemoprevention, where markers
CC are needed to identify high-risk subjects and to evaluate efficacy of
CC preventive agents. The method is further useful for identifying
CC individuals who subsequently could be enrolled in prevention intervention
CC studies using dietary supplements that are designed to impede or reverse
CC this premalignant state, and for monitoring the efficacy of the
CC interventions, by determining whether the previously detected methylation
CC biomarker persists or disappears during the course of the interventions,
CC and alkylating treatments. The method is useful for detecting the
CC aberrant methylation of the p16 gene, death-associated protein kinase
CC gene, O-6-methylguanine DNA methyltransferase gene (MGMT), RAS-associated
CC family 1 (RASSF1A) gene or other gene promoters. The present sequence is
CC a PCR primer used for amplifying RASSF1A gene
XX
XX Sequence 23 BP; 14 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 3167 GTTAGCTTGGCTTGAATCTT 3189
DB 23 GTTAGCTTGGCTTGAATCTT 1

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RESULT 2885
ABL99466/c
ID ABL99466 standard; DNA; 23 BP.
XX
XX ABL99466;
XX
XX 02-JUL-2002 (first entry)
XX
XX Left PCR primer used to target TGF-1 canine gene.
XX
XX Canine gene array; toxicological response; ss.
XX
XX Canis sp.
XX
XX WO200208453-A2.
XX
XX 31-JAN-2002.
XX

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XX 23-JUL-2001; 2001WO-US023311.
PF
XX
XX 21-JUL-2000; 2000US-0220057P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
PA
XX Farr SB, Pickett GG, Neft RE, Dunn RT,
PI WPI; 2002-217063/27.
XX
XX Identifying toxicologically relevant canine gene to determine
PT toxicological responses of agents, by obtaining and comparing gene
PT expression profiles of untreated canine cells and canine cells treated
PT with an agent.
XX
XX Example 5; Page 53; 140pp; English.
PS
XX This invention relates to identifying a toxicologically relevant canine
CC gene and the generation of an array of toxicologically relevant canine
CC genes. The gene array is useful for obtaining a gene expression profile,
CC by exposing a population of cells to an agent, obtaining cDNA from the
CC population of cells, labeling the cDNA, and contacting the cDNA with the
CC gene array. The relevant gene is useful for making and using arrays to
CC determine toxicological responses to various agents, and also useful for
CC identifying novel gene sequences and novel canine genes. The method for
CC analysing toxicological responses using the canine gene array is rapid
CC and efficient. The present sequence is related to the canine gene array
CC
SQ Sequence 23 BP; 2 A; 11 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4735 GGGCAGCTGAGAGAGAGGTC 4757
DB 23 GGCATGAGAGAGAGAGGTC 1

RESULT 2886
ABK67730
ID ABK67730 standard; DNA; 23 BP.
XX
AC ABK67730;
XX
DT 02-JUL-2002 (first entry)
XX
DE Novel transglutaminase TGz associated PCR primer #17.
XX
XX Transglutaminase; TGM; transamidation; autoimmune disease;
KM Addison's disease; AI haemolytic anaemia; AI thrombocytopenic purpura;
KM AI thyroid disease; atrophic gastritis; pernicious anaemia;
KM Chron's disease; colitis ulcerosa; Goodpasture syndrome; Iga nephropathy;
KM IgG glomerulonephritis; myasthenia gravis; partial lipodystrophy;
KM polymyositis; primary biliary cirrhosis; recurrent pericarditis;
KM progressive systemic sclerosis; recurrent pericarditis;
KM Sjogren's syndrome; relapsing polychondritis; arthritis; rheumatism;
KM sarcoidosis; SLE; splenic atrophy; diabetes; Wegener granulomatosis;
KM ulcerative colitis; vasculitis; vitiligo; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200222830-A2.
XX
XX 21-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-GB004120.
XX
XX 15-SEP-2000; 2000GB-00022768.
XX
XX 16-MAY-2001; 2001GB-00011995.
XX
XX (UYCA-) UNIV COLLEGE CARDIFF.

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XX
XX Aeschlimann DP, Grenard PM;
PI
XX
XX WPI; 2002-329954/36.
DR
XX
XX Nucleic acids which encode novel transglutaminase enzymes TG-Z and TG-Y
PT which can be used in diagnostic methods of autoimmune diseases.
XX
XX Disclosure; Page 26; 67pp; English.
PS
XX
XX The invention relates to nucleic acids which encode novel polypeptides
CC having transglutaminase activity. The compositions of polypeptides are
CC useful for transamidation reactions on peptides and polypeptides.
CC Detection of the polypeptides with transglutaminase activity are useful
CC in a diagnostic method in a subject or in cells derived from a subject
CC having an autoimmune disease. The method for detecting transglutaminase
CC proteins may be used to diagnose autoimmune diseases which include
CC Addison's disease, AI haemolytic anaemia, AI thrombocytopenic purpura, AI
CC thyroid diseases, atrophic gastritis, pernicious anaemia, Chron's
CC disease, colitis ulcerosa, Goodpasture syndrome, Iga nephropathy or IgG
CC glomerulonephritis, myasthenia gravis, partial lipodystrophy,
CC polymyositis, primary biliary cirrhosis, primary sclerosing cholangitis,
CC progressive systemic sclerosis, recurrent pericarditis, relapsing
CC polychondritis, rheumatoid arthritis, rheumatism, sarcoidosis, Sjogren's
CC syndrome, SLE, splenic atrophy, type I (insulin-dependent) diabetes
CC mellitus, Wegener granulomatosis, ulcerative colitis, vasculitis (both
CC systemic and cutaneous) and vitiligo. This sequence represents a primer
CC used in the study of transglutaminase genes in which DNA, amino acid
CC sequences and chromosomal locations of novel transglutaminases are
CC determined
XX
SQ Sequence 23 BP; 7 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4731 TGGAGCCAGCTGAGAGAGAG 4753
DB 1 TGAAGCTCAGCCGAGGTAGAG 23

RESULT 2887
ABZ95083
ID ABZ95083 standard; DNA; 23 BP.
XX
AC ABZ95083;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human adenosine A1 receptor antisense fragment no.946.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiaesthetic; hypotensive; immunosuppressive; cytotoxic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahabuddin S;

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XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.
XX PS Disclosure; SEQ ID NO 10325; 872bp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ublquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenovirus, reducing levels of adenovirus
CC receptor, producing bronchodilation, increasing levels of ublquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DY 5699 TTTGGCTTCTTCTTCTTCTTCTC 5721
DB 1 TTTTCTTCTTCTTCTTCTTCTTCTC 23
RESULT 2888
ABX93429
ID ABX93429 standard; DNA; 23 BP.
XX AC ABX93429;
XX DT 27-MAY-2003 (first entry)
XX DE Y chromosome specific sequence DY21, PCR primer Y21.
XX KW Transplanted material monitoring; urine sample analysis; kidney barrier;
KW nucleic acid detection; nucleic acid modification detection;
KW specific foetal nucleic acid; cancer; diabetes; arteriosclerosis;
KW obesity; autoimmune disease; chromosomal abnormality; genetic disease;
KW haemophilia; Alzheimer's disease; Huntington's disease; cystic fibrosis;
KW pathogen infection; genetic predisposition; cancer treatment monitoring;
KW foetus sex determination; foetal genetic disease; paternity;
KW amniocentesis; Y chromosome specific sequence; DY21; PCR; primer; ss.
OS Homo sapiens.
XX PN US6492144-B1.
XX PD 10-DEC-2002.
XX PF 03-AUG-2000; 2000US-00634732.
XX PR 30-MAY-1997; 97US-0058170P.
XX PR 03-JUN-1997; 97US-0048381P.
XX PR 29-MAY-1998; 98WO-US010965.
XX PR 04-FEB-2000; 2000US-00230704.

PR 03-JUL-2000; 2000US-00609162.
XX PA (DIAG-) DIAGEN CORP.
XX PT Unanaky SR, Lichenstein AV, Melkonyan HS;
XX DR WPI; 2003-340405/32.
XX PT Monitoring transplanted material in a patient, by analyzing urine samples
PT for nucleic acids from cell genomes of the transplanted material that are
PT different from nucleic acids of recipient and have crossed the kidney
PT barrier.
XX PS Example 3; Col 29; 32pp; English.
XX CC The invention describes a method of monitoring (M) transplanted material
CC in a patient, involving providing a urine sample suspected of containing
CC nucleic acid of the transplanted material, where the transplanted
CC material is located outside the urinary tract, and analysing the urine
CC sample for nucleic acids from the cell genome of the transplanted
CC material that are different from nucleic acids of the recipient and have
CC crossed the kidney barrier. (M) is useful for detecting the presence of
CC specific nucleic acids as well as nucleic acid modifications and
CC alterations, for detecting specific foetal nucleic acids that contain
CC modified nucleotides, for diagnosis of diseases such as cancer, diabetes,
CC arteriosclerosis, obesity and various autoimmune diseases or chromosomal
CC abnormality, genetic diseases (such as haemophilia, Alzheimer's disease,
CC Huntington's disease, cystic fibrosis) and pathogen infections, for
CC detecting genetic predisposition to various diseases, for monitoring
CC cancer treatment, for analysing specific nucleic acids in urine to track
CC the success of transplanted cells, tissue and organs, for determination
CC of foetus sex and the identification of foetal genetic diseases, such as
CC those inherited from the father for various purposes, including
CC determination of paternity, or for diagnosis of diseases caused by clonal
CC expansion of cells containing DNA modifications accompanied by death of
CC at least one subset of the cells bearing DNA modifications. (M) is a
CC safe, and simple non-invasive test, an excellent alternative to
CC amniocentesis, less expensive and more cost-effective. This sequence
CC represents a primer used to amplify fragments of the Y chromosome
CC specific DY21 sequence
XX SQ Sequence 23 BP; 2 A; 9 C; 2 G; 10 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DY 5692 CCACTGTTTGGCTTCTTCTTCTC 5714
DB 1 CCACTCTTTCATTCGCTTCTC 23
RESULT 2889
ABV74137
ID ABV74137 standard; DNA; 23 BP.
XX AC ABV74137;
XX DT 23-JAN-2003 (first entry)
XX DE Oligonucleotide used in cDNA library array.
XX KW G-protein coupled receptor; odorant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
OS Synthetic.
XX FT Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "5' polylinker"
FT misc_feature 16..21

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FT      /*tag= b
FT      /note= "each N represents A, C, G or T"
FT      22. .23
FT      misc_feature
FT      /*tag= C
FT      /note= "NN represents every possible dinucleotide
FT      combination"
XX      WO200277200-A2.
XX
XX      03-OCT-2002.
XX
XX      26-MAR-2002; 2002WO-US009559.
XX
XX      27-MAR-2001; 2001US-0279168P.
XX      31-JAN-2002; 2002US-035392P.
XX
XX      (INSC-) INSCENT INC.
XX
XX      Woods D, Dimltratos S;
XX      WPI; 2003-029930/02.
XX
XX      Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX      receptors, useful for isolating odorant binding proteins or pesticide
XX      alternatives, by analyzing sequences from a male- and female-specific
XX      nucleic acid library.
XX
XX      Disclosure; Fig 5; 83pp; English.
XX
XX      The present sequence is that of an oligonucleotide used in a method
XX      designed to rapidly array and normalize a complex cDNA library obtained
XX      from a target species. Clones are arrayed into multi-well plates. Each
XX      well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
XX      capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
XX      which allows an anchored oligonucleotide in each well to selectively
XX      hybridise only to those cDNA clones with a complementary 5' end. The
XX      unique 3' key sequences are designed to give a comprehensive level of
XX      degeneracy since they are diverse and numerous enough to ensure that
XX      every possible cDNA sequence can be bound by an individual, specific
XX      oligonucleotide in a single well. The cDNA library is heated to denature
XX      the clones into single stranded DNA, and an aliquot is added to every
XX      well. The anchored oligonucleotide serves as the 3' primer in PCR, and
XX      the common 5' region present in every cDNA clone serves as the 5' priming
XX      site. Denaturing and washing leave anchored cDNA in each well. The
XX      library is now arrayed and normalised. The method was used to identify
XX      and isolate clones encoding G-protein coupled receptors, especially
XX      odorant receptors, and active effectors involved in the olfactory
XX      pathway of invertebrates and vertebrates, e.g. odorant binding proteins,
XX      or other olfactory or neuronal proteins. The identified receptors and
XX      proteins are useful for identifying compounds that reduce a target
XX      animal's sensitivity to odours, for manufacturing compounds or devices
XX      that mask odours, or trapping invertebrates with odourants.
XX      Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
XX      with desirable effects on specific species, for the development of pest
XX      monitoring systems or non-toxic, species-specific pesticide alternatives,
XX      for controlling insect feeding and breeding behaviour, detecting the
XX      presence of small air-borne molecules, etc
XX
XX      Sequence 23 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 8 Other;
SQ
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      4464 TTTTTTTTTTTTTT 4478
XX      |||||
XX      1 TTTTTTTTTTTTTT 15
```

```
AC      ABZ21707;
XX
XX      27-FEB-2003 (first entry)
XX
XX      RBM15-MKL1 fusion protein PCR primer RBM15-1118F SEQ ID NO:23.
DE
XX
XX      Human; RBM15; RNA binding motif protein 15; megakaryoblastic leukemia 1;
XX      MKL1; fusion protein; acute megakaryoblastic leukaemia; AMKL; cytostatic;
XX      t(1;22) chromosomal rearrangement; gene therapy; chromosome 22q13;
XX      chromosome 1p13; PCR primer; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      WO200288309-A2.
XX
XX      07-NOV-2002.
XX
XX      23-APR-2002; 2002WO-US012797.
XX
XX      27-APR-2001; 2001US-0286910P.
XX
XX      (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX      (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
XX      Morris SW, Ma Z, Hitzler JK;
XX
XX      WPI; 2003-103455/09.
XX
XX      New RNA-binding motif protein-15 (RBM15)-megakaryoblastic leukemia-1
XX      (MKL1), MKL1-RBM15-S and MKL1-RBM15-S+AE fusion proteins, useful for
XX      identifying agents useful for treating patients with acute
XX      megakaryoblastic leukemia.
XX
XX      Example 1; Page 108; 109pp; English.
XX
XX      The present invention describes an RNA-binding motif protein-15 (RBM15)-
XX      megakaryoblastic leukemia-1 (MKL1) fusion protein, a MKL1-RBM15-S fusion
XX      protein, and a MKL1-RBM15-S+AE fusion protein associated with acute
XX      megakaryoblastic leukaemia (AMKL). Also described: (1) an antibody that
XX      specifically binds to the RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE
XX      fusion proteins; (2) a non-human transgenic animal that has been altered
XX      to express a gene encoding a RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE
XX      fusion protein; (3) identifying an agent capable of binding to a RBM15-
XX      MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE fusion protein; (4) detecting the
XX      t(1;22) chromosomal rearrangement associated with AMKL; and (5) screening
XX      for agents capable of (selectively) inhibiting the activity of a fusion
XX      protein arising from the t(1;22) chromosomal rearrangement associated
XX      with AMKL. The fusion proteins have cyrostatic activity and can be used
XX      in gene therapy. The RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE fusion
XX      proteins and nucleotide molecules are useful for designing and preparing
XX      agents that specifically inhibit the expression of the RBM15-MKL1 or MKL1-
XX      RBM15 genes in cells for therapeutic and other purposes. The transgenic
XX      animals are useful for identifying and testing carcinogenic or
XX      therapeutic compositions. The methods are also useful for detecting the
XX      t(1;22) chromosomal rearrangement associated with AMKL, or for
XX      identifying agents useful for treating patients with AMKL. The antibodies
XX      can be used to selectively kill cells expressing RBM15-MKL1, MKL1-RBM15-
XX      S, or MKL1-RBM15-S+AE fusion protein. RBM15 is located to chromosome
XX      1p13, and MKL1 is located to chromosome 22q13. The present sequence
XX      represents a PCR primer which is used in the generation of a fusion
XX      protein in an example from the present invention
XX
XX      Sequence 23 BP; 8 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 23;
XX      Best Local Similarity 78.3%; Pred. No. 2.2e+03;
XX      Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX      5953 CAAGCTTATCTAGAGAGACGA 5975
XX      |||||
XX      1 CATGCTTACTGTGAGACGACA 23
```

RESULT 2891

ID AB279789 standard; DNA; 23 BP.

XX AC AB279789;

DT 12-MAY-2003 (first entry)

XX Mycoplasma spp A39 16S rDNA region related PCR primer ampf.

XX Mycoplasma; 16S rDNA region; 16S rDNA; Mycoplasma spp A39; infection;

KM antibacterial; antibiotic; pleuromucalin; valnemulin; PCR primer; ss.

XX Mycoplasma sp.

OS Synthetic.

XX WO200306653-A1.

XX 23-JAN-2003.

PF 11-JUL-2001; 2001WO-GB003128.

PR 11-JUL-2000; 2000GB-00017073.

XX (WIND/) WINDSOR H.

PI Windsor H;

DR WPI; 2003-229483/22.

XX New isolated Mycoplasma spp A39 (UK NCTC number 11740), useful as a

PT control in assaying samples potentially containing Mycoplasma spp A39,

PT and for selecting agents against Mycoplasma infection.

PS Disclosure; Page 10; 40BP; English.

XX The present invention describes an isolated Mycoplasma spp A39, as

CC deposited at the UK National Collection of Type Cultures under number

CC 11740. Also described: (1) selecting an agent for treating a Mycoplasma

CC infection in a subject by assaying a sample from the subject for

CC Mycoplasma spp A39, and if the assay is positive, selecting as an agent

CC for treating the infection a pleuromucalin comprising valnemulin or its

CC analogue or derivative; (2) an oligonucleotide probe which is capable of

CC hybridising to a region of polynucleotide from Mycoplasma spp A39 and

CC substantially incapable of hybridising to a polynucleotide or

CC corresponding region from another Mycoplasma; (3) an oligonucleotide

CC primer pair for use in a PCR, capable of amplifying a target nucleic acid

CC sequence from mycoplasma spp A39 and incapable of amplifying a sequence

CC of the same length on the target sequence from another Mycoplasma; and

CC (4) assaying for Mycoplasma spp A39 by obtaining a sample potentially

CC containing Mycoplasma spp A39, determining the length of the 16S-23S

CC intergenic spacer sequence, and identifying Mycoplasma spp, where the

CC length of the 16S-23S intergenic spacer sequence is around 430 base pairs

CC (bp). The Mycoplasma spp A39 or its component can be used as a control in

Db 1 AAGCTAGTAAGCAATGTATT 23

RESULT 2892

ID AB259392/c

XX AB259392 standard; DNA; 23 BP.

XX AC AB259392;

DT 17-APR-2003 (first entry)

XX Mouse src-c probe SEQ ID NO:13.

XX Mouse; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;

KM antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;

XX antisense oligonucleotide; aberrant bone remodeling; breast cancer;

KM hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;

KM ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;

XX Kaposi's sarcoma; infection; inflammation; tumour formation; probe; ss.

XX Mus musculus.

XX WO200295053-A2.

XX 28-NOV-2002.

PF 16-MAY-2002; 2002WO-US015684.

PR 18-MAY-2001; 2001US-00860473.

XX (ISIS-) ISIS PHARM INC.

PI Bennett FC, Walt AT;

DR WPI; 2003-120806/11.

XX New antisense oligonucleotides targeted to nucleic acids encoding src-c,

PT useful for diagnosing, treating or preventing diseases associated with

PT the expression of src-c, e.g. cancer or inflammation, and in research

PT applications.

XX Example 13; Page 85; 137BP; English.

XX The present invention describes a compound (1) that is 8-50 nucleobases

CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,

CC coding region, intron region, exon region, stop codon, intron:exon

CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which

CC specifically hybridises with and inhibits the expression of src-c. (1)

CC have cytostatic, antiinflammatory, osteopathic and antibacterial

CC activities, and can be used in antisense therapy and in vaccines. The

CC antisense compounds (1) can be used for modulating the expression of src-

CC c and for treating diseases or conditions associated with expression of

CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,

CC particularly cancer, such as breast cancer, pancreatic cancer, lung

CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma

CC or Kaposi's sarcoma. (1) are also useful for diagnosing, therapeutics,

Db 30 GAGCTGCTGCAGGCT 44

Query Match 0.2%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 GAGCTGCTGCAGGCT 1

Query Match 0.2%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 GAGCTGCTGCAGGCT 1

ID ABV77669 standard; DNA; 24 BP.
 AC ABV77669;
 DT 03-FEB-2003 (first entry)
 XX
 DE Human zinc finger protein 9.79 PCR primer #1.
 XX
 KW Human; zinc finger protein 9.79; cancer; HIV infection; cytoskeletal;
 KM anti-HIV; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1343710-A.
 XX
 PD 10-APR-2002.
 XX
 PF 19-SEP-2000; 2000CN-00125246.
 XX
 PR 19-SEP-2000; 2000CN-00125246.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-548879/59.
 XX
 PT A novel human zinc finger protein 9.79 polypeptide, useful for treating
 PT several diseases e.g. cancer and HIV infection.
 XX
 PS Example 2; Page 16 (Disclosure); 31pp; Chinese.
 XX
 CC The present invention relates to human zinc finger protein 9.79 (see
 CC ABP59011). The zinc finger protein is useful for treating several
 CC diseases e.g. cancer and HIV infection. The present sequence is a PCR
 CC primer, which was used in an example from the invention
 XX
 SQ Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 24;
 Best Local Similarity 78.3%; Pred. No. 2.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4014 AATGAGAAAAAGAGAAAAACA 4036
 DB 24 AATGAAAAAAGAAAAAAGA 2
 RESULT 2896
 ABA98547/C
 ID ABA98547 standard; DNA; 24 BP.
 XX
 AC ABA98547;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Insulin-like growth factor binding protein 16.17 PCR primer #1.
 XX
 KM Insulin-like growth factor; binding protein; cytoskeletal; gene therapy;
 KM cancer; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200212301-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 11-JUN-2001; 2001WO-CN000947.
 XX
 PR 14-JUN-2000; 2000CN-00116509.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX

PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-172131/22.
 XX
 PT Insulin-like growth factor binding protein 16.17 and encoding
 PT polynucleotide, used in diagnosis and treatment of cancer.
 XX
 PS Example 2; Page 12; 37pp; Chinese.
 XX
 CC The present invention relates to insulin-like growth factor binding
 CC protein 16.17 (see AM48365). The binding protein and its coding sequence
 CC are useful for the diagnosis and treatment of cancer. The present
 CC sequence is a PCR primer, which was used in an example from the invention
 XX
 SQ Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 15; DB 1; Length 24;
 Best Local Similarity 78.3%; Pred. No. 2.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4011 TAAATGAGAAAAAGAGAAAA 4033
 DB 24 TCAAAAAAAGAAAAAGAAAA 2
 RESULT 2897
 ABV75621/C
 ID ABV75621 standard; DNA; 24 BP.
 XX
 AC ABV75621;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Argininoacyl tRNA synthetase 12.87 PCR primer 1.
 XX
 KM Argininoacyl tRNA synthetase 12.87; malignant tumour; inflammation;
 KM immunological disease; haemopathy; human immunodeficiency virus; HIV;
 KM enzyme; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN CN1347985-A.
 XX
 PD 08-MAY-2002.
 XX
 PF 11-OCT-2000; 2000CN-00125646.
 XX
 PR 11-OCT-2000; 2000CN-00125646.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-548992/59.
 XX
 PT New polypeptide argininoacyl tRNA synthetase 12.87 and encoding
 PT polynucleotide; useful for treating malignant tumors, inflammations,
 PT immunological diseases, hemopathy and human immunodeficiency virus
 PT infection.
 XX
 PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
 XX
 CC The invention relates to a novel polypeptide, argininoacyl tRNA
 CC synthetase 12.87, and the polynucleotide encoding it. The polypeptide is
 CC useful for treating various diseases, such as malignant tumours,
 CC inflammations, immunological diseases, haemopathy and human
 CC immunodeficiency virus (HIV) infection. The invention also discloses the
 CC antagonist resisting the polypeptide and its treatment effect, and
 CC application of the polynucleotide. The present sequence represents a PCR
 CC primer used to amplify the argininoacyl tRNA synthetase 12.87 gene of the
 CC invention
 XX
 SQ Sequence 24 BP; 6 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 2340 TCACACCGCGCTTCTGTGCTG 2362
23 TCACACCTGCTCTTCATGCTG 1

RESULT 2898
AAZ95163
ID AAZ95163 standard; DNA; 24 BP.
XX
AC AAZ95163;
XX
DT 05-JUN-2000 (first entry)
XX
DE Forward primer #9 used to sequence UGT2B7 polymorphic fragments.
XX
KM UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KM drug interaction; detect; human; single nucleotide polymorphism; primer;
KM ss.
XX
OS Synthetic.
XX
PM WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US016675.
XX
PR 28-JUL-1998; 98US-0094391P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions.
XX
PS Example 2; Page 22; 72pp; English.
XX
CC This sequence represents a primer used to sequence polymorphic fragments
CC of the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene. UDP-
CC glucuronosyltransferase (UGTs) are a family of enzymes that catalyze the
CC glucuronic acid conjugation of a wide range of endogenous and exogenous
CC substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms
CC in the liver. Alteration of the expression or function of UGTs may effect
CC drug metabolism. The invention relates to non-chromosomal nucleic acid
CC molecules, which comprise human UGT2B sequence polymorphisms (see
CC AA95051-295110). Probes which detect the UGT2B locus polymorphisms can
CC be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines
XX
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4023 AAAGAGAAACAAATGTTAT 4045

Db 1 AAAAAGAGAAACAAATGTTT 23

RESULT 2899
AAD46030
ID AAD46030 standard; DNA; 24 BP.
XX
AC AAD46030;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human UGT2B7 DNA sequencing forward primer #9.
XX
KM Human; UDP-glucuronosyl transferase; UGT; UGT2B7; toxicity; cancer;
KM therapy; epirubicin; cytosstatic; primer; ss.
XX
OS Homo sapiens.
XX
PM WO200259375-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002083.
XX
PR 26-JAN-2001; 2001US-0264534P.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Ratain MJ, Innocenti F, Das S, Iyer L, Sawyer M;
XX
DR WPI; 2002-691534/74.
XX
PT Determining the dose of a UGT2B7-glucuronidated drug for treating cancer,
PT comprises determining the level of UGT2B7 activity or expression in a
PT patient.
XX
PS Disclosure; Page 53; 160pp; English.
XX
CC The invention relates to an UDP-glucuronosyl transferase (UGT) enzyme,
CC UGT2B7. The invention also relates to compositions and methods for
CC optimizing UGT2B7 substrate dosings and for predicting UGT2B7 substrate
CC toxicity. The method is useful in determining the dose of a UGT2B7-
CC glucuronidated drug that may be used in treating cancer patients. It is
CC also useful in determining persons at risk for epirubicin toxicity, in
CC reducing or eliminating side effects associated with epirubicin
CC treatment, and in ways of increasing the efficacy of dosage regimens. The
CC present sequence is a primer used for sequencing human UGT2B7 DNA
XX
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4023 AAAGAGAAACAAATGTTAT 4045

Db 1 AAAAAGAGAAACAAATGTTT 23

RESULT 2900
ABK9281
ID ABK9281 standard; RNA; 24 BP.
XX
AC ABK9281;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #11.
DE Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.

XX US2002064771-A1.
PN
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABR9271-ABR9296 represent HCV NS5B replicase RNA synthesis
CC templates
XX
SQ Sequence 24 BP; 0 A; 18 C; 6 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 5774 GCCGCGCTGCTGCTGCTGCC 5796
DB 1 GCCCGCCGCCGCCGCCGCCGCC 23
XX
RESULT 2901
AB57119
ID AB57119 standard; DNA; 24 BP.
XX
AC AB57119;
XX
DT 30-JAN-2003 (first entry)
XX
DE Huma shear protein 8.91 RT-PCR primer #1.
XX
KW Human; ss; shear protein 8.91; tumour; haemopathy; HIV; PCR; primer;
KW human immunodeficiency virus infection; immunological disease;
KW inflammation; RT-PCR; reverse transcriptase PCR.
XX
OS Homo sapiens.
XX
PN CN1352095-A.

XX 05-JUN-2002.
XX
PD 06-NOV-2000; 2000CN-00127213.
XX
PF 06-NOV-2000; 2000CN-00127213.
XX
PR 06-NOV-2000; 2000CN-00127213.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-644454/70.
XX
PT New human shear protein 8.91 polypeptide for treating malignant tumors,
PT hemopathy, human immunodeficiency virus infection, immunological diseases
PT and various inflammations.
XX
PS Example 2; Page 16 (disclosure); 32pp; Chinese.
XX
CC The present invention discloses a new kind of polypeptide, human shear
CC protein 8.91, polynucleotides encoding the polypeptide and producing the
CC polypeptide by recombinant DNA technology. The present invention also
CC discloses applying the polypeptide in treating various diseases, such as
CC malignant tumors, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological diseases and various inflammations. The present
CC invention also discloses the antagonist resisting the polypeptide and its
CC treatment effect. The present invention also discloses application of the
CC polynucleotides encoding human shear protein 8.91. The present sequence
CC is a reverse transcriptase (RT)-PCR primer used to isolate nucleic acids
CC encoding human shear protein 8.91
XX
SQ Sequence 24 BP; 3 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 4459 TGGACCTTTTTTTTTTTTTTTT 4481
DB 2 TGTAAATTTTCTTCTTCTTT 24
XX
RESULT 2902
AA84260/c
ID AA84260 standard; DNA; 25 BP.
XX
AC AA84260;
XX
DT 08-SEP-1999 (first entry)
XX
DE PCR primer for human Nck associated protein 1 coding sequence.
XX
KW Nck associated protein 1; Nck1; human; apoptosis; Alzheimer's disease;
KW therapy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9931239-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-JP005646.
XX
PR 15-DEC-1997; 97JP-00363183.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (SAKA/) SAKAKI Y.
XX
PI Sakaki Y;
XX
DR WPI; 1999-395181/33.
XX

Db 1 GTGTTT TTTTCTCTCTTT 23

```
RESULT 2905
AA173048/c
ID AA173048 standard; DNA; 26 BP.
XX
XX
AC AA173048;
XX
XX
DT 24-OCT-2002 (first entry)
XX
XX
DE Scaffold oligonucleotide.
XX
XX
KM Molecular scaffold; fluorophore; fluorescence; energy transfer;
KM emission wavelength; excitation wavelength; multiple; single nucleotide;
KM polymorphism; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200222883-A1.
XX
XX
PD 21-MAR-2002.
XX
XX
PF 11-SEP-2001; 2001WO-US028967.
XX
XX
PR 11-SEP-2000; 2000US-00658077.
PR 31-JUL-2001; 2001US-0309156P.
XX
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX
PI Ju J, Li Z, Tong A, Russo JJ;
XX
XX
DR WPI; 2002-575156/61.
XX
XX
PT Composition of matter useful for multi-component analyses, comprises
PT multiple fluorophores bound to molecular scaffold at preset positions to
PT permit fluorescence energy transfer between two fluorophores.
XX
XX
PS Disclosure; Page 43; 113pp; English.
XX
XX
CC This sequence represents a molecular scaffold which may be used in a
CC composition of matter comprising multiple fluorophores. The fluorophores
CC are bound to the molecular scaffold at separate predetermined positions,
CC to permit fluorescence energy transfer between two fluorophores. The
CC fluorophores are characterized by maximum emission wavelength of one
CC being greater than the minimum excitation wavelength of the other. The
CC composition is useful for determining whether a preselected nucleotide
CC residue is present at a predetermined position within a nucleic acid. It
CC is also useful in multicomponent analysis including multiplex biological
CC analysis, and identifying multiple single nucleotide polymorphisms. The
CC presence of a number of given nucleotide residues is determined
CC simultaneously by the composition of the invention
XX
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 15; DB 1; Length 26;
Best Local Similarity 78.3%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4017 GAGAAAAAGAGAGAAAAACAAA 4039
Db 26 GAAAAAAAAAAAAAAAAAAAAA 4
RESULT 2906
AAS20672/c
ID AAS20672 standard; DNA; 26 BP.
XX
XX
AC AAS20672;
XX
XX
DT 09-APR-2002 (first entry)
XX
XX
DE Human zalphail ligand sequencing primer ZC7764b.
XX
XX
KM Cytokine; zalphail ligand; zalphail receptor; NK cell progenitor;
```

```
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KM immunostimulant; cytostatic; human; sequencing primer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN US6307024-B1.
XX
XX
PD 23-OCT-2001.
XX
XX
PF 09-MAR-2000; 2000US-00522217.
XX
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
XX
PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD,
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX
DR WPI; 2002-040208/05.
XX
XX
PT New zalphail ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX
PS Example 7; Col 139; 105pp; English.
XX
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalphail ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphail receptor and the polynucleotide
CC encoding it. The zalphail ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-15M antibodies. The
CC zalphail ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphail ligand epitopes. The zalphail ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphail ligand gene,
CC and in gene therapy. Zalphail ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence cDNA clones in the isolation of
CC human zalphail ligand
XX
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 15; DB 1; Length 26;
Best Local Similarity 78.3%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4017 GAGAAAAAGAGAGAAAAACAAA 4039
Db 26 GAAAAAAAAAAAAAAAAAAAAA 4
RESULT 2907
ABX93461/c
ID ABX93461 standard; DNA; 26 BP.
XX
XX
AC ABX93461;
XX
XX
DT 27-MAY-2003 (first entry)
XX
XX
DE L5147-specific polynucleotide sequencing related universal primer #1.
XX
XX
KM L5147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KM primer; EST clone; expressed sequence tag clone.
XX
XX
OS Synthetic.
```

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XX US2002188114-A1.
XX
XX 12-DEC-2002.
XX
XX 05-JUN-1998; 98US-00092296.
XX
XX 05-JUN-1997; 97US-0048810P.
XX
XX (BIL/) BILINGEL P.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (KLAS/) KLAAS M R.
XX (RUS/) RUSSELL J C.
XX (STRO/) STROUPE S.
XX
XX Billengel P, Cohen M, Colpitts TL, Friedman PN, Klaas MR;
XX Russell JC, Stroupe S;
XX WPI; 2003-341045/32.
XX
XX New LS147 polypeptide, useful for preparing a composition for treating
XX e.g., lung cancer.
XX
XX Example 2; Page 39; 47pp; English.
XX
XX The invention describes a purified polypeptide or its fragment derived
XX from the LS147 gene capable of selectively hybridising to the nucleic
XX acid of the gene and has at least 50% identity with the polynucleotide.
XX The LS147 polypeptide is useful for preparing a composition for treating
XX cancer, e.g. lung cancer using gene therapy. This sequence represents a
XX universal primer used to sequence LS147 expressed sequence tag (EST) -
XX clones
XX
XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 15; DB 1; Length 26;
XX Best Local Similarity 78.3%; Pred. No. 2.4e+03;
XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 4017 GAGGAAAAAGAGGAAAAACAAA 4039
XX |||||
XX 26 GAAAAA
XX
XX RESULT 2908
XX ABX12469/c
XX ID ABX12469 standard; DNA; 27 BP.
XX
XX ABX12469;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dt26v.
XX
XX Coxsackie B virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; PCR; primer; ss.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-1B003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX

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PI Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Example 5; Page 44; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a primer used to determine the
XX genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain
XX VD2921
XX
XX Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
XX
XX
XX Query Match 0.2%; Score 15; DB 1; Length 27;
XX Best Local Similarity 70.4%; Pred. No. 2.5e+03;
XX Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
XX 4011 TAAATGAGAAAAAGAGGAAAAACAA 4037
XX :|||
XX 27 BAAAAA
XX
XX RESULT 2909
XX ABN83378
XX ID ABN83378 standard; DNA; 29 BP.
XX
XX ABN83378;
XX
XX 15-AUG-2002 (first entry)
XX
XX Mononucleotide repeat locus BAT25 probe #1.
XX
XX Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 29 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "labelled with Fluorescein"
XX
XX EP1207210-A1.
XX
XX 22-MAY-2002.
XX
XX 13-NOV-2001; 2001EP-00126930.
XX
XX 15-NOV-2000; 2000EP-00124897.
XX
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Dietmaier W;
XX
XX WPI; 2002-437469/47.
XX
XX Analyzing repeat sequences in DNA using a probe which hybridizes to
XX adjacent repetitive and non-repetitive regions and determining hybrid
XX melting point is useful to detect microsatellite instability such as in
XX

```

PT hereditary cancer.
 XX
 PS Claim 16; Page 7; 19pp; English.
 XX
 CC The present invention relates to a method for analyzing a target nucleic
 CC acid consisting of repetitive and non-repetitive sequences. The method
 CC comprising hybridizing a polynucleotide probe comprising a segment
 CC complementary to a non-repetitive region and a segment complementary to
 CC an adjacent repetitive region, where the second segment consists of a
 CC defined number of repeats, and determining the melting point temperature
 CC of the hybrid. The method is used to analyse microsatellites, especially
 CC microsatellite instability, particularly as a means for detecting
 CC hereditary tumors. Alternatively, the method is used to identify an
 CC individual in a population. The present sequence is a probe for
 CC mononucleotide repeat locus BAT5, and was used to illustrate the
 CC invention
 CC
 SQ Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 29;
 Best Local Similarity 78.3%; Pred. NO. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4018 AGAAAAAGAGAGAAACAAAT 4040
 Db 5 AAAAAAAAAAAAAAAAAAAAAAT 27
 RESULT 2910
 AAS63441
 ID AAS63441 standard; DNA; 30 BP.
 XX
 AC AAS63441;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Oligonucleotide-nanoparticle probe #63.
 XX
 KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
 KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200173123-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2001; 2001WO-US010071.
 XX
 PR 28-MAR-2000; 2000US-0192699P.
 PR 26-APR-2000; 2000US-0200161P.
 PR 26-JUN-2000; 2000US-00603830.
 PR 26-JUN-2000; 2000US-0213906P.
 PR 08-DEC-2000; 2000US-0254392P.
 PR 11-DEC-2000; 2000US-0255235P.
 PR 12-JAN-2001; 2001US-00760500.
 PR 28-MAR-2001; 2001US-00820279.
 XX
 PA (NANO-) NANOSPHERE INC.
 XX
 PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
 PI Taton TA, Park S, Li Z;
 XX
 DR WPI; 2001-656926/75.
 XX
 PT Detecting and separating nucleic acid, useful e.g. for diagnosis,
 PT comprises reaction with nanoparticles that carry oligonucleotides
 PT complementary to parts of the target.
 XX
 PS Example 24; Fig 44; 404pp; English.
 XX
 CC The invention relates to a method for detection of nucleic acid (1)

CC having at least 2 portions, comprising treatment with nanoparticles that
 CC carry oligonucleotides complementary to at least 2 parts of (1), where
 CC detectable change caused by hybridisation of the oligonucleotide to (1)
 CC is observed. The method is used to detect (or to separate) specific (1),
 CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
 CC analysis etc., and generally to detect analytes other than (1). The
 CC oligonucleotide-derivatised nanoparticles are also useful for preparing
 CC nanostructures useful, for example, as biochips, biofilters, mechanical
 CC devices, separation membranes, chemical sensors, in computers, and for
 CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
 CC produced, allowing their direct use (as probes) in polymerase chain
 CC reaction, i.e. they survive multiple heating/cooling cycles so do not
 CC need to be added after amplification. (1) are detected by simple colour
 CC change, without the need for special equipment, making possible rapid
 CC field testing for e.g. pathogens. AAS63374-AAS63448 represent
 CC oligonucleotide-nanoparticle probes, and related sequences, used in the
 CC method of the invention
 CC
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 15; DB 1; Length 30;
 Best Local Similarity 78.3%; Pred. NO. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3278 AAGAGAAAAATGAACACGACC 3300
 Db 5 AAAAAAAAAAAAAAAAAAGCAGACC 27
 RESULT 2911
 AAS10385
 ID AAS10385 standard; DNA; 30 BP.
 XX
 AC AAS10385;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Oligonucleotide-cyclic disulphide linker, c1 #2.
 XX
 KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
 KW DNA isolation; genetic disease; bacterial disease; viral disease;
 KW forensic science; paternity testing; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151665-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001190.
 XX
 PR 13-JAN-2000; 2000US-0176409P.
 PR 26-APR-2000; 2000US-0200161P.
 PR 26-JUN-2000; 2000US-00603830.
 PR 12-JAN-2001; 2001US-00760500.
 XX
 PA (NANO-) NANOSPHERE INC.
 XX
 PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
 PI Taton TA, Li Z;
 XX
 DR WPI; 2001-451868/48.
 XX
 PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
 PT viral diseases, by contacting the nucleic acid with oligonucleotides
 PT attached to nanoparticles and having sequences complementary a portion of
 PT the nucleic acid.

XX Example 24; Fig 44; 323pp; English.

XX The sequence represents a cyclic disulphide linked oligonucleotide which

CC may be coupled with colloidal gold particles (nanoparticles) and used to

CC demonstrate the method of the invention. The invention relates to

CC isolating or detecting a nucleic acid of interest, in a mixture of

CC nucleic acids, by binding it to 2 or more complementary nucleotides which

CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.

CC colloidal gold) are used to both isolate and detect (e.g. by linking the

CC particle to a fluorescent probe) the resultant complex. The methods are

CC useful for detecting nucleic acids, natural or synthetic, and modified or

CC unmodified. The methods may also be applied in the diagnosis of genetic,

CC bacterial and viral diseases, in forensics, in DNA sequencing, for

CC paternity testing, for cell line authentication, and for monitoring gene

CC therapy. The methods are further useful in research and analytical

CC laboratories in DNA sequencing, in the field to detect the presence of

CC specific pathogens, for quick identification of an infection to assist in

CC drug prescription, and in homes and health centres for inexpensive first-

CC line screening. The methods, which are based on observing colour change

CC with the naked eye, are cheap, fast, simple, robust (reagents are

CC stable), do not require specialised or expensive equipment, and little or

CC no instrumentation is required

XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 15; DB 1; Length 30;

Best Local Similarity 78.3%; Pred. No. 2.7e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAAAATGAAACGAGCC 3300

5 AAAAAAAAAAAAAAAAAAGCAGACC 27

RESULT 2912

ABK65048

ID ABK65048 standard; DNA; 30 BP.

XX

AC ABK65048;

XX

DT 02-JUL-2002 (first entry)

XX

DE Nanoparticle-oligonucleotide #68.

XX

KM Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;

KW ss.

XX

OS Synthetic.

XX

PN WO200218643-A2.

XX

PD 07-MAR-2002.

XX

PF 10-AUG-2001; 2001WO-US025237.

XX

PR 11-AUG-2000; 2000US-0224631P.

PR 08-DEC-2000; 2000US-0254392P.

PR 11-DEC-2000; 2000US-0254392P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

XX

PA (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;

PI Taton TA, Garimella V, Li Z, Park S;

XX

DR WPI; 2002-256024/30.

XX

PT Detecting nucleic acid, useful for diagnosis of genetic, viral or

PT bacterial disease, comprises hybridizing nanoparticles with attached

PT oligonucleotides to nucleic acid and detecting change brought about by

PT hybridization.

XX Example 24; Fig 44; 412pp; English.

XX The invention relates to a method of detecting a nucleic acid (NA) having

CC at least 2 portions comprising: (a) providing nanoparticles (NP) with

CC attached oligonucleotides (OGN), where OGN has a sequence complementary

CC to the sequence of NA; (b) contacting NA and NP under conditions

CC effective to allow hybridisation of OGN with NA; and (c) observing a

CC detectable change brought about by hybridisation of OGN with NA. The

CC method is useful for detecting a nucleic acid, separating a selected

CC nucleic acid from others and methods of nanofabrication. Detecting

CC analytes such as nucleic acids and proteins are useful for the diagnosis

CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use

CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.

CC In particular assays using OGN-NP conjugates prepared using linkers

CC comprising a steroid residue attached to a cyclic disulphide have been

CC found to be approximately 10 times more sensitive than assays employing

CC conjugates prepared using alkanethiols or acyclic disulphides as the

CC linker. The OGN-NP conjugates are stable allowing them to be used

CC directly in PCR solutions. Therefore conjugates added as probes to a DNA

CC target to be PCR amplified can be carried through the 30 or 40 heating

CC cooling cycles of the PCR and are still able to detect the amplicons

CC without opening the tubes and causing contamination. ABK64981-ABK65055

CC represent nanoparticle-oligonucleotides of the invention

XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 15; DB 1; Length 30;

Best Local Similarity 78.3%; Pred. No. 2.7e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAAAATGAAACGAGCC 3300

5 AAAAAAAAAAAAAAAAAAGCAGACC 27

RESULT 2913

ABS64686

ID ABS64686 standard; DNA; 30 BP.

XX

AC ABS64686;

XX

DT 15-NOV-2002 (first entry)

XX

DE Nucleic acid detection method associated polynucleotide #68.

XX

KM Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

KW nanoparticle; viral RNA detection; bacterial DNA detection;

KW fungal DNA detection; nanoprobe conjugate; ss.

XX

OS Synthetic.

XX

PN WO200246472-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-US046418.

XX

PR 08-DEC-2000; 2000US-0254392P.

PR 08-DEC-2000; 2000US-0254418P.

PR 11-DEC-2000; 2000US-0255235P.

PR 11-DEC-2000; 2000US-0255236P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

PR 09-APR-2001; 2001US-0282640P.

PR 10-AUG-2001; 2001US-00927777.

XX

PA (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;

PI Taton TA, Garimella V, Li Z, Park S;

XX

DR WPI; 2002-608256/65.

XX Detecting nucleic acid having two portions, by providing nanoparticles
 PT having oligonucleotides attached to it, contacting nucleic acid and
 PT nanoparticles to allow hybridization, and observing detectable change.
 XX
 XX
 XX Example 24; Fig 44; 442pp; English.

CC The invention describes a method of detecting (M1) a nucleic acid having
 CC two portions, involving providing nanoparticles having oligonucleotides
 CC attached to it, which has a sequence complementary to sequence of two
 CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
 CC allow hybridization of oligonucleotides with two or more portions of
 CC nucleic acid, and observing a detectable change brought about by
 CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide
 CC conjugates (II) and the aggregate probe are useful for detecting two or
 CC more nucleic acids (from a biological source) having at least two
 CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
 CC with a disease, synthetic, or structurally-modified natural or synthetic
 CC RNA or DNA, or a product of a polymerase chain reaction amplification.
 CC (II) is useful for preparing a nanoprobe conjugate for detecting an
 CC analyte, and for detecting a nucleic acid bound to an electrode surface.
 CC (I) and (II) are useful for fabrication, and for separating a selected
 CC nucleic acid having two portions from other nucleic acids. (I), (II) and
 CC the aggregate probe are useful for detecting an analyte (especially
 CC polyvalent analyte) in a sample. This sequence represents a
 CC polynucleotide used to demonstrate the method of the invention
 CC
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 30;
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAATGAAACCGAGCC 3300
 |||||
 Db 5 AAAAAAAAAAAAAAGCAGACC 27

RESULT 2914

AA61658
 ID AAL61658 standard; DNA; 30 BP.

AC AAL61658;

DT 22-SEP-2003 (first entry)

DE Oligonucleotide #19 used in the nucleic acid detection method.

XX Nucleic acid detection; fabrication; ss.

XX Unidentified.

XX WO2003035829-A2.

XX 01-MAY-2003.

XX 08-OCT-2002; 2002WO-US032088.

XX 09-OCT-2001; 2001US-0327864P.

XX 07-DEC-2001; 2001US-00008978.

XX (NANO-) NANOSPHERE INC.

XX Park S, Taton TA, Mirkin CA;

XX WPI; 2003-430409/40.

XX Detecting nucleic acid having two portions, by providing nanoparticles
 PT having oligonucleotides attached to it, contacting nucleic acid and
 PT nanoparticles to allow hybridization, and observing detectable change.

XX Example 24; Fig 44; 467pp; English.

CC The invention relates to a method of detecting a nucleic acid having two
 CC portions. The method involves providing nanoparticles having
 CC oligonucleotides attached to it which has a sequence complementary to
 CC sequence of two portions of nucleic acid, contacting nucleic acid and
 CC nanoparticles to allow hybridization of oligonucleotides with two or more
 CC portions of nucleic acid and observing a detectable change brought about
 CC by hybridization. The method and aggregate probes are useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic or structurally modified natural or
 CC synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. The invention is useful for preparing a nanoprobe
 CC conjugate for detecting an analyte and for detecting a nucleic acid bound
 CC to an electrode surface. It is also useful for fabrication and for
 CC separating a selected nucleic acid having two portions from other nucleic
 CC acids. The present sequence is an oligo used to illustrate the method of
 CC the invention
 CC
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 30;
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAATGAAACCGAGCC 3300
 |||||
 Db 5 AAAAAAAAAAAAAAGCAGACC 27

RESULT 2915

AAQ30395
 ID AAQ30395 standard; DNA; 18 BP.

AC AAQ30395;

DT 25-MAR-2003 (revised)

DT 07-DEC-1992 (first entry)

XX Oligomer LAP312 for forming triplex with HUMINT02 target duplex.

XX Human leukocyte adhesion protein; P150.95 alpha subunit gene;

XX herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis;

XX inflammation; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 2

FT /*tag= a

FT /mod_base= OTHER

FT /*tag= N6 methyl-8-oxo 2' deoxyadenine"

FT 3

FT /*tag= b

FT /mod_base= OTHER

FT /*tag= N6 methyl-8-oxo 2' deoxyadenine"

FT 9..10

FT /*tag= 1

FT /note= "o-xyloso dimer synthon linkage"

FT 9

FT /*tag= c

FT /mod_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT 10..18

FT /*tag= h

FT /label= inverted_polarity_region

FT /note= "see comments"

FT 10

FT /*tag= d

FT /mod_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT 13

FT /*tag= e

FT /mod_base= OTHER

```

FT modified_base /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 15 /tag= f
FT /mod_base= OTHER
FT modified_base /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 17 /*tag= g
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US008811.
XX
XX 23-NOV-1990; 90US-00617907.
XX 18-JAN-1991; 91US-00643382.
XX 08-APR-1991; 91US-00683420.
XX 17-APR-1991; 91US-00686544.
XX 17-APR-1991; 91US-00686546.
XX 17-APR-1991; 91US-00686547.
XX 27-SEP-1991; 91US-00766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with G-C
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX herpes malignancy and inflammation.
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at physiological
XX pH with a purine rich target sequence by coupling into the major groove
XX of the duplex. The specific target sequence of this oligomer is the human
XX leukocyte adhesion protein p150, 95 alpha subunit gene (HUMINT02)
XX beginning at nucleotide 677 contg. a purine rich sequence concd. on one
XX strand of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterized by specific DNA duplex
XX targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and
XX inflammation. The triple helices form under mild conditions thus assays
XX may be carried out without subjecting the test specimen to harsh
XX conditions. The oligomer contains an inverted polarity region formed from
XX an o-xylosa dimer synthon. The linking gp. is o-xylosa (nucleotides have
XX the 3' positions of xylose sugars linked via the o-xylosa ring). Two
XX nucleotides are coupled through a xylose residue to form the dimer
XX synthon. This additional modifications may render the oligomer stable to
XX nuclease activity. The oligomer is able to inhibit gene expression, as
XX verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 7 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 6682 TTAATTTTAAATTAATAT 6699
XX | | | | | | | | | |
XX 1 TAAATTTTAAATTAATAT 18
XX
XX RESULT 2916
XX AAQ38707 standard; RNA; 18 BP.
XX
XX AAQ38707;
XX
XX 25-MAR-2003 (revised)

```

```

DT 15-JUL-1993 (first entry)
XX
XX First chimeric primer for adding poly A tails.
XX
XX oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;
XX treatment; diagnosis; testing; assay; Candida; papillomavirus;
XX cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;
XX liver disease; human immunodeficiency virus; herpes simplex virus; HSV;
XX human immunodeficiency virus; HIV; AIDS; Influenza virus;
XX genetic disease; genetic abnormalities.
XX
XX Synthetic.
XX
XX WO9305182-A1.
XX
XX 18-MAR-1993.
XX
XX 04-SEP-1992; 92WO-US007489.
XX
XX 05-SEP-1991; 91US-00755485.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bruce TW;
XX
XX WPI; 1993-101001/12.
XX
XX Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule
XX - for use in therapeutics, diagnostics and research reagents.
XX
XX Disclosure; Page 27; 61pp; English.
XX
XX This sequence was used as a PCR primer in order to add a polyA tail to
XX the 3' end of the highest specific activity selected oligonucleotide in
XX order to form a first strand. The primer is comprised of a 5' known
XX sequence and a 3' polynucleotide portion corresp. to the polynucleotide
XX tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4460 GGAAGCTTTTATTTTATTTT 4477
XX | | | | | | | | | |
XX 1 GGAAGCTTTTATTTTATTTT 18
XX
XX RESULT 2917
XX AAQ92177
XX ID AAQ92177 standard; DNA; 18 BP.
XX
XX AAQ92177;
XX
XX 12-JAN-1996 (first entry)
XX
XX p53 detection probe, (codon 273 CGT to TGT).
XX
XX Primer; polymerase chain reaction; amplify; mutant; K-ras; PCR;
XX flanking region; amplification; probe; detection; sputum; diagnosis;
XX benign; malignant; neoplasm; lung; lung cancer; head; neck; ss.
XX
XX Synthetic.
XX
XX WO9513397-A1.
XX
XX 18-MAY-1995.
XX
XX 10-NOV-1994; 94WO-US012947.
XX
XX 12-NOV-1993; 93US-00152313.
XX

```


PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MED.
 XX
 PI Sidrensky D;
 XX
 DR WPI; 1995-194114/25.
 XX
 PT Detecting target nucleic acid in mammalian sputum - particularly for
 PT diagnosis of lung neoplasia involving mutation(s) in the K-ras oncogene
 PT or p53 tumour suppressor.
 XX
 PS Example 1; Page 34; 122pp; English.
 XX
 CC The sequences given in AA092112-211 are probes which were used in the
 CC detection of a mutant p53 gene sequence. The DNA to be detected is
 CC amplified using PCR and then these probes which are pref. labeled using
 CC 32-P gamma-ATP are used to detect the mutant sequences. The primers and
 CC probes given in AA092098-219 are used in the method of the invention for
 CC detecting mammalian target DNA in sputum samples. Analysis of the target
 CC DNA is used to diagnose benign or malignant neoplasms of the lung. It is
 CC also useful for screening people at high risk or for monitoring progress
 CC of treatment of lung neoplasms. The method is based on the discovery that
 CC mutant target DNA associated with lung cancer is present at detectable
 CC levels in sputum. Cells shed into sputum from head and neck cancers may
 CC also be detected
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7309 TTGAGATTGTTGTTGNG 7326
 DB 1 TTGAGCTGTGTGTTGNG 18
 XX
 RESULT 2918
 AA083415
 ID AA083415 standard; DNA; 18 BP.
 XX
 AC AA083415;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE c-fos antisense oligonucleotide.
 XX
 KM c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
 KM phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO9502051-A2.
 XX
 PD 19-JAN-1995.
 XX
 PF 06-JUL-1994; 94WO-EP002218.
 XX
 PR 10-JUL-1993; 93EP-00111059.
 XX
 PA (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1995-066896/09.
 XX
 PT Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
 PT treating neuronal injury, degeneration, cell death and/or neoplasms.
 XX
 XX Claim 2; Page 61; 86pp; English.
 XX
 CC Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
 CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a

CC causal role in neuronal injury, degeneration, cell death and/ or
 CC neoplasms, can be used to prevent and treat such conditions. c-jun
 CC antisense sequences are described in AA083267-321 and AA083440-43; jun-B
 CC antisense sequences are described in AA083332-63 and AA083444-45; and c-
 CC fos antisense sequences are described in AA083364-439 and AA083446- 51.
 CC Preferably the antisense sequences are phosphorothioate oligonucleotides
 CC since these are not destroyed as fast by endogenous factors as naturally
 CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 0 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4299 CATCTTTTCCCTCCCT 4316
 DB 1 CATCTTATTCCTTCCCT 18
 XX
 RESULT 2919
 AAT96107
 ID AAT96107 standard; DNA; 18 BP.
 XX
 AC AAT96107;
 XX
 DT 31-MAR-1998 (first entry)
 XX
 DE First chimeric primer.
 XX
 KM Determination; oligonucleotide; specific activity; therapy;
 KM target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;
 KM chimeric; primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5686242-A.
 XX
 PD 11-NOV-1997.
 XX
 PF 27-OCT-1994; 94US-00330000.
 XX
 PR 05-SEP-1991; 91US-00755485.
 PR 04-SEP-1992; 92WO-US007489.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Lima WF, Bruice TW;
 XX
 DR WPI; 1997-558135/51.
 XX
 PT Determination of oligo-nucleotide with specific activity for target bio-
 PT molecule - using set of randomised oligo-nucleotide(s).
 XX
 PS Disclosure; Col 27-28; 22pp; English.
 XX
 CC The present sequence was used in the development of a method of
 CC determining an oligonucleotide having specific activity for a target
 CC biomolecule. The method comprises assaying a set of randomised
 CC oligonucleotides for activity against a target biomolecule, separating
 CC active from inactive oligonucleotides and recovering, amplifying and
 CC determining the nucleic acid sequence of the active oligonucleotides. The
 CC oligonucleotides can be used for therapeutic, diagnostic and research
 CC purposes
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4460 GGACTTTTCTTTTCTTTT 4477
 ||| |||||

Db 1 GGATGTTTTTTTTTTTT 18

RESULT 2920
AAK63294/c
ID AAK63294 standard; RNA; 18 BP.

XX
AC AAK63294;

XX
DT 16-JUL-1999 (first entry)

XX
DE Delta-9 desaturase haltrin ribozyme substrate SEQ ID NO:1169.

XX
KM Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;
KM granule bound starch synthase; hammerhead ribozyme; haltrin ribozyme;
KM modulation; gene expression; transgenic plant; cleavage; canola plant;
KM caffeine synthesis; coffee plant; nicotine production; tobacco;
KM fruit ripening; flower pigmentation; lignin production; ss.

XX
OS Zea mays.

XX
PN WO9710328-A2.

XX
PD 20-MAR-1997.

XX
PF 12-JUL-1996; 96WO-US011689.

XX
PR 13-JUL-1995; 95US-0001135P.

XX
PA (RIBO-) RIBOZYME PHARM INC.
(DOMC) DOWELANCO.

XX
PI Zwack MG, Edington BE, Mcswigen JA, Merlo PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;

XX
DR WPI; 1997-202224/18.

XX
PT Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.

XX
PS Claim 40; Page 93; 155pp; English.

XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene.
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant

XX
SQ Sequence 18 BP; 2 A; 10 C; 6 G; 0 T; 0 U; 0 Other;

XX
Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 65 GCTGCGGCGGCGGCGGCG 82
Db 18 GCTGCTGCGGCGGCGGCG 1

RESULT 2921

AAK8679
ID AAK8679 standard; DNA; 18 BP.

XX
AC AAK8679;

XX
DT 10-SEP-1999 (first entry)

XX
DE Human chromosome 18q YAC clone primer.

XX
KM Human chromosome 18q; mood disorder; polymorphic marker; detection;
KM identification; trinucleotide repeat expansion; schizophrenia;
KM anxiety disorder; adjustment disorder; personality disorder;
KM nucleotide triplet repeat; ss.

XX
OS Synthetic.

XX
OS Homo sapiens.

XX
PN WO932643-A2.

XX
PD 01-JUL-1999.

XX
PF 17-DEC-1998; 98WO-EF008543.

XX
PR 18-DEC-1997; 97GB-00026804.

XX
PA (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOC.

XX
PI Van Broeckhoven C, Raeymaekers P, Del-Favero J;

XX
DR WPI; 1999-418934/35.

XX
PT Detecting nucleotide triplet repeats in human chromosome 18q.

XX
PS Disclosure; Page 56; 87pp; English.

XX
CC The present invention describes detecting nucleotide triplet repeats in a
CC region of human chromosome 18q disposed between polymorphic markers
CC D18S68 and D18S979 to identify a human gene associated with a mood
CC disorder or related disorder. AAX88542 to AAX88705 represents human
CC chromosome 18q YAC clones and primers corresponding to them, used in the
CC exemplification of the present invention. YAC clones comprising a portion
CC of the region of human chromosome 18q between markers D18S68 and D18S979
CC are used to identify at least one human gene associated with a mood
CC disorder or related disorder. The mood disorder or related disorder, is
CC chosen from the Diagnostic and Statistical Manual of Mental Disorders,
CC version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4,
CC 311, 301.13, 295.70), schizophrenia and related disorders (295, 297.1,
CC 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3),
CC adjustment disorders (309.XX) and personality disorders (codes 301.XX).
CC Probes derived from genes associated with the mood disorder or related
CC disorder can be used to detect pathological mutations or genetic
CC variations in patients. The methods, probes and antibodies can be used to
CC determine the susceptibility of an individual to a mood disorder or
CC related disorder. The nucleic acids and proteins of the human gene can be
CC used to treat mood disorders and related disorders

XX
SQ Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

XX
Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5795 CTTGCTGCTGCTGCTGTC 5812
Db 1 CTTGCTGCTGCTGCTGTC 18

RESULT 2922

AAZ35875
ID AAZ35875 standard; DNA; 18 BP.

XX
AC AAZ35875;

XX
DT 03-FEB-2000 (first entry)

XX
DE Human sentrin phosphorothioate antisense oligonucleotide SEQ ID NO:17.

XX
KM Human; sentrin; antisense oligonucleotide; phosphorothioate; inhibition;
KM modulation; expression; diagnosis; ss.

```

XX XX Synthetic.
OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX US5985664-A.
XX
XX 16-NOV-1999.
XX
XX 17-DEC-1998; 98US-00213768.
XX
XX 17-DEC-1998; 98US-00213768.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowsett LM,
XX
XX WPI; 2000-022284/02.
XX
XX Antisense compound which modulates human sentrin expression, useful for
XX treating diseases associated with sentrin expression.
XX
XX Claim 3; Col 38; 29pp; English.
XX
XX The present invention describes an antisense compound (I) 8-30
XX nucleotides long targeted to a nucleic acid molecule encoding human
XX sentrin. The antisense compound comprises a phosphorothioate antisense
XX oligonucleotide which inhibits expression of human sentrin. (I) is useful
XX for inhibiting expression of sentrin in human cells or tissues in vitro,
XX for treating humans or other animals suspected of having or being prone
XX to a disease associated with sentrin expression. (I) can also be used for
XX research or diagnostic purposes. The present sequence represents a human
XX sentrin phosphorothioate antisense oligonucleotide from the present
XX invention
XX
XX Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 328 CTGGCCCAATTACTTTGAG 345
XX |||||
XX 1 CTGTCCAMTGACTTTGAG 18
XX
XX RESULT 2923
XX AA265529
XX ID AA265529 standard; DNA; 18 BP.
XX
XX AC AA265529;
XX
XX 30-MAR-2000 (first entry)
XX
XX Immunosuppressant inhibitor oligonucleotide TGF-beta1-98-17.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
XX prostaglandin E2; PGE2; immune response; tumor; asthma; Crohn's disease;
XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
XX glomerulonephritis; acute respiratory distress syndrome; se;
XX atherosclerosis.
XX
XX Unidentified.
XX
XX OS
XX PN WO963975-A2.
XX
XX PD 16-DEC-1999.
XX

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PF 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiefen K, Schlingensiefen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
XX adversely affects the immune response, for treating cancers and
XX infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
XX used in the invention. The invention relates to a composition which
XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.
XX transforming growth factor TGF-beta, vascular endothelial growth factor
XX VEGF, interleukin-10, IL-10, prostaglandin E2 PGE2, or their receptors)
XX that adversely affects the immune response. The composition also includes
XX at least one stimulant that positively affects the immune response. This
XX oligonucleotide is an example of an inhibitor that is used in the
XX composition. The composition is used as an immunostimulant for the
XX treatment of neoplasms and infections, particularly hyperproliferation;
XX leukemias, (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
XX most of which are directed against TGFbeta or VEGF, are inhibitors of
XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
XX colitis, diabetes, glomerulonephritis, acute respiratory distress
XX syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 CTGGCAGCTGCGCGGCG 19
XX |||||
XX 1 CCGGCAGCGCGCGCGGCG 18
XX
XX RESULT 2924
XX AA259187/c
XX ID AA259187 standard; DNA; 18 BP.
XX
XX AC AA259187;
XX
XX 15-SEP-2003 (revised)
XX
XX 20-APR-2000 (first entry)
XX
XX Reverse primer for construct MWp-MWpms DNA.
XX
XX Fusion protein; Bacillus; cell wall protein; promoter; cleavage site;
XX TEV protease; PCR primer; se.
XX
XX Brevibacillus brevis.
XX
XX JF11341991-A.
XX
XX 14-DEC-1999.
XX
XX 30-MAR-1999; 99JP-00089488.
XX
XX 31-MAR-1998; 98JP-00087339.
XX
XX (ITOH-) ITOHAM FOODS INC.
XX

```

PA (UDAK/) UDAKA S.
XX Sato S, Higashikuni N, Kudo T, Kondo M;
XX WPI, 2000-101697/09.
DR A DNA coding a new fused protein and preparation of a useful peptide
XX through its expression.
PT Example 3; Page 10; 43pp; Japanese.
XX
XX The invention relates to a DNA construct encoding a fusion protein
CC comprising a Bacillus species cell wall protein fused to a cleavage
CC peptide and a heterologous protein. The fusion construct is placed
CC downstream of a Bacillus species promoter sequence. This sequence
CC represents a PCR primer for the MWBP-MWpmp5 part of the construct MWBP-
CC MWpmp5-Mec-Proinsulin, which comprises the Bacillus brevis middle wall
CC protein mp5 linked to the human proinsulin protein. (Updated on 15-SEP-
CC 2003 to standardise OS field)
XX
SQ Sequence 18 BP; 0 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCA 7432
DB 18 GCAGCAGCAGCAGCAGCA 1
RESULT 2925
AAZ48498
ID AAZ48498 standard; DNA; 18 BP.
XX
AC AAZ48498;
XX
XX 31-MAR-2000 (first entry)
DT
XX Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18891.
DE
XX Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX US6007995-A.
PN
XX 28-DEC-1999.
PD
XX 26-JUN-1998; 98US-00106038.
PE
XX 26-JUN-1998; 98US-00106038.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Baker BF, Cowser LM;
PI WPI, 2000-105333/09.
DR
XX Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors.
XX
XX Example 10; Col 24; 34pp; English.
PS
XX The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid
CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research

CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. Sequences AAZ48498-555
CC represent antisense oligos used for inhibition of the human TNFR1 mRNA
XX
SQ Sequence 18 BP; 5 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7410 CATCAGCAGCAGCAGCAG 7427
DB 1 CACGACGGCGCAGCAGCAG 18
RESULT 2926
AAZ71698/C
ID AAZ71698 standard; DNA; 18 BP.
XX
AC AAZ71698;
XX
XX 10-SEP-2001 (first entry)
DT
XX Human biallelic marker upstream amplification primer SEQ ID NO:6054.
DE
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO954500-A2.
PN
XX 28-OCT-1999.
PD
XX 21-APR-1999; 99WO-1B000822.
PE
XX 21-APR-1998; 98US-0082614P.
PR
XX 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI WPI, 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1521; 2745pp; English.
PS
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 10 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5704 CTTCCTTTCTCTCTC 5721
18 CTTCCTTTCTCTCTC 1

RESULT 2927
AAZ76847/c
ID AAZ76847 standard; DNA; 18 BP.

XX AAZ76847;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:11203.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

XX WO954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumentfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

XX Claim 9; Page 2619; 2745pp; English.

XX AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA269579 to AA277440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. CC Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the CC differential efficacious responses to and side effects from CC pharmaceutical agents acting on a disease as well as other treatment. CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and CC 3367, are not actually given a sequence in the Sequence Listing from the present invention

XX Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2341 CACACCCGCTTTCTGT 2358
18 CACACACCCCTTTCTGT 1

RESULT 2928

AAZ8678
ID AAZ8678 standard; DNA; 18 BP.

XX AAZ8678;

XX 11-MAY-2000 (first entry)

XX Chimeric primer #1.

XX Primer; detection; diagnosis; ss.

XX Unidentified.

XX US6022691-A.

XX 08-FEB-2000.

XX 07-NOV-1997; 97US-00965908.

XX 05-SEP-1991; 91US-00755485.

XX 04-SEP-1992; 92WO-US007489.

XX 27-OCT-1994; 94US-00330000.

XX (ISIS-) ISIS PHARM INC.

XX Lima WF, Bruce TW;

XX WPI; 2000-170669/15.

XX Assay for a chemical or drug in a sample comprises detecting binding of an oligonucleotide selected from a set of randomized oligonucleotides.

XX Disclosure; Col 27-28; 20pp; English.

XX This invention describes a novel method (1) for specifically detecting a chemical or drug in a sample comprising contacting the sample with an oligonucleotide having specific activity for a target biomolecule and detecting the presence or absence of binding where the presence of binding indicates the presence of the chemical or drug in the sample. The CC oligonucleotide is identified by: (a) assaying a prepared set of CC randomized oligonucleotides for activity against a target biomolecule; CC (b) separating active from inactive oligonucleotides; (c) recovering the CC active oligonucleotides; and (d) characterizing the recovered CC oligonucleotides by microanalytical structure determination. The method CC can be used for diagnostic or research purposes

XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GGACTTTTTTTTTTTT 4477
1 GGATGTTTTTTTTTTT 18

RESULT 2929
AAA30403/c

ID AAA30403 standard; DNA; 18 BP.

XX AAA30403;

XX 21-AUG-2000 (first entry)

XX Human NF-kappa-B p65 subunit antisense oligodeoxynucleotide ISIS# 23770.

XX Human; anti-inflammatory; cytostatic; antimicrobial; infection;

XX antisense inhibition; inflammation; transcription factor; apoptosis;

XX cancer; ss.

XX Homo sapiens.

```

FH Key location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /note= "all or some internucleoside bonds are
FT phosphorothioate and optionally some sugars may be 2'
FT methoxyethyl"
XX
XX US6069008-A.
XX
XX 30-MAY-2000.
XX
XX 25-NOV-1998; 98US-00199859.
XX
XX 25-NOV-1998; 98US-00199859.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowseert LM, Montia BP;
XX
XX WPI, 2000-410858/35.
XX
XX Antisense compounds which inhibit the expression of the human NF-kappa-B
XX p65 subunit (p65) useful for treating diseases associated with p65
XX expression and as prophylaxis to prevent of delay infection, inflammation
XX or tumor formation.
XX
XX Example 15; Col 41; 33pp; English.
XX
XX The present sequence is one of a number of oligonucleotides designed to
XX target different regions of the human NF-kappa-B p65 subunit, which is a
XX member of the Rel/NF-kappa-B family of transcription factors. Rel/NF-
XX kappa-B proteins are involved in a diverse set of signaling pathways
XX involving stress, apoptosis, cancer, growth, infection and inflammation.
XX Antisense oligonucleotides are able to inhibit expression of the p65
XX subunit and may therefore be used in the treatment of disorders
XX associated with NF-kappa-B p65 subunit expression. They may be used as a
XX prophylaxis to prevent or delay infection, inflammation or tumor
XX formation. Antisense compounds may also be used for research and
XX diagnostics because they hybridize to nucleic acids encoding NF-kappa-B
XX p65 subunit. The effect of antisense oligonucleotides on NF-kappa-B p65
XX subunit mRNA levels was measured using real-time quantitative PCR and
XX Northern blot analysis. Antisense oligonucleotides were synthesised on an
XX automated DNA synthesiser
XX
XX Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2124 TGAAGACTTGTCTACAT 2141
XX ||||| ||||| |||||
XX 18 TGAAGACTTGTCTACAT 1
XX
XX RESULT 2930
XX AAA8376
XX ID AAA8376 standard; DNA; 18 BP.
XX
XX AAA8376;
XX
XX 21-AUG-2000 (first entry)
XX
XX Human Ets-2 phosphorothioate antisense oligonucleotide, SEQ ID NO:35.
XX
XX Ets-2; human; transcription factor; chromosome 21q22.3; cancer; invasion;
XX metastasis; skeletal abnormality; Down's syndrome; expression inhibition;
XX phosphorothioate; antisense; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN US6054316-A.
XX

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PD 25-APR-2000.
XX
XX 25-JUN-1999; 99US-00344579.
XX
XX 25-JUN-1999; 99US-00344579.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowseert LM;
XX
XX WPI, 2000-338495/29.
XX
XX Antisense compound, 8-30 nucleobases in length, inhibiting the expression
XX Ets-2 is useful for treating cancer and detecting Ets-2 expression.
XX
XX Claim 3; Col 39; 31pp; English.
XX
XX Sequences AAA8349-A3838 represent antisense oligonucleotides targeted
XX to the human Ets-2 gene, which inhibit its expression. The antisense
XX oligonucleotides were designed to target different regions of the human
XX Ets-2 RNA, and were analysed for their effect on Ets-2 mRNA levels by
XX quantitative real-time PCR. The Ets-domain transcription factors are a
XX family of proteins which are involved in controlling key cellular events
XX such as proliferation, differentiation and development. The Ets domain is
XX a DNA-binding domain shared by all members of this family. Through this
XX motif, Ets family members bind to the promoter regions of various genes
XX at a GCA consensus sequence, thereby acting as either repressors or
XX activators of the gene. All but one Ets family protein bind to DNA as a
XX monomer. Ets-2 has been implicated in the regulation of cellular
XX proliferation and differentiation. The Ets-2 gene is located at
XX chromosome 21q22.3, which is within a region known to undergo
XX translocations associated with malignancies. Ets-2 has been found to be
XX upregulated in several cancers, including lymphoblastic leukaemia. It may
XX also play a role in the cancer phenotype, as it activates the tyrosine
XX kinase activator (vpr) promoter and the promoters of
XX metalloproteinases in response to epidermal growth factor (EGF)
XX stimulation. High levels of vpr and metalloproteinases are associated
XX with tumor invasion and metastasis in breast cancers. As the Ets-2 gene
XX is located on chromosome 21, which is triplicated in Down's syndrome, it
XX is also thought to be responsible for the skeletal abnormalities present
XX in this condition. The antisense oligonucleotides of the invention are
XX useful for the treatment or prophylaxis of conditions associated with Ets
XX -2 expression, especially cancer
XX
XX Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 7231 ATCCCTCTCAAGTCCAGC 7248
XX ||||| ||||| |||||
XX 1 ATCCGCTCTCAAGTCCAGC 18
XX
XX RESULT 2931
XX AAD17190/c
XX ID AAD17190 standard; DNA; 18 BP.
XX
XX AAD17190;
XX
XX 29-NOV-2001 (first entry)
XX
XX S. nouresei PKS-encoding Nysc DNA amplifying PCR antisense primer ERD2.
XX
XX Polyketide synthase; PKS; macrolide; mycristin; PKS gene cluster;
XX antifungal; antibiotic; enoylreductase; ER; PCR primer; ss.
XX
XX Streptomycetes nouresei.
XX
XX OS
XX PN WO200159126-A2.
XX
XX 16-AUG-2001.
XX

```

XX 08-FEB-2001; 2001MO-GB000509.
 XX
 PF 08-FEB-2000; 2000GB-00002840.
 XX
 PR 10-APR-2000; 2000GB-00008786.
 PR 14-APR-2000; 2000GB-00009387.
 XX
 PA (UNIV-) UNIV NORGES TEKNIK NATURVITENSKAPELIGE.
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
 PA (ALPH-) ALPHARMA AS.
 PA (SINV-) SINVENT AS.
 PA (DZIE/) DZIELEWSKA H.
 PA (ZOTC/) ZOTCHEV S B.
 PA (SEKV/) SEKUROVA O N.
 PA (FJAE/) FJAEVRIK E.
 PA (BRAU/) BRAUTASET T.
 PA (STRO/) STROM A R.
 PA (VALT/) VALTA S.
 XX
 PI Zotchev SB, Sekurova ON, Fjaervik E, Brautaset T, Strom AR,
 PI Valla S, Ellingsen TE, Sletta H, Gulliksen O;
 XX
 DR WPI; 2001-557614/62.
 XX
 PT New mystatin polyketide synthase polynucleotides and polypeptides, useful
 PT as antibiotics and antifungals.
 XX
 PS Example 2; Page 69; 266pp; English.
 XX
 CC The present invention relates to the cloning and sequencing of the gene
 CC cluster encoding a modular type I polyketide synthase (PKS) enzyme
 CC involved in the biosynthesis of the macrocyclic antibiotic mystatin. The
 CC mystatin PKS is useful as antifungal antibiotics. The present sequence is
 CC a PCR primer which is used for the amplification of the DNA fragment
 CC representing the coding sequence for the C-terminal part of the
 CC enoylreductase (ER) domain in module 5 of Streptomyces noursei PKS-
 CC encoding Nysc
 XX
 SQ Sequence 18 BP; 4 A; 10 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5542 GGTGTCATGCAATG 5559
 DB 18 GGTGTCATGCGGCTG 1
 RESULT 2932
 ID AAA46048 standard; DNA; 18 BP.
 XX
 AC AAA46048;
 XX
 OS
 DT 12-SEP-2001 (first entry)
 XX
 DE Synthetic oligonucleotide 23.
 XX
 KW Synthetic oligonucleotide; dinucleotide repeat; cytosatic; apoptosis;
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 KW lymphoma; ss.
 XX
 OS Synthetic.
 XX
 PN MO200144465-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 12-DEC-2000; 2000MO-CA001467.
 XX
 PR 13-DEC-1999; 99US-0170325P.
 XX

PR 29-AUG-2000; 2000US-0228925P.
 XX
 PA (BION-) BIONICHE LIFE SCI INC.
 XX
 PI Phillips NC, Pilon MC;
 XX
 DR WPI; 2001-398150/42.
 XX
 PT Composition comprising synthetic oligonucleotides which comprise multiple
 PT repeats of dinucleotides such as GT, TG, etc., useful for treating cancer by
 PT inducing cell cycle arrest, inhibiting proliferation, activating
 PT caspases.
 XX
 PS Example 19; Page 32; 77pp; English.
 XX
 CC The present sequence is that of a synthetic oligonucleotide useful to the
 CC invention. The invention relates to a composition, comprising a 2 to 20
 CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
 CC repeats of dinucleotides such as GT, TG, etc., according to specific
 CC formula and having cytosatic activity. The oligonucleotide compositions
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,
 CC activation of caspases and induction of apoptosis or production of
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
 CC cancer such as primary carcinoma, secondary carcinoma, breast, sarcoma
 CC and secondary sarcoma such as, leukemia, lymphoma, prostate,
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
 CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(Ink4B), p16(Ink4), drug
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 CC
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 15 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3623 GGGTGGGGTGGGAGAG 3640
 DB 1 GGGTGGGGTGGGCTG 18
 RESULT 2933
 ID ABA91529 standard; DNA; 18 BP.
 XX
 AC ABA91529;
 XX
 OS
 DT 23-APR-2002 (first entry)
 XX
 DE DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
 XX
 KW DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 8..9
 FT /tag= a
 FT /label= RNA
 XX
 PN MO200206531-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 12-JUL-2001; 2001MO-US022166.
 XX
 PR 14-JUL-2000; 2000US-00616761.
 PR 30-MAR-2001; 2001US-00823647.
 XX
 PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
 XX
 PI Datagapcta N;
 XX

```
XX WPI; 2002-171819/22.
XX
XX Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.
XX
XX Example 4; Page 49; 72pp; English.
XX
XX The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC the set had a different number of ribonucleotides, 2 in the present case.
CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC minutes. The results showed that 4 ribonucleotides were the minimum
CC number for RNA cleavage. The invention provides probes for nucleic acid
CC hybridisation. The probes form a hairpin structure comprising a double-
CC stranded stem and a single-stranded loop, and are capable of both
CC intramolecular and intermolecular hybridisation. The double-stranded stem
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC can be removed. Arrays and methods for nucleic acid hybridisation using
CC the probes are provided.
XX
XX Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 4464 TTTTTTTTTTTTTTTTTT 4481
Db 1 TTTTTTAAATTTTTTTT 18
RESULT 2934
ABLA0838
ID ABL40838 standard; DNA; 18 BP.
XX
XX ABL40838;
AC
XX 03-JUN-2002 (first entry)
DT
XX
XX P. putida exdB and exdD genes amplifying RT-PCR primer.
DE
XX
XX exdB; exdD; tonB; antibiotic; toluene; pHBA; aromatic compound; parabene;
KM para-hydroxybenzoic acid; RT-PCR; primer; ss.
XX
XX Pseudomonas putida.
OS
XX
XX WO200229034-A2.
PN
XX
XX 11-APR-2002.
PD
XX
XX 28-SEP-2001; 2001WO-US031180.
PF
XX
XX 30-SEP-2000; 2000US-0236879P.
PR
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA
XX
XX Ramos JL, Ben-Bassat A, Godoy P, Ramos-Gonzales MI, Duque E;
PI WPI; 2002-340103/37.
XX
XX Novel isolated nucleic acid of the tonB operon from Pseudomonas, useful
PT for producing transformed bacterial strains which are more sensitive to
PT antibiotics, and toluene.
XX
XX Disclosure; Page 80; 81pp; English.
```

```
XX The invention relates to a novel gene cluster comprising the exdB, exdD
CC and tonB genes from P. putida. These genes are useful for producing
CC bacterial cells more sensitive to antibiotics, toluene, pHBA (para-
CC hydroxybenzoic acid), aromatic compounds, parabenes, and aromatic amino
CC acids. Methods are also provided to identify pHBA tolerant genes, and
CC pHBA tolerant strains, useful for producing pHBA. The present sequence
CC represents a primer for RT-PCR amplification of P. putida exdB and exdD
CC mRNA.
XX
XX Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 7419 CAGCAGCAGCAGCAGCAGC 7436
Db 1 CAGCAGCAGCAGCAGCAGC 18
RESULT 2935
AAS62957
ID AAS62957 standard; DNA; 18 BP.
XX
XX AAS62957;
AC
XX
XX 29-JAN-2002 (first entry)
DT
XX
XX Esophageal adenocarcinoma diagnostic oligonucleotide #56.
DE
XX
XX Human; cancer; gastrointestinal adenocarcinoma;
KM esophageal adenocarcinoma; gastrointestinal dysplasia;
KM esophageal dysplasia; gastrointestinal metaplasia; diagnostic;
KM Cpg-island methylation; esophageal metaplasia; PCR primer;
KM Barrett's intestinal tissue; loss of heterozygosity; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200175172-A1.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 02-APR-2001; 2001WO-US010658.
PF
XX
XX 31-MAR-2000; 2000US-0193839P.
PR
XX
XX (USC-) UNIV SOUTHERN CALIFORNIA.
PA
XX
XX Laird P, Bads C;
PI WPI; 2002-010805/01.
XX
XX Diagnosing cancer or cancer-related conditions, e.g., gastrointestinal
PT and esophageal adenocarcinoma, comprises performing methylation assay of
PT a tissue sample obtained from a test tissue or region to be diagnosed.
XX
XX Claim 3; Page 32; 80pp; English.
XX
XX The invention relates to a method of diagnosing cancer or cancer-related
CC conditions from tissue samples. The method comprises obtaining a sample
CC from test tissue or region to be diagnosed, performing a methylation
CC assay of the sample, where the assay determines methylation state of
CC genomic Cpg sequences, and making a diagnostic or prognostic prediction
CC of the cancer based at least in part upon the methylation state of the
CC genomic Cpg sequences. The method is useful for diagnosing cancer or
CC cancer-related conditions such as gastrointestinal or esophageal
CC adenocarcinoma, gastrointestinal or esophageal dysplasia,
CC gastrointestinal or esophageal metaplasia, Barrett's intestinal tissue,
CC pre-cancerous conditions in normal esophageal squamous mucosa, or their
CC combinations, from tissue samples. Preferably, the cancer diagnosed is
CC esophageal adenocarcinoma, and making a diagnostic or prognostic
CC prediction of the cancer, based upon the methylation state of the genomic
```


CC Cpg sequences provides for classification of the adenocarcinoma by grade
CC or stage. The method provides an opportunity for early intervention, in
CC patients identified with cancer, or an elevated risk for developing
CC cancer. Cpg-island methylation can easily be detected in a field of
CC normal cell contamination as a gain of signal, unlike loss of gene
CC expression (e.g., loss of heterozygosity (LOH) and deletion analysis),
CC which is difficult to resolve in a sample with contaminating normal
CC cells. AAS62902-AAS62966 represent oligonucleotide sequences used in
CC diagnosis of esophageal adenocarcinoma as described in the method of the
CC invention
CC
XX
SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2194 CGCATCATCTTCTACCGA 2211
Db 1 CGCCTCATCTTCTCCCGA 18
RESULT 2936
ABLT43181
ID ABLT43181 standard; DNA; 18 BP.
XX
AC ABLT43181;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:225.
XX
KW Human: chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; 88.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PE 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAKAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 9; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multwell plates numbered for discrimination are mixed in each of the
CC multwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multwell
CC plates; (e) the clones in the multwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABLT42957 to ABLT45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABLT45323 to ABLT45634

CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 18 BP; 5 A; 1 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6870 GCGAGGAGAGAGGCTGG 6887
Db 1 GCGAGGAGAGAGGCTGG 18
RESULT 2937
ABT04994
ID ABT04994 standard; DNA; 18 BP.
XX
AC ABT04994;
XX
DT 11-OCT-2002 (first entry)
XX
DE TNFR1 expression modulation related antisense oligo SEQ ID No 24.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
PN WO200248168-A1.
XX
PD 20-JUN-2002.
XX
PE 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowseert LM, Zhang H, Dean NM;
XX
DR WPI; 2002-583481/62.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS Example 10; Page 44; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 5 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7410 CACACAGCAGCAGCAGG 7427
Db 1 CACACAGCAGCAGCAGG 18

RESULT 2938
 ID ABX80015 standard; cDNA, 18 BP.
 AC ABX80015;
 XX 17-APR-2003 (first entry)
 DT
 DE EST polymorphic DNA repeat polynucleotide #340.
 XX
 DE EST, expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 XX US6472154-B1.
 XX
 XX 29-OCT-2002.
 XX
 XX 31-DEC-1999; 99US-00475947.
 XX
 XX 31-DEC-1999; 99US-00475947.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Garner HR, Wren JD, Manna JD, Fondon JW;
 XX WPI; 2003-208818/20.
 DR
 XX
 PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 PS Example; Col 1165; 588bp; English.
 XX
 CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 7415 GCAGCAGCAGCAGCAGCA 7432
 DB 1 GCAGCAGCAGCAGCAGCA 18
 AC
 RESULT 2939
 ID AB211028 standard; DNA; 18 BP.
 XX
 XX AB211028;
 AC

XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related oligonucleotide #1168.
 XX
 KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200277272-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-EP003401.
 XX
 XX 26-MAR-2001; 2001US-0278333P.
 XX
 XX (EPIG-) EPIDEMIOLOGICAL AG.
 XX
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 XX Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 XX Lewin A, Lipschick E, Maier S, Model F, Mueller V, Otto T, Pelet C;
 XX Schwabe I, Ziebarth H;
 XX WPI; 2003-018942/01.
 DR
 XX
 PT Detecting and differentiating between haematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX
 PS Claim 15; Page 77; 117p; English.
 XX
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. AB209861 to AB211118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 18 BP; 3 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 3210 TGAGAAAGTGGTGGAG 3227
 DB 1 TGAGTAAGTGGTGGAG 18
 AC
 RESULT 2940
 ID AB211030/c
 XX
 XX AB211030 standard; DNA; 18 BP.
 XX


```
XX 12-JUN-2003.
PD 06-DEC-2002; 2002US-00314405.
PF 15-NOV-2000; 2000US-00713616.
XX (INOK/) INOKO H.
XX Inoko H, Tamiya G, Matsuzaka Y,
DR WPI; 2003-616782/58.
XX
PT New oligonucleotide primer capable of specifically hybridizing to a DNA
PT having the sequence of the flanking regions of a microsatellite (e.g.
PT M29), useful for HLA-related research, e.g. transplantation matching.
XX
XX Example 2; Page 5; 20pp; English.
XX
CC The invention relates to an oligonucleotide primer capable of
CC specifically hybridizing to a DNA having the sequence of the flanking
CC regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
CC 11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-4-25, M2-4-26, M2-2-
CC 29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-2-36, M2-5-11, M2-2-
CC 46, and M2-2-48. The primer is useful for determining the number of
CC repeat units of the microsatellite cited above. The primer is useful in
CC HLA-related research, such as genetic mapping of HLA class II-associated
CC diseases, transplantation matching, population genetics, and
CC identification of recombination hot spots as well as linkage
CC disequilibrium studies. The present sequence represents the human
CC microsatellite repeat M2_3_8.
XX
SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 65 GCTGGGGGGGGGGGGCGG 82
DB 1 GCGGGGGGGGGGGCGGCG 18
XX
RESULT 2943
ADBS4474
ID ADBS4474 standard; DNA; 18 BP.
XX
AC ADBS4474;
XX
DT 04-DEC-2003 (first entry)
XX
DE Hybridisation oligonucleotide 12 used to analyse genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytosstatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
KW probe.
XX
XX Unidentified.
XX
OS WO2003072821-A2.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimnich I, Becker E, Leeche R,
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.
```

```
XX Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
XX Claim 36; Page 27; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may be useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the hybridisation
CC oligonucleotide of the invention which was used to analyse the genomic
CC DNA region.
XX
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6672 TTGGGGGACGTATTTT 6689
DB 1 TTGGGGGATGTATTGTT 18
XX
RESULT 2944
ADCS69952
ID ADCS69952 standard; DNA; 18 BP.
XX
AC ADCS69952;
XX
DT 18-DEC-2003 (first entry)
XX
DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 441).
XX
KW PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
KW cytosine methylation state.
XX
XX Unidentified.
XX
OS WO2003052135-A2.
XX
PN WO2003052135-A2.
XX
PD 26-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP014026.
XX
PR 14-DEC-2001; 2001DE-01061625.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Field UK, Genc B, Liloglou T, Lipacher E, Maier S,
PI Nimnich I;
XX
DR WPI; 2003-533029/50.
XX
PT Detecting and differentiating cytosine methylation state of genomic DNA,
PT useful for diagnosing, treating prognosticating and/or monitoring lung
PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT carcinoma.
XX
PS Claim 15; SEQ ID NO 441; 58pp; English.
XX
```

CC This invention relates to a novel method for detecting and
 CC differentiating between lung cell proliferative disorders associated with
 CC at least one gene and/or their regulatory regions. Specifically, it
 CC refers to a method comprising contacting a target nucleic acid in a
 CC biological sample with at least one reagent, wherein the reagent is able
 CC to distinguish between methylated and non-methylated CpG dinucleotides
 CC present in the target DNA. As such, it is possible to further
 CC differentiate and diagnose medical conditions including adenocarcinoma
 CC and squamous cell carcinoma, and their respective adjacent lung tissue.
 CC The present invention describes cytosolic oligomers and PNA-oligomers
 CC that are useful as probes for determining the cytosine methylation state
 CC or single nucleotide polymorphisms (SNPs) of the target sequence. This
 CC oligonucleotide sequence is a primer oligomer used for the analysis of
 CC CpG positions within genomic DNA, used in an exemplification of the
 CC invention.

CC Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6672 TTGGGCGACGTATTATT 6689

1 TTGGGCGACGTATTATT 18

RESULT 2945

AD843413/c

ID AD843413 standard; DNA; 18 BP.

AC AD843413;

29-JAN-2004 (first entry)

Human SNCG sequencing primer, SEQ ID 18.

Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;

Alzheimer's disease; neuroprotective; nontoxic; gene therapy;

Chromosome 10; PCR; primer; ss.

Homo sapiens.

WO2003054143-A2.

03-JUL-2003.

25-OCT-2002; 2002WO-US034679.

25-OCT-2001; 2001US-0339525P.

08-NOV-2001; 2001US-0336928P.

08-NOV-2001; 2001US-0338010P.

09-NOV-2001; 2001US-0338363P.

04-DEC-2001; 2001US-0337052P.

28-MAR-2002; 2002US-0368919P.

(NEUR-) NEUROGENETICS INC.

(GEHO) GEN HOSPITAL CORP.

Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzl RE, Bertram L;

Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;

WPI; 2003-559131/52.

Determining a predisposition for or the occurrence of neurodegenerative

disease, e.g. Alzheimer's disease by detecting in a target nucleic acid

the presence or absence of an allelic variant of one or more polymorphic

regions.

Example 2; Page 265; 848bp; English.

The present invention relates to a method (M1) for determining a

predisposition for or the occurrence of neurodegenerative disease in a

CC subject. The method comprises detecting in a target nucleic acid obtained
 CC from the subject the presence or absence of an allelic variant of one or
 CC more polymorphic regions of one or more genes selected from uPA
 CC (urokinase plasminogen activator), SNCG (gamma-synuclein), IDB (insulin-
 CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
 CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 CC presence of at least one of the allelic variant of one or more
 CC polymorphic regions is indicative of a predisposition for or the
 CC occurrence of neurodegenerative disease. The genes are all located on
 CC chromosome 10. M1 is useful for determining a predisposition for or the
 CC occurrence of, and for treating neurodegenerative disease, particularly
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used
 CC in the method of the invention.

CC Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6860 CTTCTCCCTGGGAGGGA 6877

18 CTTCTCTGGGAGGGA 1

RESULT 2946

AAN2724

ID AAN2724 standard; DNA; 19 BP.

AC AAN2724;

31-OCT-2002 (revised)

14-MAY-1990 (first entry)

Probe fixed via 400nt poly-dT linker to a nylon filter to identify target

Beta-thalassemia allele.

Probe; fixed; oligo-nucleotide; hybridisation; ss.

Synthetic.

WO8911548-A.

30-NOV-1989.

18-MAY-1989; 89WO-US002170.

-20-MAY-1988; 88US-00197000.

04-MAY-1989; 89US-00347495.

(CETU) CETUS CORP.

Salki RK, Erlich HA;

WPI; 1989-370739/50.

Assay reagent cong. oligo-nucleotide probe attached via spacer - each

probe having hybridisation region complementary to specific analyte

sequence, e.g. for diagnosis of genetic disease.

Example; Page 29; 47bp; English.

Probe fixed to a filter allows simultaneous non radioactive detection of

50 or more specific nucleotide sequences in a single test sample.

(Updated on 31-OCT-2002 to add missing OS field.)

Sequence 19 BP; 5 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6716 CAGATGCTAGTGAAT 6733

DR WPI; 1993-382240/48.
XX Detection method of gene without using radio-isotope - by hybridisation
PT of nucleic acid probe which is single strand having complementary
XX sequence of gene and single strand denatured sample DNA.
PS Disclosure; Page 21; 26pp; Japanese.
XX
CC The sequences (AA053077-Q53136) are used in the invention to detect
CC specific genes without the use of radio-isotopes. Detection is carried
CC out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic
CC acid probe, complementary to the target sequence. Hybridisation occurs on
CC the surface of an electrode or optical fibre and detection is visualised
CC by the addition of an entity that recognises (ds) hybridised DNA and is
CC electrochemically / photochemically active
XX
SQ Sequence 19 BP; 3 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 510 CACTGTCACAGACTGCC 527
Db 19 CCCTGTCAAGACTGCC 2
RESULT 2950
AAA85905
ID AAA85905 standard; DNA; 19 BP.
XX
XX AAA85905;
AC
XX 04-DEC-2000 (first entry)
DT
XX Cdc 25 hs ribozyme binding site #13.
DE
XX
XX Rbomyze; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KM
OS Mammalia.
XX
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tiltz R, Welch PJ, Barber JR, Robbins JM;
PI
XX WPI; 2000-412314/35.
DR
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1.
XX
XX Disclosure; Page 99; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA082415 to AA086787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 3 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1215 TACCTACCTTCCCTTAGA 1232
Db 1 TACCTCTTTTCCCTTAGA 18
RESULT 2951
AAA82490/C
ID AAA82490 standard; DNA; 19 BP.
XX
XX AAA82490;
AC
XX 04-DEC-2000 (first entry)
DT
XX cdk1 ribozyme binding site #76.
DE
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KM
OS Mammalia.
XX
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tiltz R, Welch PJ, Barber JR, Robbins JM;
PI
XX WPI; 2000-412314/35.
DR
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1.
XX
XX Disclosure; Page 47; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA082415 to AA086787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 9 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6736 CTTCCTTTTAAATCTG 6753
Db 19 CTTCCTTTTAAATCTG 2
RESULT 2952
AAA85904
ID AAA85904 standard; DNA; 19 BP.
XX
XX AAA85904;
AC
XX 04-DEC-2000 (first entry)
DT
XX Cdc 25 hs ribozyme binding site #12.
DE
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KM

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XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DR WPI; 2000-412314/35.
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PT PCNA and Cyclin B1.
XX PS Disclosure; Page 99; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AA82415 to AA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1215 TACCTACCTTCCCTAGA 1232
Db 2 TACCTCTTCCCTAGA 19

RESULT 2953
AAZ71461
ID AAZ71461 standard; DNA; 19 BP.
XX AC AAZ71461;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:5817.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX PA Homo sapiens.
XX OS Homo sapiens.
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;

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XX DR WPI; 2000-013267/01.
XX PT Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX PS Claim 8; Page 1471; 2745pp; English.
XX CC AA265654 to AA269578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AA269579 to AA277440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterisation of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence Listing from the
XX CC present invention
XX SQ Sequence 19 BP; 0 A; 7 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5702 GCCTTCTTTCCTTC 5719
Db 1 GCCTTCTTTCCTTTC 18

RESULT 2954
AAC65640/C
ID AAC65640 standard; DNA; 19 BP.
XX AC AAC65640;
XX DT 16-FEB-2001 (first entry)
XX DE Human AFLP primer E51.
XX KW Human; AFLP; polymorphic loci; SNP; single nucleotide polymorphism;
XX KW amplification fragment length polymorphism; genetic marker; primer; ss.
XX OS Homo sapiens.
XX PN WO200061801-A2.
XX PD 19-OCT-2000.
XX PF 10-APR-2000; 2000WO-NL000235.
XX PR 09-APR-1999; 99EP-00201112.
XX PA (KEYG-) KEYGENE NV.
XX OS Homo sapiens.
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;

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This invention describes a novel method for determining (D) genotypes of polymorphic loci amplified in a restriction fragment mixture (M), using an oligonucleotide sequence (OS) complementary to part of target

CC restriction fragment (TF), and located adjacent to polymorphism to be
 CC detected. The method involves hybridization of TF and OS, adding labeled
 CC nucleotide (N) or its analog (A) to (M), to extend OS, and detecting the
 CC hybrid and/or of OS with (N) or (A). The method is useful for detecting
 CC single nucleotide polymorphisms in constant amplification fragment length
 CC polymorphism-fragments. The method is useful for detecting single
 CC nucleotide polymorphisms (SNPs) located in constant amplification
 CC fragment length polymorphism (AFLP) fragments such that useful non-
 CC polymorphic bands, which ordinarily do not provide any useful information
 CC when conventional AFLP-finger printing is used, are made. SNPs are also
 CC informative as genetic markers

SO Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1826 TGGGATGCTAGCGCAGT 1843
 19 TGGGATGCTAGCGCAGT 2

RESULT 2955
 AAS42915
 ID AAS42915 standard; DNA; 19 BP.
 AC AAS42915;
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX
 DE Human G Protein-Coupled Receptor (GPCR) PCR primer #49.
 XX
 KW Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
 KW attention deficit disorder; anxiety; depression; bipolar disorder; ss;
 KW neurological disorder; Huntington's disease; dementia; obesity; anorexia;
 KW metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
 KW type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
 KW cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
 KW viral infection; immunostimulant; neuroleptic; nootropic; tranquilizer;
 KW antidepressant; anorectic; PCR primer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W0200162797-A2.
 PD
 XX 30-AUG-2001.
 PF
 XX 23-FEB-2001; 2001WO-US005676.
 XX
 PR 23-FEB-2000; 2000US-0184247P.
 PR 23-FEB-2000; 2000US-0184303P.
 PR 23-FEB-2000; 2000US-0184304P.
 PR 23-FEB-2000; 2000US-0184305P.
 PR 23-FEB-2000; 2000US-0184397P.
 PR 02-MAR-2000; 2000US-0186457P.
 PR 03-MAR-2000; 2000US-0186810P.
 PR 09-MAR-2000; 2000US-0188064P.
 PR 13-MAR-2000; 2000US-0188880P.
 PR 03-APR-2000; 2000US-0194344P.
 PR 23-JUN-2000; 2000US-0213861P.
 PR 11-JUL-2000; 2000US-0217369P.
 PR 11-JUL-2000; 2000US-0217370P.
 PR 14-JUL-2000; 2000US-0218337P.
 PR 20-JUL-2000; 2000US-0218492P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogel I G, Wood LS, Parodi LA, Lind P;
 XX WPI; 2001-570628/64.
 DR
 XX New isolated nucleic acid encoding a new G-protein coupled receptor
 PT

PT polypeptide for detecting receptor modulators that can treat mental
 PT disorders, such as schizophrenia, anxiety, depression, or obesity.
 XX
 PS Example 5; Page 124; 279pp; English.
 XX
 CC Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for
 CC cDNA molecules encoding human G-protein coupled receptor (GPCR)
 CC polypeptides. The protein and DNA sequences of the invention can be used
 CC to identify compounds which bind to GPCR polypeptides and in screening
 CC for compounds that modulate GPCR activity. By screening a human subject
 CC for the presence of mutations in GPCR DNA, a GPCR-related disorder or a
 CC genetic predisposition can be diagnosed. The sequences can also be used
 CC for treatment and prevention of mental disorders such as schizophrenia,
 CC attention deficit disorder, anxiety, depression, dementia and bipolar
 CC disorder, neurological disorders such as Huntington's disease,
 CC Parkinson's disease and Tourette's syndrome, metabolic disorders such as
 CC obesity, anorexia and type 2 diabetes, cardiovascular disorders such as
 CC thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,
 CC viral infections caused by HIV and cancers

SO Sequence 19 BP; 7 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3638 AGGAGGTAGTGGGAG 3655
 1 AGCAGGTAGTGGGAG 18

RESULT 2956
 AAC83562
 ID AAC83562 standard; DNA; 19 BP.
 XX
 AC AAC83562;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE DNA synthesis method linker/primer sequence SEQ ID NO: 1.
 XX
 KW DNA synthesis; directional complementary DNA library; linker; PCR primer;
 KW ss.
 KW
 XX
 OS Synthetic.
 XX
 PN US6143531-A.
 PD
 XX 07-NOV-2000.
 PF
 XX 22-JUL-1997; 97US-00899029.
 XX
 PR 19-SEP-1988; 88US-00246567.
 PR 02-MAY-1991; 91US-00700066.
 PR 23-NOV-1992; 92US-00981931.
 PR 02-SEP-1993; 93US-00116049.
 XX
 PA (STRA-) STRATAGENE.
 XX
 PI Hansen CJ, Huse WD;
 XX WPI; 2001-006435/01.
 DR
 XX Double stranded DNA synthesis with specific orientation comprises
 PT synthesizing a first strand of DNA complementary to a selected DNA or RNA
 PT template and synthesizing second strand complementary to first one.
 XX
 PS Example 1; Fig 1; 14pp; English.
 XX
 CC The present invention describes an improved method of DNA synthesis which
 CC provides double stranded DNA where the predetermined orientation of the
 CC sequence is preserved. This can be used in the construction of
 CC complementary DNA and directional DNA libraries

XX	Seq	Sequence	19 BP; 1 A, 2 C, 2 G, 14 T, 0 U, 0 Other;
XX	Query Match		0.2%; Score 14.8; DB 1; Length 19;
XX	Best Local Similarity	88.9%;	Ped. No. 1.9e+03;
XX	Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0
OY		4459	TGGACTTTTTTTTTTTT 4476
DB		2	TGCACTTTTTTTTTTTT 19
RESULT 2957			
AAH61067			
ID	AAH61067	standard; DNA; 19 BP.	
AC	AAH61067;		
XX			
DT	10-SEP-2001	(first entry)	
XX			
DE	Cdc35 hs ribozyme binding site SEQ ID NO:3491.		
XX			
KW	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;		
KW	recognition site; target; ribozyme binding site; eye disease; vulnery;		
KW	proliferative diseases; skin disease; psoriasis; diabetic retinopathy;		
KW	cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;		
KW	matrix metalloproteinase; growth factor; reductase; scarring; cyostatic;		
KW	antipsoriatic; dermatologic; antiseborrheic; antiabetic; virucide;		
KW	antisickling; ophthalmological; keratolytic; gene therapy; viral wart;		
KW	atopic dermatitis; actinic keratosis; squamous cell carcinoma;		
KW	basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;		
KW	sickle cell retinopathy; ss.		
OS	Homo sapiens.		
OS	Synthetic.		
PN	WO200130362-A2.		
XX			
PD	03-MAY-2001.		
PF	26-OCT-2000; 2000MO-US029500.		
XX			
PR	26-OCT-1999; 99US-0161532P.		
XX			
PA	(IMMU-) IMMUSOL INC.		
PI	Robbins JM, Tritz R;		
DR	WTI; 2001-300427/31.		
XX			
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes		
PT	that cleave RNA encoding cytokines involved in inflammation, matrix		
PT	metalloproteinases, growth factors and cell-cycle dependent kinases.		
PS			
XX	Example 1; Page 325; 408pp; English.		
CC	The present invention describes a method for treating a proliferative		
CC	skin or eye disease and scarring. The method involves administering a		
CC	ribozyme (I) which cleaves RNA encoding a cytokine involved in		
CC	inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle		
CC	dependent kinase, growth factor or a reductase, or administering a		
CC	nucleic acid molecule (II) comprising a promoter operably linked to a		
CC	nucleic acid segment encoding (I). (I) can have antipsoriatic,		
CC	dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,		
CC	ophthalmological, vulnerary, keratolytic and virucide activities, and		
CC	cleaves RNA encoding cytokine involved in inflammation. (I) can be used		
CC	in gene therapy. (I) and (II) are useful for treating proliferative skin		
CC	diseases such as psoriasis, atopic dermatitis, actinic keratosis,		
CC	squamous or basal cell carcinoma and viral or seborrheic wart. They can		
CC	also be used for treating proliferative eye diseases such as diabetic		
CC	retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of		
CC	prematurity and retinal detachment, and for treating and preventing		
CC	scarring such as keloid, adhesion and hypertrophic or hypertrophic burn		

CC	scar.	AAH57577	to AAH62099	represent sequences used in the
CC	exemplification	of the present invention		
XX				
SO	Sequence	19 BP; 3 A; 8 C; 1 G; 7 T; 0 U; 0 Other;		
OY	Query Match	0.2%; Score 14.8; DB 1; Length 19;		
	Best Local Similarity	88.9%; Pred. No. 1.9e+03;		
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Dd	1215 TACCTACTTCCCTAGA 1232			
	1 TACCTCCTTTCCCTAGA 18			
RESULT 2958				
AAH57652/C				
ID	AAH57652 standard; DNA; 19 BP.			
AC				
XX	AAH57652;			
DT	10-SEP-2001 (first entry)			
DE	Cell-cycle dependent kinase cdk1 ribozyme binding site SEQ ID NO:76.			
XX				
KW	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;			
KW	recognition site; target; ribozyme binding site; eye disease; vulnery;			
KW	proliferative disease; skin disease; psoriasis; diabetic retinopathy;			
KW	cyclokin; inflammation; cell-cycle dependent kinase; cyclin; MMP;			
KW	matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;			
KW	antiprolastic; dermatological; antiseborrheic; antidiabetic; virucide;			
KW	antisickling; ophthalmological; keratolytic; gene therapy; viral wart;			
KW	atopic dermatitis; actinic keratosis; squamous cell carcinoma;			
KW	basal cell carcinoma; seborehic wart; vitreoretinopathy; scar;			
KW	sickle cell retinopathy; ss.			
OS	Homo sapiens.			
OS	Synthetic.			
XX				
PN	WO200130362-A2.			
PD	03-MAY-2001.			
XX				
PF	26-OCT-2000; 2000WO-US029500.			
XX				
PR	26-OCT-1999; 99US-0161532P.			
XX				
PA	(IMMU-) IMMUSOL INC.			
XX				
PI	Robbins JM, Tritz R;			
XX				
DR	WPI; 2001-300427/31.			
XX				
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes			
PT	that cleave RNA encoding cytokines involved in inflammation, matrix			
PT	metalloproteinases, growth factors and cell-cycle dependent kinases.			
XX				
PS	Example 1; Page 77; 408bp; English.			
XX				
CC	The present invention describes a method for treating a proliferative			
CC	skin or eye disease and scarring. The method involves administering a			
CC	ribozyme (I) which cleaves RNA encoding a cytokine involved in			
CC	inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle			
CC	dependent kinase, growth factor or a reductase, or administering a			
CC	nucleic acid molecule (II) comprising a promoter operably linked to a			
CC	nucleic acid segment encoding (I). (I) can have antiprolastic;			
CC	dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,			
CC	ophthalmological, vulnerary, keratolytic and virucide activities, and			
CC	cleaves RNA encoding cytokine involved in inflammation. (I) can be used			
CC	in gene therapy. (I) and (II) are useful for treating proliferative skin			
CC	diseases such as psoriasis, atopic dermatitis, actinic keratosis,			
CC	squamous or basal cell carcinoma and viral or seborehic wart. They can			
CC	also be used for treating proliferative eye diseases such as diabetic			
CC	retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of			

CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX

SO Sequence 19 BP; 9 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6736 CTTCCTCTTAATCG 6753
Db 19 CTTCCTTTTGAATCTG 2

RESULT 2959
AAH61066
ID AAH61066 standard; DNA; 19 BP.
XX
AC AAH61066;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3490.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KM recognition site; target; ribozyme binding site; eye disease; vulnery;
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KM matrix metalloproteinase; growth factor; reductase; scarring; cytosolic;
KM antiproliferative; dermatological; antiseborrheic; antidiabetic; vitruide;
KM anti-bleeding; ophthalmological; keratolytic; gene therapy; viral wart;
KM atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KM basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
KM sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
FI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 325; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiseborrheic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,
CC ophthalmological, vulnery, keratolytic and vitruide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seboreic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX

SO Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1215 TACCTACCTCCCTAGA 1232
Db 2 TACCTCCTTCCCTAGA 19

RESULT 2960
AAS09985
ID AAS09985 standard; DNA; 19 BP.
XX
AC AAS09985;
XX
DT 24-OCT-2001 (first entry)
XX
DE PCR primer P4 used in RT-PCR-SSCP of PAX2 exon 8.
XX
XX PAX2; mouse; PCR primer; nervous system; excretory system;
KM optic nerve coloboma; renal hyperplasia; apoptosis; chemotherapy;
KM radiation therapy; cancer; prostate; ovary; bladder; kidney;
KM cystic kidney disease; ss.
XX
XX Nhs musculus.
XX
PN WO200146405-A2.
XX
XX 28-JUN-2001.
XX
PD 21-DEC-2000; 2000WO-CA001545.
XX
PF 22-DEC-1999; 99US-0171443P.
XX
PR 24-JUL-2000; 2000US-0220161P.
XX
PA (UYMC-) UNITV MCGILL.
XX
PI (UYOT-) UNITV OTAGO.
XX
PI Goodyer P, Eccles RM, Torban E;
XX
DR WPI; 2001-441672/47.
XX
XX
XX The sequence represents PCR primer P4 used in reverse transcription PCR
CC single strand conformation polymorphism (RT-PCR-SSCP) of PAX2 exon 8.
CC PAX2 is a transcription factor involved in the development of the nervous
CC and excretory systems and mutations of PAX2 have been associated with
CC optic nerve colobomas and renal hyperplasia. These mutations are
CC associated with increased apoptosis. The method of the invention involves
CC modulating resistance to apoptosis, rescuing cells from apoptosis, and
CC enhancing resistance of normal tissues to apoptotic cell death induced by
CC chemotherapy or radiation therapy. This is achieved by administering to a
CC patient, a nucleic acid (I) encoding a molecule which selectively
CC inhibits and/or prevents the function of the PAX2 gene. The method can be
CC used to modulate resistance to apoptosis of cancer cells (prostate,
CC ovarian, bladder, kidney cancer cells and/or cystic kidney diseases) or
CC cystic kidney cells in a patient in which PAX2 is expressed at higher
CC level than in a healthy patient, for rescuing cells from apoptosis in a

CC patient, and for enhancing resistance of normal tissues to apoptotic cell
 CC death induced by chemotherapy or radiation therapy. (1) is also useful
 CC for treating cancer in a cystic kidney disease in a patient
 XX

Sequence 19 BP; 3 A; 1 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2872 AGGAGGAGTGTGGGTAG 2889

Db 2 AGGGTGGAGTGGGTAG 19

RESULT 2961

ABL88900

ABL88900 standard; DNA; 19 BP.

AC ABL88900;

DT 22-MAY-2002 (first entry)

XX HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO.122.

XX Binding molecule; HIV-1; human immunodeficiency virus type 1;

XX reverse transcriptase; binding group; ss.

OS Human immunodeficiency virus 1.

XX Synthetic.

XX EPI174518-A1.

XX 23-JAN-2002.

XX 20-JUL-2000; 2000EP-00202611.

XX 20-JUL-2000; 2000EP-00202611.

XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.

XX Loukachov VV, Van Gemen B, Goudamit J;

XX WPI; 2002-156696/21.

XX Collection of binding groups for determining or typing samples,

XX especially clinical samples, has groups capable to identify essentially

XX all members of the family of nucleic acids of relatively high

XX significance.

XX Disclosure; Page 36; 16pp; English.

XX The present invention describes a collection of binding groups for a

XX family of nucleic acids comprising members of relative high and relative

XX low significance, where the binding groups are selected to be capable to

XX identify, alone or in combination, essentially all members of the family

XX of nucleic acids of relatively high significance. The collection of

XX binding groups is useful for typing of nucleic acid in a clinical sample,

XX by contacting the nucleic acid with the collection and determining

XX whether one or more binding groups bound to the nucleic acid of the

XX sample. This method is useful for determining whether the sample

XX comprises at least a part of a member of relatively high significance of

XX a family of nucleic acids. The collection of binding groups is useful for

XX diagnosing the severity of a disease caused by a pathogen containing a

XX member of a family of nucleic acids. ABL88779 to ABL89321 represent

XX oligonucleotide sequences used in the exemplification of the present

XX invention

XX Sequence 19 BP; 12 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 19;

XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6170 CATTAAGAGAAAGAGTG 6187

Db 2 CATTAAGAGAAAGAGAG 19

RESULT 2962

ABA97625/C

ABA97625 standard; DNA; 19 BP.

AC ABA97625;

DT 11-APR-2002 (first entry)

XX Probe d.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

XX JP2001286300-A.

XX 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

XX 24-AUG-1999; 99JP-00236666.

XX 30-AUG-1999; 99JP-00242693.

XX 01-FEB-2000; 2000JP-00028896.

XX (BIOT-) BIOINDUSTRIY KYOKAI SH.

XX (KANK-) KANKYO ENG KK.

XX (KEIZ-) KEIZAI SANGYOUSHO SANGYO GIYUTSU SOGO KEN.

XX WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

XX the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

XX nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

XX decreases the fluorescence of the fluorochrome when hybridised with a

XX target nucleic acid, the decrease in the fluorescence is measured. The

XX method can be used for measuring a target nucleic acid

XX Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 19;

XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6682 TTATTTTATTTATATAT 6699

Db 19 TTTTATTTTATTTATAT 2

RESULT 2963

AA151775/C

AA151775 standard; DNA; 19 BP.

AC AA151775;

DT 24-APR-2003 (first entry)

XX TNF alpha PCR primer #2.

XX Screening; G protein-coupled receptor; cholesterol metabolism; ss;

XX inflammatory disease; transplantation rejection; immune insufficiency;

XX infection; PCR; primer; TNF alpha.

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OS Unidentified.
XX
XX WO200284286-A1.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-JP003513.
XX
XX 12-APR-2001; 2001JP-00114203.
XX 14-JUN-2001; 2001JP-00180562.
XX 16-JUL-2001; 2001JP-00214922.
XX 27-DEC-2001; 2001JP-00397767.
XX 22-FEB-2002; 2002JP-00045728.
XX
XX (TAKES ) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fujii R, Kawamata Y, Miwa M, Hosoya M,
XX
XX WPI; 2003-075569/07.
XX
XX
XX Screening method for agonists or antagonists to alter binding properties
XX of novel G protein-coupled receptor protein in controlling cholesterol
XX metabolism, used to diagnose and treat inflammatory diseases or
XX infections.
XX
XX Disclosure; Page 174; 186pp; Japanese.
XX
XX The invention comprises a method for screening for compounds that are
XX capable of changing the binding properties of a G protein-coupled
XX receptor protein. The method of the invention is useful for screening
XX agonists or antagonists to alter binding properties of novel G protein-
XX coupled receptor proteins in controlling cholesterol metabolism. The
XX method of the invention is useful in the diagnosis and treatment of
XX inflammatory diseases, excessive immune reaction after transplantation,
XX immune insufficiency and infections. The present DNA sequence represents
XX a TNF alpha PCR primer
XX
XX Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1269 GAAGCTGACGACGACCA 1286
XX 18 GAAGCTGACGACCA 1
XX
XX RESULT 2964
XX ADA25292/c
XX ID ADA25292 standard; RNA; 19 BP.
XX
XX ADA25292;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human PKC-alpha short interfering nucleic acid target SEQ ID NO:23.
XX
XX short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
XX RNA interference; cytostatic; vasotrophic; nephrotropic; modulation;
XX inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
XX prostate cancer; glioblastoma; proliferative disease; restenosis;
XX polycystic kidney disease; human; ribozyme; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070983-A1.
XX
XX 28-AUG-2003.
XX
XX 11-FEB-2003; 2003WO-US004034.
XX

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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 18-SEP-2002; 2002US-0411707P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Ncswigen J, Beigelman L,
XX
XX WPI; 2003-679891/54.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer and restenosis, downregulates expression of the
XX protein kinase C-alpha gene.
XX
XX Example 3; Page 118; 143pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
XX that downregulates expression of a protein kinase C-alpha (PKC-alpha)
XX gene by RNA interference. Also described: (1) a siNA that modulates
XX expression and/or activity of genes for other isoforms of PKC or genes
XX involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
XX siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
XX express siNA. The siNA sequences have cytostatic, vasotropic and
XX nephrotropic activities, and can be used in the modulation (inhibition)
XX of expression of the PKC-alpha gene by RNA interference. The siNA can be
XX used to modulate expression of PKC-alpha genes. They are potentially
XX useful in treating a variety of cancers including e.g. breast cancer,
XX cancers of the head and neck, ovarian cancer, lung cancer, prostate
XX cancer, and glioblastoma and for treating other proliferative diseases
XX and conditions, such as restenosis and polycystic kidney disease. The
XX siNA may also be useful for diagnosis, drug screening, target
XX identification and validation, genetic engineering, studying gene
XX function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
XX The present sequence represents a human PKC-alpha siNA target, which is
XX used in the exemplification of the present invention.
XX
XX Sequence 19 BP; 6 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3937 TCCCTTGATGCTAAGTC 3954
XX 19 TCCCTTGATGATTAAGTC 2
XX
XX RESULT 2965
XX ADA25417
XX ID ADA25417 standard; RNA; 19 BP.
XX
XX ADA25417;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human PKC-alpha short interfering nucleic acid SEQ ID NO:148.
XX
XX short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
XX RNA interference; cytostatic; vasotropic; nephrotropic; modulation;
XX inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
XX prostate cancer; glioblastoma; proliferative disease; restenosis;
XX polycystic kidney disease; human; ribozyme; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070983-A1.
XX

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PD 28-AUG-2003.
 XX 11-FEB-2003; 2003WO-US004034.
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 18-SEP-2002; 2002US-0411707P.
 PR 15-JAN-2003; 2003US-0440129P.
 PA (SIRN-) SIRNA THERAPEUTICS INC.
 PA Mcswigen J, Beigelman L;
 PI WPI; 2003-679891/64.
 DR New short interfering nucleic acid, useful e.g. for treatment and
 XX diagnosis of cancer and restenosis, downregulates expression of the
 PT protein kinase C-alpha gene.
 PT
 XX
 PS Example 3; Page 118; 143pp; English.
 XX
 CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a protein kinase C-alpha (PKC-alpha)
 CC gene by RNA interference. Also described: (1) a siNA that modulates
 CC expression and/or activity of genes for other isoforms of PKC or genes
 CC involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
 CC siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
 CC express siNA. The siNA sequences have cytostatic, vasotropic and
 CC nephroretropic activities, and can be used in the modulation (inhibition)
 CC of expression of the PKC-alpha gene by RNA interference. The siNA can be
 CC used to modulate expression of PKC-alpha genes. They are potentially
 CC useful in treating a variety of cancers including e.g. breast cancer,
 CC cancers of the head and neck, ovarian cancer, lung cancer, prostate
 CC cancer, and glioblastoma and for treating other proliferative diseases
 CC and conditions, such as restenosis and polycystic kidney disease. The
 CC siNA may also be useful for diagnosis, drug screening, target
 CC identification and validation, genetic engineering, studying gene
 CC function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
 CC The present sequence represents a human PKC-alpha siNA, which is used in
 CC the exemplification of the present invention.
 CC
 XX
 SQ Sequence 19 BP; 4 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 61.1%; Pred. No. 1.9e+03;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3937 TCCCTTGATGCTCAAGTC 3954
 Db 1 UCCCUUGAGUAGUAAAGUC 18
 RESULT 2966
 ID ADE27307 standard; RNA; 19 BP.
 XX ADE27307;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX
 DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:251.
 XX
 KW short interfering nucleic acid; siNA, downregulation; inhibition; SCD;
 KW stearyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
 KW antiatherosclerotic; cytostatic; virucide; obesity; diabetes;
 KW atherosclerosis; cancer; viral infection; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 OS Synthetic.

XX
 PN WO2003070885-A2.
 XX 28-AUG-2003.
 PD
 XX 13-FEB-2003; 2003WO-US004034.
 PF
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 20-SEP-2002; 2002US-0412304P.
 PR 15-JAN-2003; 2003US-0440129P.
 PA (RIBO-) RIBOZYME PHARM INC.
 PA Mcswigen J, Beigelman L, Thompson J;
 PI WPI; 2003-721687/68.
 DR New short interfering nucleic acid, useful e.g. for treatment and
 XX diagnosis of obesity or diabetes, downregulates expression of the
 PT stearyl-CoA desaturase gene.
 PT
 XX
 PS Example 3; SEQ ID NO 251; 139pp; English.
 XX
 CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
 CC by RNA interference. Also described: (1) modulating expression of SCD
 CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
 CC siNAs have anorectic, antidiabetic, antiatherosclerotic, cytostatic and
 CC virucide activities. The siNAs can be used to modulate expression of SCD
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
 CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
 CC They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents an SCD siNA, which is
 CC used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 19 BP; 1 A; 0 C; 3 G; 0 T; 15 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 5.6%; Pred. No. 1.9e+03;
 Matches 1; Conservative 15; Mismatches 2; Indels 0; Gaps 0;
 QY 4471 TTTTCTTTTCTTCTT 4488
 Db 1 UUUUUUUUUUUUGGCUU 18
 RESULT 2967
 ID ADE27597/c standard; RNA; 19 BP.
 XX ADE27597;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX
 DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:541.
 XX
 KW short interfering nucleic acid; siNA, downregulation; inhibition; SCD;
 KW stearyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
 KW antiatherosclerotic; cytostatic; virucide; obesity; diabetes;
 KW atherosclerosis; cancer; viral infection; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 OS Synthetic.

```
PN WO2003070865-A2.
XX
XX 28-AUG-2003.
PD
XX
XX 13-FEB-2003; 2003WO-US004317.
PF
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Mcswiggen J, Belgelman L, Thompson J;
PI
XX WPI; 2003-721687/68.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearyl-CoA desaturase gene.
XX
XX Example 3; SEQ ID NO 541; 139pp; English.
PS
XX
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 15 A; 3 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4471 TTTTCTTTTCTCTT 4488
DB 19 TTTTCTTTTCTCTT 2
RESULT 2968
AAN81957/c
ID AAN81957 standard; DNA; 20 BP.
XX
XX AAN81957;
AC
XX
XX 25-MAR-2003 (revised)
DT 22-OCT-1990 (first entry)
XX
DE Probe pool LFI to detect Human Lymphocyte Function Associated Antigen-3.
XX
XX Lymphocyte function associated antigen-3; adhesion inhibition; probe;
KM T-lymphocytes; immune suppression; ss.
XX
XX Synthetic.
XX
XX WO8809820-A.
PN
XX 15-DEC-1988.
PD
```

```
XX
XX 03-JUN-1988; 88WO-US001924.
PF
XX
XX 03-JUN-1987; 87US-00057615.
PR
XX
XX (BIOJ ) BIOGEN NV.
PA (DAND ) DANA FARBER CANCER INST.
PA (DAND ) DANA FARBER CANCER INST INC.
PA (DAND ) DANA FARBER CANCER INST INC.
XX
XX Wallner BP, Springer TA, Hession C, Tizard R, Mattaliano R;
XX WPI; 1988-368634/51.
DR
XX
XX DNA sequences encoding Lymphocyte Function Associated Antigen-3 - which
PT inhibits adhesion between T-lymphocytes and target cells.
PT
XX Disclosure; Page 7; 46pp; English.
PS
XX
XX Probe pool LFI is a 32-fold degenerate 20-mer. Probe was labelled with
CC gamma-32P-ATP and polynucleotide kinase. It was used together with pool
CC LFI2 (AAN81958) for screening libraries. See also AAN81956-N81958; esp.
CC AAN81958. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
SQ Sequence 20 BP; 1 A; 3 C; 1 G; 10 T; 0 U; 5 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 65.0%; Pred. No. 2e+03;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 6344 AACATTAAGCCGAGAGAGGT 6363
DB 20 AATGGAACACCAAAAGAGT 1
RESULT 2969
AAQ03650
ID AAQ03650 standard; DNA; 20 BP.
XX
XX AAQ03650;
AC
XX
XX 25-MAR-2003 (revised)
DT 07-AUG-1990 (first entry)
XX
XX Probe NN-D for use in Church-Gilbert sequencing of cDNA encoding PI-
DE linked LFA-3.
XX
XX PI-linked lymphocyte function associated antigen 3 polypeptide;
KM phage lambda P24; T-cells; autoimmune disease; graft versus host disease;
KM allograft rejection; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9002181-A.
PN
XX
XX 08-MAR-1990.
PD
XX
XX 24-AUG-1989; 89WO-US003652.
PF
XX
XX 26-AUG-1988; 88US-00237309.
PR
XX
XX (BIOJ ) BIOGEN INC.
PA
XX
XX Wallner BP, Hession C;
PI
XX
XX WPI; 1990-099405/13.
DR
XX
XX New DNA sequences and recombinant DNA - expressing PI-1-linked lymphocyte
PT function associated antigen-3 polypeptide.
PT
XX Disclosure; Fig 5; 34pp; English.
XX
```

CC Probe NN-D for was used along with 3 other 20-nucleotide long probes, and
 CC NotI digestion, for sequencing by Church-Gilbert approach, of the ends of
 CC an inserted sequence in pNN01. This plasmid is a subclone of P24 contg.
 CC cDNA encoding PI-linked LFA-3. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 CC XX

SQ Sequence 20 BP; 3 A; 1 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

OY 7307 CTTTGAGATTGTGTGTTG 7324
 Db 1 CTTTGAGATTGTGTGTTG 18

RESULT 2970
 AAQ03648/C
 ID AAQ03648 standard; DNA; 20 BP.

AC AAQ03648;

DT 25-MAR-2003 (revised)
 DT 07-AUG-1990 (first entry)

DE Probe NN-B for use in Church-Gilbert sequencing of cDNA encoding PI-
 DE linked LFA-3.

KW PI-linked lymphocyte function associated antigen 3 polypeptide;
 KW phage lambda P24; T-cells; autoimmune disease; graft versus host disease;
 KW allograft rejection; ss.

OS Homo sapiens.

PN WO9002181-A.

PD 08-MAR-1990.

PP 24-AUG-1989; 89WO-US003652.

PR 26-AUG-1988; 88US-00237309.

PA (BIOJ) BIOGEN INC.

PI Wallner BP, Hession C;

DR WPI; 1990-099405/13.

PT New DNA sequences and recombinant DNA - expressing PI-linked lymphocyte
 PT function associated antigen-3 polypeptide.

PS Disclosure; Fig 5; 34pp; English.

CC Probe NN-B for was used along with 3 other 20-nucleotide long probes, and
 CC NotI digestion, for sequencing by Church-Gilbert approach, of the ends of
 CC an inserted sequence in pNN01. This plasmid is a subclone of P24 contg.
 CC cDNA encoding PI-linked LFA-3. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 CC XX

SQ Sequence 20 BP; 8 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

OY 7307 CTTTGAGATTGTGTGTTG 7324
 Db 20 CTTTGAGATTGTGTGTTG 3

RESULT 2971
 AAQ03651/C

ID AAQ03651 standard; DNA; 20 BP.

AC AAQ03651;

DT 25-MAR-2003 (revised)

DT 07-AUG-1990 (first entry)

DE Probe LF-1 for cDNA encoding PI-linked LFA-3 (3'-5').

KW PI-linked lymphocyte function associated antigen 3 polypeptide;
 KW phage lambda P24; T-cells; autoimmune disease; graft versus host disease;
 KW allograft rejection; ss.

OS Homo sapiens.

PN WO9002181-A.

PD 08-MAR-1990.

PP 24-AUG-1989; 89WO-US003652.

PR 26-AUG-1988; 88US-00237309.

PA (BIOJ) BIOGEN INC.

PI Wallner BP, Hession C;

DR WPI; 1990-099405/13.

PT New DNA sequences and recombinant DNA - expressing PI-linked lymphocyte
 PT function associated antigen-3 polypeptide.

PS Disclosure; Fig 5; 34pp; English.

CC Probe LF-1 is a 32-fold degenerate 20-mer derived from the sequence of
 CC LFA-3 purified from human erythrocytes. The probe was used to screen
 CC libraries of PBL cDNA for clones encoding PI-linked LFA-3. (Updated on 25
 CC -MAR-2003 to correct PA field.)
 CC XX

SQ Sequence 20 BP; 1 A; 3 C; 1 G; 10 T; 0 U; 5 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 65.0%; Pred. No. 2e+03; Mismatches 5; Indels 0; Gaps 0;

OY 6344 AACATAAGCCGAAGAGT 6363
 Db 20 AAYAGRAARACRAARAAGT 1

RESULT 2972
 AAQ14994/C
 ID AAQ14994 standard; DNA; 20 BP.

AC AAQ14994;

DT 24-FEB-1992 (first entry)

DT 07-AUG-1990 (first entry)

DE Oligonucleotide #9 for modulating HIV-1 gag/pol frameshifting.

KW human immunodeficiency virus; phosphorothioate linkage; retrovirus;
 KW ribosomal frame shift; gag; pol; fusion protein; ss.

OS Synthetic.

PN WO9117246-A.

PD 14-NOV-1991.

PP 04-MAY-1990; 90US-00518929.

PR 04-MAY-1990; 90US-00518929.

XX

PA (ISIS-) ISIS PHARM INC.
XX Ecker DJ;
XX WPI; 1991-353768/48.
XX
PT Modulating gene expression for HIV treatment - comprises binding
PT oligonucleotide(s) to RNA portions which have sec. structure.
XX
XX Example 3; Page 26; 40pp; English.
XX
XX This oligonucleotide and its analogue, having phosphorothioate bonds,
CC were designed to specifically bind to the gag-pol frameshift region and
CC interfere with translation and/or frameshifting. There is potential for
CC significant RNA secondary structure near the site of frameshifting in HIV
CC -1. The inhibitory effect of the oligo and its analogue has not yet been
CC determined
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1178 ATCTGCGCTGCTACAG 1195
DB 19 ATCTGCGCTGCTACAG 2

RESULT 2973
AAQ29648/c
ID AAQ29648 standard; DNA; 20 BP.
XX
AC AAQ29648;
XX
XX 25-MAR-2003 (revised)
DT 16-MAR-1993 (first entry)
XX
DE PCR primer #55 for identifying Hepatitis C virus.
XX
XX Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening; PCR;
KM primer; polymerase chain reaction; ss.
XX
XX Hepatitis C virus.
OS
XX
XX EBS10952-A1.
PN
XX
XX 28-OCT-1992.
PD
XX
XX 23-APR-1992; 92EP-00303625.
PF
XX
XX 26-APR-1991; 91JP-00191376.
PR
XX
XX (IMMO) IMMUNO JAPAN INC.
PA
XX
XX Okamoto H, Nakamura T;
PI
XX
XX WPI; 1992-359137/44.
DR
XX
XX Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide
PT primers with nucleotide sequences corresp. to part. of the viral RNA.
XX
XX Disclosure; Page 36; 54pp; English.
PS
XX
XX This PCR primer was used with AAQ29645 to detect the presence of
CC Hepatitis C viral RNA in a sample. (Updated on 25-MAR-2003 to correct PN
CC field.)
CC
XX
SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2943 AACAGGCGCAGCAAGCA 2960
DB 20 AGCAGGCGCAGCAAGAA 3

RESULT 2974
AAQ24460/c
ID AAQ24460 standard; DNA; 20 BP.
XX
XX AAQ24460;
AC
XX
XX 09-NOV-1992 (first entry)
DT
XX
XX NANB hepatitis virus primer 9.
DE
XX
XX non-A, non-B hepatitis virus; NANBH; HC-J5; PCR;
KM amplification polymerase chain reaction; ss.
XX
XX
XX Non-A.
OS
XX non-B hepatitis virus.
OS
XX
XX EP485209-A.
PN
XX
XX 13-MAY-1992.
PD
XX
XX 07-NOV-1991; 91EP-00310297.
PF
XX
XX 08-NOV-1990; 90JP-00304405.
PR
XX
XX (IMMO) IMMUNO JAPAN INC.
PA
XX
XX Okamoto H, Nakamura T;
PI
XX
XX WPI; 1992-160959/20.
DR
XX
XX Recombinant cDNA of NANBH virus strain HC-J5 and corresp. peptides -
PT useful for diagnosis and in vaccines and immunological pharmaceuticals.
XX
XX
XX Disclosure; Page 7; 42pp; English.
PS
XX
XX The sequences given in AAQ24460 and AAQ24461 are PCR primers which are
CC used to amplify the 5' region of non-A, non-B hepatitis virus (NANBH)
CC strain HC-J5. These probes amplify the region corresponding to
CC nucleotides 867-1154 of the entire nucleotide sequence and were used to
CC produced clones C5164, C5303 and C5331. The nucleotide sequences derived
CC from this amplification can be used to detect NANBH infection which
CC could not be detected by conventional methods. The detection kits allow
CC highly specific and sensitive detection at an early phase of infection
XX
SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2943 AACAGGCGCAGCAAGCA 2960
DB 20 AGCAGGCGCAGCAAGAA 3

RESULT 2975
AAQ31484/c
ID AAQ31484 standard; DNA; 20 BP.
XX
XX AAQ31484;
AC
XX
XX 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
XX NANB hepatitis virus PCR primer #55.
DE
XX
XX Polymerase chain reaction; non-A non-B hepatitis; detection; ss.

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XX OS Synthetic.
XX PN BP516270-A2.
XX PD 02-DEC-1992.
XX PF 09-APR-1992; 92EP-00303186.
XX PR 10-APR-1991; 91JP-00196175.
XX PA (IMMO ) IMMUNO JAPAN INC.
XX PI Okamoto H, Nakamura T;
XX DR WP1; 1992-400636/49.
XX PT Non-A, non-B hepatitis virus related antigens, their polynucleotide(s)
XX PT and antibodies - are useful for detecting NANBH virus in blood samples
XX PT intended for transfection.
XX PS Example; Page 6; 23pp; English.
XX CC The sequence is that of PCR primer #55 which was used to determine the 5'
XX CC terminus sequence from nucleotides 867-1354 of non-A, non-B hepatitis
XX CC (NANBH) virus strain HC-J5. These nucleotide sequences encode structural
XX CC proteins of NANBH virus and these proteins can be analysed to locate and
XX CC provide polypeptides useful as antigens for detection of NANBH virus via
XX CC antibody-antigen complex detection. Mutants, variants or fragments of the
XX CC sequence can be used for very sensitive detection. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
   Best Local Similarity 88.9%; Pred. No. 2e+03;
   Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2943 AACGAGGCCACGACGACA 2960
   20 AGCAGGGCCACGACGAGAAA 3

RESULT 2976
AAQ43865/c
ID AAQ43865 standard; DNA; 20 BP.
XX AC AAQ43865;
XX PI
XX DR 21-OCT-1993 (first entry)
XX PT NANB hepatitis viral gene HC-OM PCR primer #55.
XX KM Non-A, non-B; virus; polymerase chain reaction; detection; sensitive;
XX KM specific; ss.
XX OS Synthetic.
XX PN JP05091884-A.
XX PD 16-APR-1993.
XX PF 10-APR-1991; 91JP-00196175.
XX PR 12-JUN-1990; 90JP-00153401.
XX PR 08-NOV-1990; 90JP-00304405.
XX PA (NAKA/) NAKAMURA T.
XX DR WP1; 1993-199637/25.
XX PT Antigen related to non-A and non-B hepatitis virus - comprises non-
XX PT translation region comprising 340 - 341 mole. of nucleotides, non-

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PT translation region comprising 1885 - 2551 mole. of nucleotides including
PT region 1,149 and, etc.
XX AC Example; Page 7; 73pp; Japanese.
XX CC The sequence is that of PCR primer #55 which was used in the
XX CC amplification by PCR of nucleotides 867-1354 of the non-A, non-B
XX CC hepatitis virus gene HC-OM
XX SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
   Best Local Similarity 88.9%; Pred. No. 2e+03;
   Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2943 AACGAGGCCACGACGACA 2960
   20 AGCAGGGCCACGACGAGAAA 3

RESULT 2977
AAQ74282/c
ID AAQ74282 standard; DNA; 20 BP.
XX AC AAQ74282;
XX DT 25-MAR-2003 (revised)
XX DT 12-JUN-1995 (first entry)
XX DE Amyloid precursor protein exon 14 forward PCR primer.
XX KM Amyloid precursor protein, APP; exon 14 PCR primer;
XX KM beta-amyloidosis animal models; Down's syndrome; Alzheimers disease;
XX KM yeast artificial chromosome; ss.
XX OS Synthetic.
XX PN W09423049-A2.
XX PD 13-OCT-1994.
XX PF 01-APR-1994; 94WO-US003619.
XX PR 02-APR-1993; 93US-00042390.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Gearhart JD, Lamb BT;
XX DR WP1; 1994-333207/41.
XX PT Introduction and expression of large genomic sequences in transgenic
XX PT animals - which may be used as animal models of beta-amyloidosis in
XX PT Alzheimer's disease and Down's syndrome.
XX PS Example 1; Page 24; 60pp; English.
XX CC AAQ74282 and AAQ74283 are the forward and reverse PCR primers for human
XX CC amyloid precursor protein (APP) exon 14, these were used to screen yeast
XX CC artificial chromosome (YAC) libraries for APP. Isolated APP clones were
XX CC then injected into blastocysts, from the same species as the embryonic
XX CC cells which contained the YAC library. Transgenic animals which could be
XX CC used as models of beta-amyloidosis (prevalent in individuals with Down's
XX CC syndrome and Alzheimers disease), were then generated from the injected
XX CC blastocysts. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
   Best Local Similarity 88.9%; Pred. No. 2e+03;
   Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 704 TGAGGCACTGGCATCA 721

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Db 19 TGAGGCATGCAATTC A 2

RESULT 2978
AAQ98015/c
ID AAQ98015 standard; DNA; 20 BP.
XX
AC AAQ98015;
XX
DT 25-MAR-2003 (revised)
DT 19-OCT-1995 (first entry)
XX
DE PNA oligomer targeting HIV gag/pol frameshift.
XX
KM Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
KM antiviral; antisense; triple helix; ss.
XX
OS Synthetic.
XX
FH Key Location/qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "at least one (and preferably all) of the backbone
subunits are composed of N-acetyl N-(2-aminoethyl)glycine
peptide residues, the nucleobase being attached
covalently to the acetyl group and the peptide linkage
being formed by condensation of the glycine carboxy group
of one residue with the amino group of the 2-aminoethyl
moiety in the next residue"

XX
FN W09504068-A1.
XX
XX 09-FEB-1995.
XX
PD
PF 28-JUL-1994; 94WC-US008517.
XX
XX 29-JUL-1993; 93US-00099718.
XX
XX (ISIS-) ISIS PHARM INC.
XX
PA
PI Ecker DJ;
XX
DR WPI; 1995-082179/11.
XX
XX
PT Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid
PT sub:unit - binds in complementary manner to DNA and RNA, and useful for
PT modulating HIV viral activity, e.g. in treating AIDS.
XX
XX
PS Claim 2; Page 177; 186pp; English.
XX
CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC of naturally occurring nucleobases covalently bound to a polyamide
CC backbone and (b) hybridise to the translation initiation AUG region, 5'
CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice
CC junctions or coding sequence of a human immunodeficiency virus gene
CC chosen from env, gag, pol, rev and tat. The PNAs can be used to target
CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene
CC regulation moieties. They have utility as gene-targeted drugs for
CC modulating HIV processes. Hence they can be used to treat AIDS and other
CC viral infections. They are also useful in diagnostic applications and as
CC research tools. PNA oligomers have high affinity for complementary single
CC stranded DNA. They are also able to form triple helices in which a first
CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the
CC resulting double helix or with the first PNA strand. The PNAs possess no
CC significant charge and are water soluble, which facilitates cellular
CC uptake. Further, since they contain amides of non-biological amino acids,
CC they are biostable and resistant to enzymatic degradation by proteases.
CC The present sequence is a specifically claimed PNA sequence (represented
CC by the sequence of nucleobases) targeting the HIV gag/pol frameshift.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1178 ATCTGCGCTGCTACAG 1195
DB 19 ATCTGCGCTTCTTACAG 2

RESULT 2979
AAT41212
ID AAT41212 standard; DNA; 20 BP.
XX
AC AAT41212;
XX
DT 03-DEC-1996 (first entry)
XX
DE Human gene signature HUMGS01132-derived anti-sense primer.
XX
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KM human; cloning; mapping; non-biased library; diagnosis; detection;
KM cell typing; abnormal cell function; primer; PCR; amplification;
KM polymerase chain reaction; ss.
XX
OS Synthetic.
XX
FN W09514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WC-JP001916.
XX
XX 12-NOV-1993; 93JP-00355504.
XX
XX (MATS/) MATSUBARA K.
XX (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
XX
PT Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT directed human cDNA library that reflects relative abundance of corresp.
PT mRNA in specific human tissues.
XX
XX
PS Example 7; Fig 8; 2245pp; Japanese.
XX
CC Primers T41001-T41382 are derived from novel human gene signature (GS)
CC sequences which did not match with sequences deposited in Genbank release
CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC libraries prepared from various human tissues; synthesis of cDNA was
CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC Each library is constructed so as to reflect accurately the relative
CC abundance of different mRNAs in the particular tissue from which it was
CC derived. The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS sequences)
CC as a means of diagnosing abnormal cell function or for recognising
CC different cell types. The primers T41211-2 amplify clone pm0647 which
CC comprises the GS HUMGS001132 (T20132), located on chromosome 20
XX
SQ Sequence 20 BP; 6 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1936 ATCTAGTCCACACCG 1953
DB 1 ATCTAGTCCACACCG 18

RESULT 2980

AAT28903
 ID AAT28903 standard; DNA; 20 BP.
 AC AAT28903;
 XX
 DT 10-FEB-1997 (first entry)
 XX
 DE Factor XIII subunit "a" gene, exon 1, forward primer.
 XX
 KM Primer: amplification; factor XIII "a" gene; deletion;
 KM splice donor/acceptor site; translational frameshift; substitution;
 KM nonsense mutation; transition; diagnosis; bleeding; haemorrhage;
 KM miscarriage; clot formation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9617953-A2.
 XX
 PD 13-JUN-1996.
 XX
 PF 07-DEC-1995; 95WO-GB002857.
 XX
 PR 08-DEC-1994; 94GB-00024823.
 XX
 PA (UTLE-) UNIV LEEDS.
 XX
 PI Markham AF;
 XX
 DR WPI; 1996-287196/29.
 XX
 PT Genetic study of Factor XIII activity - used for diagnosis and treatment
 PT of Factor XIII disorders, e.g. bleeding, haemorrhage, miscarriage or clot
 PT formation.
 XX
 PS Example; Table 1; 44pp; English.
 XX
 CC The sequences given in AAT28903-32 are primers which were used in the
 CC amplification of the exons of the factor XIII "a" gene. This allows
 CC analysis of the factor XIII gene and identification of differences in the
 CC gene sequence which are known to segregate with a reduction or
 CC enhancement of factor XIII activity. All fifteen exons were amplified
 CC from five unrelated families showing factor XIII disorders. The PCR
 CC products obtained for each exon of each individual were found to be of
 CC the expected size, indicating that there are no gross insertions or
 CC deletions in the factor XIII "a" gene of these patients. Three mutations
 CC which may be the cause of "a" subunit deficiency have been described. The
 CC first is a two base pair deletion at a splice donor acceptor site. This
 CC deletion does not grossly affect the splicing of the factor XIII pre
 CC mRNA, but causes a translational frameshift resulting in early
 CC translation termination. The second mutation is a G to A substitution at
 CC a splice donor site. The mechanism of how this mutation causes factor
 CC XIII deficiency is yet to be determined. The third mutation is a nonsense
 CC mutation in which a C to T transition at position 598, in an Arg codon,
 CC results in a stop codon TGA. A further eight mutations have been
 CC identified and include a deletion/insertion event, a nonsense mutation
 CC and missense/silent mutations. These primers may be used in the diagnosis
 CC and treatment of disorders involving factor XIII e.g. bleeding,
 CC haemorrhage, miscarriage or clot formation
 XX
 SO Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5294 TACTCCGACCAAGTT 5311
 1 TACTCCGACCAAGTT 18

Db 1 TACTCCGACCAAGTT 18

RESULT 2981
 AAT33418
 ID AAT33418 standard; cDNA; 20 BP.

XX
 AC AAT33418;
 XX
 DT 16-MAY-1997 (first entry)
 XX
 DE Human vascular endothelial growth factor antisense oligonucleotide.
 XX
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;
 KM degeneration; expression inhibitor; ss.
 XX
 OS Synthetic.
 XX
 PN WO9627006-A2.
 XX
 PD 06-SEP-1996.
 XX
 PF 29-FEB-1996; 96WO-US002840.
 XX
 PR 02-MAR-1995; 95US-00398945.
 XX
 PR 08-DEC-1995; 95US-00569926.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 PI Robinson GS;
 XX
 DR WPI; 1996-412773/41.
 XX
 PT Human vascular endothelial growth factor anti-sense oligonucleotide -
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced
 PT neovascularisation and angiogenesis associated disease states.
 XX
 PS Disclosure; Page 14; 92pp; English.
 XX
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the
 CC expression of human vascular endothelial growth factor (VEGF). The
 CC synthetic oligonucleotides contain phosphorothioate linkages and
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the
 CC expression of VEGF is useful in the treatment of hypoxia induced
 CC neovascularisation and angiogenesis associated disease states,
 CC retinopathy of prematurity, diabetic retinopathy and age related macular
 CC degeneration
 XX
 SO Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2402 CTGGGACCACTGAGACA 2419
 2 CTGGGACCACTGAGACA 19

Db 2 CTGGGACCACTGAGACA 19

RESULT 2982
 AAT33421
 ID AAT33421 standard; cDNA; 20 BP.
 XX
 AC AAT33421;
 XX
 DT 16-MAY-1997 (first entry)
 XX
 DE Human vascular endothelial growth factor antisense oligonucleotide.
 XX
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;
 KM degeneration; expression inhibitor; ss.
 XX
 OS Synthetic.
 XX
 PN WO9627006-A2.
 XX
 PD 06-SEP-1996.

XX 29-FEB-1996; 96WO-US002840.
 XX 02-MAR-1995; 95US-00398945.
 PR 08-DEC-1995; 95US-00569926.
 XX (HYBR-) HYBRIDON INC.
 XX PI Robinson GS;
 XX WPI; 1996-412773/41.
 DR Human vascular endothelial growth factor antisense oligo:nucleotide -
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced
 PT neovascularisation and angiogenesis associated disease states.
 XX PS Disclosure; Page 14; 92pp; English.
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the
 CC expression of human vascular endothelial growth factor (VEGF). The
 CC synthetic oligonucleotides contain phosphorothioate linkages and
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the
 CC expression of VEGF is useful in the treatment of hypoxia induced
 CC neovascularisation and angiogenesis associated disease states;
 CC retinopathy of prematurity, diabetic retinopathy and age related macular
 CC degeneration
 CC XX
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;
 QY 5921 CCCAGAGATGTCACCTG 5938
 DB 2 CCCAAGATGCCACCTG 19
 RESULT 2983
 AAT33412
 ID AAT33412 standard; cDNA; 20 BP.
 XX
 AC AAT33412;
 XX
 DT 16-MAY-1997 (first entry)
 XX
 DE Human vascular endothelial growth factor antisense oligonucleotide.
 XX
 KW Antisense; VEGF; vascular endothelial growth factor; hypoxia;
 KW neovascularisation; angiogenesis; metastasis; retinopathy; macular;
 KW degeneration; expression inhibitor; ss.
 XX
 OS Synthetic.
 XX
 PN WO9627006-A2.
 XX
 PD 06-SEP-1996.
 XX
 PF 29-FEB-1996; 96WO-US002840.
 XX
 PR 02-MAR-1995; 95US-00398945.
 PR 08-DEC-1995; 95US-00569926.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 PI Robinson GS;
 XX WPI; 1996-412773/41.
 DR Human vascular endothelial growth factor anti:sense oligo:nucleotide -
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced
 PT neovascularisation and angiogenesis associated disease states.
 XX

PS Disclosure; Page 14; 92pp; English.
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the
 CC expression of human vascular endothelial growth factor (VEGF). The
 CC synthetic oligonucleotides contain phosphorothioate linkages and
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the
 CC expression of VEGF is useful in the treatment of hypoxia induced
 CC neovascularisation and angiogenesis associated disease states;
 CC retinopathy of prematurity, diabetic retinopathy and age related macular
 CC degeneration
 CC XX
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;
 QY 5921 CCCAGAGATGTCACCTG 5938
 DB 2 CCCAAGATGCCACCTG 19
 RESULT 2984
 AAT48412
 ID AAT48412 standard; DNA; 20 BP.
 XX
 AC AAT48412;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Oligonucleotide H-14 specific for human VEGF nucleic acid.
 XX
 KW Vascular endothelial growth factor; inhibition; decrease; antisense;
 KW neovascularisation; retinopathy; age-related macular degeneration;
 KW diabetes; ss.
 XX
 OS Synthetic.
 XX
 PN WO9623065-A2.
 XX
 PD 01-AUG-1996.
 XX
 PF 26-JAN-1996; 96WO-US001189.
 XX
 PR 26-JAN-1995; 95US-00378860.
 XX
 PA (HYBR-) HYBRIDON INC.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Robinson GS, Smith LEH;
 XX WPI; 1996-362689/36.
 XX
 PT Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -
 PT for treatment of retinopathies and age-related macular degeneration.
 XX
 PS Disclosure; Page 12; 66pp; English.
 CC Neovascularisation can be reduced by blocking vascular endothelial growth
 CC factor (VEGF) expression using a synthetic oligonucleotide specific for
 CC VEGF. Inhibiting neovascularisation is useful for treatment of
 CC retinopathy of prematurity, diabetic retinopathy and age-related macular
 CC degeneration. The present sequence is an example of a suitable
 CC oligonucleotide specific for human VEGF
 CC XX
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;
 QY 5921 CCCAGAGATGTCACCTG 5938
 DB 2 CCCAAGATGCCACCTG 19

DR WP1; 1998-594573/50.

XX New isolated LDL-receptor related protein - used to develop products for
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT disorders, inflammation or Alzheimer's disease.

XX
PS Claim 12; Page 106; 200pp; English.

XX
CC The present invention describes LRP5 (low density lipoprotein (LDL)
CC receptor related protein, previously designated LRP-3). AAV85587 to
CC AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic
CC acid molecules (NMs) encoding LRP5 can be used for determining if an
CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).
CC The NMs or proteins can be used for reducing triglyceride levels in the
CC serum of an individual. Therapies that affect LRP5 may also be useful in
CC the treatment of autoimmune diseases such as glomerulonephritis, diseases
CC and disorders involving disruption of endocytosis and/or antigen
CC presentation, cytokine clearance and/or inflammation, viral infection,
CC pathogenic bacterial toxin contamination, elevation of free fatty acids
CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
CC disease and cardiovascular disease. Products from the present invention
CC can also be used for detection, diagnosis and drug screening

XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2075 GCCGATCTGCTGCTACTG 2092
|||||
1 GCCAAGACTGTGCTACTG 18

DB

RESULT 2988

AAV85871
ID AAV85871 standard; DNA; 20 BP.

XX
AC AAV85871;

XX
DT 10-FEB-1999 (first entry)

DE LRP5 SNP primer 58-8 1f.

XX
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX insulin dependent diabetes mellitus; autoimmune disease;
XX glomerulonephritis; inflammation; viral infection; osteoporosis;
XX hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX PCR primer; ss.

XX
XX Synthetic.

OS Homo sapiens.

OS
XX
XX WO9846743-A1.

PN
XX
XX 22-OCT-1998.

PD
XX
XX 15-APR-1998; 98WO-GB001102.

PF
XX
XX 15-APR-1997; 97US-0043553P.

PR
XX
XX 05-JUN-1997; 97US-0048740P.

PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.

XX
XX
XX Todd JA, Hese JM, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzger ML, Nakagawa Y;
PI Phillips MS, Twells RCF;
XX
XX WP1; 1998-594573/50.

DR
XX
XX New isolated LDL-receptor related protein - used to develop products for
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT disorders, inflammation or Alzheimer's disease.

disorders, inflammation or Alzheimer's disease.

Claim 12, Page 111, 200pp; English.

The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). AAV85823 to CC AAV85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid molecules (NMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM).

The NM or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving clearance of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and drug screening

Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2075 GCCGATCTGTGCTACTG 2092
||| |||||
1 GCCAAGACTGTGCTACTG 18

RESULT 2989
AAV52002
ID AAV52002 standard; DNA; 20 BP.
XX AC AAV52002;
XX XX AAV52002;
DT 02-FEB-1999 (first entry)
DE Zea mays genome reverse PCR primer #298.
XX Zea mays
XX polymorphic marker; allele-specific probe; amplification; PCR primer;
KW hybridisation; plant; hybrid certification; genetic contribution;
KM progeny; back-cross; hybrid; ancestry; corn; ss.
OS Synthetic.
OS Zea mays.
XX WO9824796-A1.
PN 11-JUN-1998.
PD 01-DEC-1997; 97WO-US021782.
PF 02-DEC-1996; 96US-0032069P.
PR 07-MAR-1997; 97US-00813507.
XX (AFRY-) AFFYMETRIX INC.
PA Lemieux B, Landry BS, Sapolsky RJ, Muirgoux A;
PI WPI; 1998-33352/29.
XX Braasica species allele-specific oligonucleotide probes and primers -
PT useful for plant breeding.
XX Example 1; Page 55; 65pp; English.
PS AAV51705-VS2008 are reverse PCR primers used to amplify fragments of the
CC Zea mays genome in order to detect polymorphic markers. Such markers can
CC be used in the construction of allele-specific primers and probes for
CC amplification or hybridisation, e.g. to determine common or disparate
CC ancestry between 2 or more plants, to monitor the genetic contribution of
CC an ancestral plant, to trace the progeny of proprietary plants, in

CC certification of a hybrid plant or to identify the progeny of a back-
CC crossed plant with an ancestral plant
XX
SQ Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1/54 AGCTCATTTGTCATCC 1771
DB 1 AGCTCATTTGTCCTCC 18
RESULT 2990
AAV35084/c
ID AAV35084 standard; DNA; 20 BP.
XX
AC AAV35084;
XX
XX 28-AUG-1998 (first entry)
DT
XX Antisense MDR1 oligonucleotide #24.
DE
XX P-glycoprotein; multiple drug resistance; MDR; cellular uptake; cancer;
KW gene expression; chemotherapy; treatment; hyper-proliferative disease;
KM primer; 88.
XX
XX Synthetic.
XX
XX WO9814615-A1.
XX
XX 09-APR-1998.
PD
XX 01-OCT-1997; 97WO-US017800.
PE
XX 04-OCT-1996; 96US-00731199.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean NM, Manoharan M;
PI
XX WPI; 1998-240109/21.
DR
XX Anti-sense oligo:nucleotide(s) targeted to multiple drug resistance gene
PT - are modified by lipophilic substituent, on sugar and/or with non-
PT natural linkages, used to improve activity of anti-proliferative agents
PT against tumours.
XX
XX Example 1; Page 21; 64pp; English.
PS
XX AAV35061-V35101 are primers which have a sequence complementary to the
CC translocation initiation or termination region of a nucleic acid encoding a
CC P-glycoprotein associated with multiple drug resistance (MDR) and
CC inhibits expression of the glycoprotein. These primers are composed of 8-
CC 30 covalently linked nucleotides and includes at least 1 of the
CC following; a 2'-modification, a lipophilic group (lg) that improves
CC cellular uptake, and at least 1 covalent link that is a phosphorothioate,
CC phospho di- or tri-ester, methylphosphonate, methylene (methylimino),
CC morpholino, polyamide, short chain alkyl or heteroatomic inter-sugar
CC link, or cycloalkyl or heterocyclic inter-sugar link. The primers are
CC used to modulate human MDR gene expression in cells and tissues, i.e. to
CC improve chemotherapeutic treatment of an animal with hyper-proliferative
CC disease, particularly cancer, to prevent development of MDR and to re-
CC sensitise an animal that has developed MDR to a chemotherapeutic agent
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1103 AGAGTGACGACGCTGTGS 1120

DB 19 AGAGTGACGACGCTGTGS 2
RESULT 2991
AAV70043/c
ID AAV70043 standard; DNA; 20 BP.
XX
XX AAV70043;
AC
XX 04-FEB-1999 (first entry)
DT
XX Rat c-Fos protein antisense oligonucleotide #97.
DE
XX Rat; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis;
KW antisense oligonucleotide; phosphorothioate; regulation;
KM malignant tumour; cell cycle expression; hyperproliferative disease; ss.
XX
XX Synthetic.
OS
XX Rattus sp.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX WO9846272-A1.
XX
XX 22-OCT-1998.
PD
XX 14-APR-1998; 98WO-US007386.
PE
XX 14-APR-1997; 97US-00837201.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean NM, McKay R, Miraglia L, Baker B;
PI
XX WPI; 1998-609906/51.
DR
XX Antisense oligonucleotides regulating Activating Protein 1 subunits -
PT hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
PT cycle expression and hyperproliferative disease.
PT
XX
XX Example 9; Page 57; 120pp; English.
PS
XX AAV70042 to AAV70052 represent antisense oligonucleotides which are
CC specifically hybridisable with a region of a nucleic acid encoding rat c-
CC Fos protein. The antisense compound regulates the expression of the c-Fos
CC protein. The present invention also describes antisense oligonucleotides
CC which regulate the c-jun protein. The antisense oligonucleotides are used
CC for the diagnosis and treatment of diseases or disorders associated with
CC Activating Protein 1 expression, of which c-Fos and c-Jun are subunits.
CC The antisense oligonucleotides are used in compositions as c-Fos and/or c-
CC -jun together with a carrier and a chemotherapeutic agent. They are used
CC to regulate the expression of c-Fos or c-jun in cells or tissues,
CC preferably by inhibiting metastasis. They also regulate cell cycle
CC expression and can be used to treat an animal with, or being prone to, a
CC hyperproliferative disease
XX
SQ Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1284 CCAGACTCGACCATGAT 1301
DB 19 CCAAAACGACGACCATGAT 2
RESULT 2992
AAV22586


```

ID  AAV22586 standard; DNA; 20 BP.
XX
AC  AAV22586;
XX
DT  08-JUL-1998 (first entry)
XX
DE  Antisense oligonucleotide designed to target the R1 message.
XX
KM  R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
XX  antisense; growth; inhibition; sensitivity; hydroxyurea;
XX  chemotherapeutic drug; methotrexate; PMA; treatment; ss.
XX
OS  Synthetic.
XX  Homo sapiens.
XX
PN  WO9805769-A2.
XX
PD  12-FEB-1998.
XX
PF  01-AUG-1997; 97MO-CA000540.
XX
PR  02-AUG-1996; 96US-0023040P.
XX  07-MAR-1997; 97US-0039595P.
XX
PA  (GENE-) GENESENSE TECHNOLOGIES INC.
XX
FI  Wright JA, Young AH;
XX
XX  WPI; 1998-145609/13.
XX
PT  Antisense oligonucleotides to ribonucleotide reductase genes - used to
XX  modulate tumour growth and inhibit tumour cell proliferation.
XX
PS  Claim 8; Page 49; 79pp; English.
XX
CC  AAV22531-89 represent antisense oligonucleotides which are targeted
XX  against the mRNA of the R1 subunit sequence of ribonucleotide reductase.
XX  Aberrant expression of the R2 gene, which encodes the second subunit of
XX  the ribonucleotide reductase gene, can determine the malignant
XX  characteristics of cells. Suppression of R2 and R1 gene expression was
XX  found to reduce transformed properties of tumour cells. The antisense
XX  oligonucleotides can be used for modulating tumour cell growth, or for
XX  inhibiting tumour cell proliferation. They can also be used for
XX  increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
XX  (especially to hydroxyurea, methotrexate (MTX), and PMA). The antisense
XX  oligonucleotides may be used to treat proliferative disorders including
XX  leukaemias, lymphomas, sarcomas, melanomas, various other forms of
XX  cancer, papillomas, atherosclerosis, psoriasis, polychemia, mastocytosis,
XX  autoimmune diseases, angiogenesis, bacterial infections and viral
XX  infections (including HIV hepatitis, or herpes infections)
XX
SQ  Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4463 CTTTTTTTTTTTTTTTTT 4480
DB 3 CGTTTTTTTTTTCTTTT 20

```

```

XX
OS  Synthetic.
XX  Homo sapiens.
XX
PN  WO9804689-A1.
XX
PD  05-FEB-1998.
XX
PF  31-JUL-1996; 96MO-US012516.
XX
PR  31-JUL-1996; 96MO-US012516.
XX
PA  (UROC-) UROCOR INC.
XX
PI  Veltri R, Ohara SM, An G, Ralph D;
XX
XX  WPI; 1998-130681/12.
XX
DR  Human prostate cancer marker - useful for detection and treatment of
XX  human prostate cancer.
XX
PT  Example 4; Page 121; 229pp; English.
XX
PS  This primer is used in the relative quantitative RT-PCR to examine the
XX  expression of the genes which is used for the identification of markers
XX  of human prostate cancer. Isolated nucleic acid segments shown in
XX  CC AAV16881 to AAV16885, AAV16890 to AAV16903, AAV26351 and AAV26352 which
XX  can act as human prostate cancer markers are provided in the
XX  CC specification. The specification also provides methods for identifying
XX  markers for human prostate cancer and for detection of prostate cancer
XX  cells. The markers can be identified by amplifying human prostate RNA to
XX  provide nucleic acid amplification products, separating the products and
XX  CC identifying those RNA that are differentially expressed between human
XX  prostate cancers versus normal or benign human prostate. Prostate cancer
XX  cells in a sample can be detected by detecting a nucleic acid in a
XX  CC sample, the nucleic acid being a prostate cancer marker. Primers and
XX  CC probes derived from this marker can be used for the detection of prostate
XX  CC cancer cells in a sample. Antibodies against the protein encoded by the
XX  CC marker nucleic acid fragments, inhibitors of the protein and
XX  CC oligonucleotides antisense to the markers can be used in the treatment of
XX  CC prostate cancer. The antibodies can also be used for the diagnosis of
XX  human prostate cancer
XX
SQ  Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3414 CTTATTCCTCTGTGCA 3431
DB 19 CATATTCCTTTGTGCA 2

```

```

RESULT 2993
AAV26329/c
ID  AAV26329 standard; DNA; 20 BP.
XX
AC  AAV26329;
XX
DT  07-AUG-1998 (first entry)
XX
DE  Human prostate cancer marker UC Band #201 identifying RT-PCR primer 2.
XX
XX  Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.
XX

```

```

RESULT 2994
AAV26076/c
ID  AAV26076 standard; DNA; 20 BP.
XX
AC  AAV26076;
XX
DT  20-MAY-1999 (first entry)
XX
DE  Prostate disease marker gene fragment amplifying RT-PCR primer.
XX
XX  Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;
XX  KM differentiation; Reverse Transcription Polymerase Chain Reaction;
XX  KM diagnostic; progression; cancer; metastasis; RT-PCR; primer; ss.
XX
OS  Synthetic.
XX  Homo sapiens.
XX
XX  US5882864-A.
XX

```

```

PD 16-MAR-1999.
XX
XX 31-JUL-1996; 96US-00692787.
XX
XX 31-JUL-1995; 95US-0001655P.
XX
XX (UROC-) UROC INC.
XX
XX Veltre R, Ralph D, An G, O'hara SM;
XX
XX WPI; 1999-214055/18.
XX
XX Diagnosing prostate cancer and benign prostatic hyperplasia cells - using
XX oligonucleotide probes specific for marker genes associated with tumor
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction analysis.
XX
XX Example 4; Col 66; 74pp; English.
XX
XX The invention relates to methods for diagnosing prostate cancer or benign
XX prostatic hyperplasia cells in a biological sample. The method uses
XX oligonucleotides specific for marker genes associated with tumour
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX for detecting and monitoring the progression of benign prostatic
XX hyperplasia and human prostate cancer (the most prevalent form of cancer
XX and a major cause of death in males) prior to the tumor undergoing
XX metastasis, therefore allowing the optimal method of treatment to be
XX determined before the condition becomes life threatening
XX
XX Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 3414 CTTATTCCTCTGTGCCA 3431
Db 19 CATATCTCTTTGTCCA 2
XX
XX RESULT 2995
XX ID AAX29179 standard; DNA; 20 BP.
XX
XX AAX29179;
XX
XX 18-JUN-1999 (first entry)
XX
XX Human osteopontin (OPN) specific probe hOPN-PI.
XX
XX Osteopontin; antisense; restenosis; coronary arterial tissue; CASMC;
XX inflammation; coronary artery smooth muscle cell; angioplasty; human;
XX OPN; probe; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9907844-A2.
XX
XX 18-FEB-1999.
XX
XX 07-AUG-1998; 98WO-US016569.
XX
XX 07-AUG-1997; 97US-0054967P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Mukherjee AB, Kundu GC, Panda DK;
XX
XX WPI; 1999-190049/16.
XX
XX New osteopontin antisense sequences - useful to treat restenosis,
XX

```

```

PT particularly following vascular surgery.
XX
XX Example 1; Page 29; 72pp; English.
XX
XX The invention relates to antisense osteopontin oligonucleotide sequences
XX which are complementary to at least a portion of the human osteopontin
XX (OPN) cDNA sequence (AAX29191). The antisense sequences are used to
XX prevent restenosis in tissue, particularly coronary arterial tissue,
XX especially where the patient is undergoing angioplasty, particularly
XX percutaneous trans-luminal coronary angioplasty or directional coronary
XX atherectomy. They prevent secretion of osteopontin by monocytes and
XX macrophages which infiltrate to sites of inflammation following surgery.
XX Osteopontin probably causes restenosis by inducing coronary artery smooth
XX muscle cells (CASMC) to migrate to, and proliferate at, angioplasty
XX injury sites. The present sequence represents a probe specific for human
XX osteopontin cDNA sequence
XX
XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 904 TTCATGTGTGAGTGTG 921
Db 1 TCCATGTGTGAGTGTGATG 18
XX
XX RESULT 2996
XX ID AAZ04197/c
XX
XX AAZ04197 standard; DNA; 20 BP.
XX
XX AAZ04197;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX paratrachoma; inclusion conjunctivitis; genital disease; peritropatitis;
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
XX Chlamydia trachomatis.
XX
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffiths R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1669; 1755pp; English.
XX
XX PCR primers AAZ01426-206209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX

```

CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases

XX
SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5010 GAATGAGGCTCTGGGA 5027

Db 19 GAATGAGGCTCTGGGA 2

RESULT 2997

AAZ05197/c

ID AAZ05197 standard; DNA; 20 BP.

XX AAZ05197;

DT 07-OCT-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;
KM paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KM bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

OS Synthetic.

OS Chlamydia trachomatis.

XX MO928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB001939.

XX 28-NOV-1997; 97FR-00015041.

XX 17-DEC-1997; 97FR-00016034.

XX 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

XX Disclosure; Page 1751; 1755pp; English.

CC PCR primers AAZ01426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nongonococcal urethritis, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis;
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases

XX
SQ Sequence 20 BP; 2 A; 10 C; 0 G; 8 T; 0 U; 0 Other;

Query March 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

QY 3638 AGAGGTAGATGGGAG 3655

Db 18 AGAGGAGATGGGAG 1

RESULT 2998

AAZ04690/c

ID AAZ04690 standard; DNA; 20 BP.

XX AAZ04690;

DT 07-OCT-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;
KM paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KM bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

OS Synthetic.

OS Chlamydia trachomatis.

XX MO928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB001939.

XX 28-NOV-1997; 97FR-00015041.

XX 17-DEC-1997; 97FR-00016034.

XX 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

XX Disclosure; Page 1709; 1755pp; English.

CC PCR primers AAZ01426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nongonococcal urethritis, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis;
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases

XX
SQ Sequence 20 BP; 0 A; 8 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAG 4030

Db 20 AGAGGAGAAAAAGAG 3

RESULT 2999

AAZ04201/c

ID AAZ04201 standard; DNA; 20 BP.

XX AAZ04201;

```

XX 07-OCT-1999 (first entry)
DT
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
DE
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
PN
XX MO9928475-A2.
PD
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1669; 1755pp; English.
XX
XX PCR primers AA201426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumonia; in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
XX
SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2851 CCAATCCAGAGGACA 2868
XX |||||
XX 20 CCAATCCAGAGGACA 3
XX
XX
RESULT 3000
AA201618
ID AA201618 standard; DNA; 20 BP.
XX
XX AA201618;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
OS

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OS Chlamydia trachomatis.
XX
XX MO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1457; 1755pp; English.
XX
XX PCR primers AA201426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumonia; in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2652 CCACCTGTGACAGCA 2669
XX |||||
XX 1 CCACCTGTGACAGCA 18
XX
XX
RESULT 3001
AA203279
ID AA203279 standard; DNA; 20 BP.
XX
XX AA203279;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
OS Chlamydia trachomatis.
PN
XX MO9928475-A2.
PD
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX

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```
XX (GEST ) GENSET.
XX Griffais R;
XX WPI; 1999-371125/31.
XX Genome sequence of Chlamydia trachomatis.
XX PT Disclosure; Page 1593; 1755bp; English.
XX PS PCR primers AA201426-206209 were used to amplify open reading frames
XX CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
XX CC encode polypeptides (see AA136754-137949) which can be used as vaccines
XX CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX CC be used to control growth of the microorganism. Chlamydia trachomatis is
XX CC responsible for a large number of diseases, e.g. eye diseases such as
XX CC conjunctivitis; genital diseases such as nongonococcal urethritis,
XX CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis,
XX CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX CC The polypeptides of the invention may be of use in treating these
XX CC diseases
XX SQ Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5426 AAGGATTCAGCTTGGG 5443
XX Db 2 AAGGATTCAGCTTGGG 19
XX
XX RESULT 3002
XX AA24878
XX ID AA24878 standard; DNA; 20 BP.
XX AC AA24878;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KM neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.
XX XX WO9927105-A2.
XX XX 03-JUN-1999.
XX XX 20-NOV-1998; 98WO-IB001890.
XX XX 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX XX
XX PA (GEST ) GENSET.
XX PT Griffais R;
XX DR WPI; 1999-357842/30.
XX XX
XX PT Genome sequence of Chlamydia pneumoniae.
XX PS Page 1704; Disclosure; 1912pp; English.
XX CC AA291991-X97517 represent PCR primers used to amplify open reading frames
XX CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
```

```
CC (see AA291990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AA24584- AA25879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1356 GAAAGATCCAGCTACAA 1373
XX Db 2 GAAAGATCCAGCTACAA 19
XX
XX RESULT 3003
XX AA247569/c
XX ID AA247569 standard; DNA; 20 BP.
XX AC AA247569;
XX DT 23-MAR-2000 (first entry)
XX DE Antisense oligonucleotide 24 targeted to human MDR1 P-glycoprotein.
XX KW Multidrug resistance gene; MDR1; human; hyperproliferative disease;
XX KM cancer; autoradiography; phosphorochiolate; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /note="Phosphorothioate internucleoside linkage"
XX
XX US6001991-A.
XX PD 14-DEC-1999.
XX XX 30-SEP-1997; 97US-00940250.
XX PR 04-OCT-1996; 96US-00731199.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX Manoharan M, Dean NM;
XX PI WPI; 2000-061907/05.
XX DR
XX PT Antisense oligonucleotide specific for multidrug resistance P-
XX PT glycoprotein is useful for treating hyperproliferative diseases and
XX PT disorders e.g. cancer.
XX PS Claim 1; Col 13; 24pp; English.
XX XX
XX CC This sequence is an antisense oligonucleotide that specifically
XX CC hybridises to nucleic acids encoding a human multidrug resistance P-
XX CC glycoprotein (MDR1). The oligonucleotide inhibits expression of the P-
XX CC glycoprotein, which functions as an ATP driven efflux pump. The antisense
XX CC oligonucleotides of the invention have a phosphorothioate modified
XX CC backbone, and may contain residues with 2' modifications selected from 2'-
XX CC methoxyethoxy, 2'-fluoro, 2'-O-fluoro or 2'-propyl. Some antisense
XX CC oligonucleotides have cholesterol bound at the 3' end which ensures
XX CC resistance to 3' exonucleases, enhances cellular uptake, and leaves the
XX CC 5' termini available for conjugation of additional functional groups. The
XX CC oligonucleotides may be used in research, diagnosis or as therapeutic
```

CC	involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC	located on chromosome 9q31, and mutations in this gene are associated
CC	with two genetic HDL (high density lipoprotein) deficiency disorders,
CC	Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
CC	are distinguishable in that TD is an autosomal recessive disorder, while
CC	FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC	cholesterol") in the blood correlate with a high risk of cardiovascular
CC	disease, particularly coronary artery disease, but also cerebrovascular
CC	disease, coronary restenosis, and peripheral vascular disease.
CC	Conversely, a high level of HDL has protective effects against
CC	cardiovascular disease. The invention provides genetic constructs and
CC	transgenic cells and non-human animals comprising human ABC1 nucleic
CC	acids, and methods of gene therapy for the treatment or prevention of
CC	cardiovascular disease comprising the administration of an expression
CC	vector encoding ABC1 or an active fragment thereof. The invention also
CC	encompasses compounds which mimic ABC1 activity, compounds which
CC	stimulate ABC1 expression and methods of screening for such compounds. It
CC	further relates to methods for determining whether a patient has an
CC	increased risk for cardiovascular disease due to polymorphisms in the
CC	ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC	prevent cardiovascular disease, especially coronary artery disease,
CC	cerebrovascular disease, coronary restenosis or peripheral vascular
CC	disease. They may also be used in the treatment of diseases associated
CC	with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC	disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC	The invention specifically excludes proteins with the exact amino acid
CC	sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC	acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC	present sequence represents a human ABC1 gene PCR primer which may be
CC	used to amplify an exon of the human ABC1 gene
XX	
XX	Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
XX	
Qy	Query Match 0.2%; Score 14.8; DB 1; Length 20;
Db	Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	2810 TGGATGAGAGAAAGCTT 2827
	20 TGGATTGAGAGAAAGCTT 3
RESULT 3005	
AAA13124	
ID	AAA13124 standard; DNA; 20 BP.
AC	AAA13124;
XX	
DT	17-JUL-2000 (first entry)
XX	
DE	PI3K antisense inhibitor oligonucleotide ISIS# 32136.
XX	
KW	Phosphatidylinositol 3 kinase; PI3K; antisense oligonucleotide; p110;
KM	catalytic subunit; treatment; rheumatoid arthritis; asthma; research;
XX	diagnostic; infection; inflammation; tumour formation; inhibitor; ss.
OS	Synthetic.
XX	
XX	
FT	Key Location/Qualifiers
FT	FT misc_feature 1..20
FT	FT misc_feature /*tag= a
FT	FT modified_base /note= "Phosphorothioate internucleoside linkage"
FT	FT modified_base 1..5
FT	FT modified_base /*tag= b
FT	FT catalytic_base OTHER /mod_base= OTHER
FT	FT modified_base /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"
FT	FT modified_base 16..20
FT	FT modified_base /*tag= c
FT	FT /mod_base= OTHER
FT	FT /note= "optionally 2'-methoxyethyl (2'-MOE) nucleotides"
XX	
XX	US6046049-A.

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PD 04-APR-2000.
XX
XX 19-JUL-1999; 99US-00357070.
XX
XX 19-JUL-1999; 99US-00357070.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Coweert LM;
XX
XX WPI; 2000-282691/24.
XX
XX New antisense compounds targeting nucleic acids encoding human PI3 kinase
XX p110 delta useful for treating a disease or condition associated with PI3
XX kinase p110 delta expression, e.g. rheumatoid arthritis, asthma.
XX
XX Claim 16; Col 41; 35pp; English.
XX
XX This sequence represents a phosphatidylinositol 3 kinase (PI3K)
XX targeting antisense oligonucleotide. Phosphatidylinositol 3 kinases act
XX as downstream effectors of hormone and growth factor receptors, and have
XX been implicated in growth factor mediated cell transformation.
XX CC mitogenesis, protein trafficking, cell survival and proliferation, and
XX CC many other cellular activities. PI3K is a heterodimer, consisting of a
XX CC 110kD catalytic subunit (p110), and an 85kD regulatory subunit (p85). The
XX CC invention relates to antisense oligonucleotides which target the p110
XX CC delta mRNA of PI3K. The antisense oligonucleotides specifically hybridise
XX CC with various regions of the PI3K mRNA sequence, and inhibit the
XX CC expression of PI3K. The antisense oligonucleotides may be used to treat
XX CC an animal, particularly human, suspected of having or being prone to a
XX CC disease or condition associated with the expression of PI3K, e.g.
XX CC rheumatoid arthritis or asthma. The treatment works through the
XX CC modulation (preferably inhibition) of the expression of PI3K. The
XX CC antisense oligonucleotides may also be used for research and diagnostics,
XX CC in pharmaceutical compositions and formulations, in the preparation of
XX CC kits for detecting the level of PI3K in a sample, and as prophylaxis,
XX CC e.g. to prevent or delay infection, inflammation or tumour formation.
XX CC Antisense oligonucleotides, which are able to inhibit gene expression,
XX CC specifically, are used to elucidate the function of particular genes, and
XX CC to distinguish between functions of various members of a biological
XX CC pathway.
XX
XX Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3378 GTTGCTCTCTCCCGCAGCT 3395
XX ||||| ||||| |||||
XX 2 GTTGCTCTCTCTCCAGCT 19
XX
XX RESULT 3006
XX AAA96416
XX ID AAA96416 standard; DNA; 20 BP.
XX
XX AAA96416;
XX
XX 08-FEB-2001 (first entry)
XX
XX Primer used to amplify a sar47/48 polymorphic microsatellite repeat.
XX
XX Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
XX KM ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;
XX KM insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;
XX KM Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma;
XX KM thyroditis; postpartum thyroditis; rheumatoid arthritis;
XX KM Hashimoto's disease; coeliac disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200056856-A2.

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XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US007938.
XX
XX 25-MAR-1999; 99US-0126215P.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Ling V, Wu P, Gray GS;
XX
XX WPI; 2000-628257/60.
XX
XX Determining predisposition of humans to develop autoimmune disease
XX PT involves detecting polymorphic microsatellite repeat sequence within
XX PT human costimulatory receptor gene locus.
XX
XX Claim 18; Page 155; 160pp; English.
XX
XX PCR primers AAA96415-16 were used to amplify polymorphic microsatellite
XX CC repeat (PMR) sequences from the human costimulatory receptor gene locus
XX CC (hCGRL). The primers are used in the method of the invention. The
XX CC specification describes a method for determining the predisposition of a
XX CC human subject to develop autoimmune disease. The method comprises
XX CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the
XX CC human costimulatory receptor gene locus (hCGRL). PMR sequences vary in
XX CC length among individuals and can be amplified to generate products that
XX CC differ in size. These products can then be detected by rapid and
XX CC convenient high resolution processes. The method is useful for
XX CC determining the predisposition of insulin-dependent diabetes mellitus
XX CC (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism,
XX CC myasthenia gravis, thymoma, lupus, thyroditis, postpartum thyroditis,
XX CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.
XX CC PMR sequences within hCGRL are useful as markers in a variety of assays
XX CC and in the field of forensic medicine, disease diagnosis and human genome
XX CC mapping.
XX
XX Sequence 20 BP; 1 A; 10 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 5098 TGCCCTGTCCATGCGCTT 5115
XX ||||| ||||| |||||
XX 1 TCCTCTCTCATTCGCTT 18
XX
XX RESULT 3007
XX AA287562/c
XX ID AA287562 standard; DNA; 20 BP.
XX
XX AA287562;
XX
XX 19-APR-2000 (first entry)
XX
XX Primer specific for cancer biomarker UC Band #201.
XX
XX Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;
XX KM benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;
XX KM diagnosis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9964631-A1.
XX
XX 16-DEC-1999.
XX
XX 11-JUN-1999; 99WO-US013151.
XX
XX 12-JUN-1998; 98US-00097199.
XX
XX (UROC-) UROCOR INC.

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XX An G, O'hara SM, Ralph D, Veltri RM;
XX WPI; 2000-116557/10.
XX
XX Novel RNA biomarkers for diagnosis, prognosis and management of prostate,
XX breast and bladder cancer.
XX
XX Example 2; Page 110; 191pp; English.
XX
XX The invention provides nucleic acid markers of prostate, breast and
XX bladder cancer. The markers are indicators of malignant transformation of
XX prostate, breast and bladder tissues and are diagnostic of the potential
XX for metastatic spread of malignant prostate tumours. The nucleic acid can
XX also be used as targets for therapeutic intervention in prostate cancer,
XX benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The
XX markers may be used to design specific probes and primers, for the rapid
XX analysis of prostate, bladder or breast biopsy samples. The probes and
XX primers may also be used for in situ hybridization or in situ PCR
XX detection and diagnosis. They may also be used to identify and isolate
XX full length gene sequences from various DNA libraries. Antibodies against
XX the polypeptide products of the markers can be used to treat prostate
XX cancer, bladder cancer or breast cancer. The encoded proteins may be used
XX to detect antibodies. The proteins and antibodies can be used in
XX immunodetection methods for detecting or quantifying the cancers, and for
XX clinical diagnosis of these cancers. The antibodies may also be used for
XX radioimaging to quantify and localize the encoded proteins
XX
XX Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 2;
XX
XX 3414 CTTATCTCTCTCTGTCCA 3431
XX | | | | | | | | | |
XX 19 CATAATCTCTTTGTCCA 2
XX
XX RESULT 3008
XX ID AAA11286 standard; DNA; 20 BP.
XX
XX AA11286;
XX
XX 08-NOV-2000 (first entry)
XX
XX Human TRPC7 gene intron 1/exon 2 junction.
XX
XX Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;
XX calcium channel function; human; gene therapy; periodic psychosis;
XX mutation; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX intron 1..10
XX /*tag= a
XX /number= 1
XX exon 11..20
XX /*tag= b
XX /number= 2
XX
XX WO200029571-A1.
XX
XX 25-MAY-2000.
XX
XX 11-NOV-1999; 99WO-JP006289.
XX
XX 12-NOV-1998; 98JP-00321200.
XX
XX (EIKE ) EIKEN KAGAKU KK.
XX

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PI Shimizu N, Nagamine K;
XX WPI; 2000-387784/33.
XX
XX Nucleic acids encoding transmembrane protein TRPC7 expressed in brain and
XX homologous to transient receptor potential protein useful in the of
XX treatment of associated diseases such as periodic psychosis.
XX
XX Example 7; Page 38; 77pp; Japanese.
XX
XX The invention relates to the isolation of a nucleic acid (AA11284)
XX coding for a transmembrane protein TRPC7 (AA92944) which is expressed in
XX brain and is homologous to transient receptor potential (TRP) protein.
XX This suggests that the TRPC7 protein may have a calcium channel function.
XX The genomic sequence has been shown to contain 31 introns. This sequence
XX represents an exon/intron junction from the genomic TRPC7 sequence. The
XX DNA and protein can be used in the diagnosis and treatment of disorders
XX associated with TRPC7, especially the screening, monitoring and treatment
XX (by gene therapy) of periodic psychosis, which appears to be associated
XX with mutations in the TRPC7 gene
XX
XX Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 2;
XX
XX 3676 ACCTCCAGCCAGAAAGCC 3693
XX | | | | | | | | | |
XX 3 ACCTTCAGCAAGAAAGCC 20
XX
XX RESULT 3009
XX ID AA273463 standard; DNA; 20 BP.
XX
XX AA273463;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker upstream amplification primer SEQ ID NO:7819.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 1898; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA269579 to AA277440 represent amplification
XX

```


CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies.
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

XX
SQ Sequence 20 BP; 1 A; 10 C; 1 G; 8 T; 0 U; 0 Other;

Qy Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dy 2860 GAGGACGACGAGGAGG 2877
20 GAGGAGGCAAGAGGAGG 3

Db

RESULT 3010
AAC73675/c
ID AAC73675 standard; DNA; 20 BP.
XX
AC AAC73675;
XX
DT 02-FEB-2001 (first entry)
XX
DE Murine IL-5 antisense oligonucleotide ISIS #17981.
XX
KM Mouse; interleukin-5; IL-5; signal transduction;
XX antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
KM IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
KM inflammation; cancer; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO200058512-A1.
XX
PS 05-OCT-2000.
PD
PF 17-MAR-2000; 2000WO-US007318.
XX
PR 26-MAR-1999; 99US-00280799.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Karraas JG, McKay R;
XX
DR WPI; 2000-594648/56.
XX
PT Antisense oligonucleotide compound used to treat asthma and eosinophilic
PT syndrome in humans modulates interleukin-5 signal transduction.
XX
XX Example 14; Page 53; 156pp; English.

XX
PS The present sequence is an oligonucleotide used for antisense modulation
CC of interleukin-5 (IL-5) signal transduction. Oligonucleotides were
CC designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha.
CC The antisense oligonucleotides may be used for the treatment of diseases
CC associated with IL-5 signal transduction, IL-5 expression or IL-5
CC receptor-alpha expression. Such diseases include asthma and eosinophilic
CC syndrome. The oligonucleotides are also useful for research uses and to
CC prevent or delay infection, inflammation or tumour formation

XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5272 ATTAGGACGACGTTGGCAG 5289
20 AGACGAGCAGCGTGGCAG 3

Db

RESULT 3011
AAC60575
ID AAC60575 standard; DNA; 20 BP.
XX
AC AAC60575;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human fra-1 mRNA antisense oligonucleotide ISIS 109066.
XX
KM Human; fra-1; antisense oligonucleotide; phosphorothioate; cytostatic;
KM antiinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;
KM ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6124133-A.
XX
PD 26-SEP-2000.
PD
PF 15-OCT-1999; 99US-00418641.
XX
PR 15-OCT-1999; 99US-00418641.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Taylor JK, Cowseart LM;
XX
DR WPI; 2000-601552/57.
XX
PT Novel antisense compound 8-30 nucleobases in length targeted to human fra
PT -1 and which specifically hybridizes with and inhibits the expression of
PT human fra-1, useful for modulating the expression of fra-1 in cells.
XX
XX Example 15; Col 42; 38pp; English.

XX
PS The present sequence is one of a large number of antisense
CC oligonucleotides which are targeted to nucleic acids encoding fra-1. The
CC sequences may be oligodeoxyribonucleotides or chimeric oligonucleotides,
CC containing a central gap region consisting of ten 2'-deoxynucleotides,
CC which is flanked on both sides by 2'-methoxyethyl (2'-MOE) wings. The
CC oligonucleotides have a phosphorothioate backbone and the cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense
CC oligonucleotides are useful for inhibiting the expression of fra-1 in
CC human cells or tissues. They can be used for diagnostics, therapeutics,
CC prophylaxis and as research reagents and in kits. Use of the antisense
CC compounds may also be useful prophylactically, e.g. to prevent or delay
CC infection, inflammation or tumour formation

XX
SQ Sequence 20 BP; 4 A; 1 C; 10 G; 5 T; 0 U; 0 Other;

Qy Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dy 4175 TAGGAGCGGCGTGTAT 4192
1 TAGGAGCGGTGTGTAT 18

Db

RESULT 3012
AAA90815
ID AAA90815 standard; DNA; 20 BP.
XX

```

AC  AAA90815;
XX
DT  20-DEC-2000 (first entry)
XX
DE  Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.
XX
XX  Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
XX  R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
XX
OS  Synthetic.
XX
PN  WO200047733-A1.
XX
PD  17-AUG-2000.
XX
PF  09-FEB-2000; 2000WO-CA000120.
XX
PR  11-FEB-1999; 99US-00249730.
XX
PA  (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI  Wright JA, Young AH;
XX
DR  WPI; 2000-558216/51.
XX
PT  New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
XX  tumor cell growth.
XX
PS  Example 3; Page 32; 137bp; English.
XX
CC  The present sequence is an antisense oligonucleotide directed against the
CC  mRNA encoding the R1 component of mammalian ribonucleotide reductase.
CC  Ribonucleotide reductase catalyses the conversion of ribonucleotides to
CC  their corresponding deoxyribonucleotides and thus plays an important role
CC  in DNA synthesis and cell proliferation. Regulation of ribonucleotide
CC  reductase is altered in cultured malignant cells and increased levels of
CC  R2 protein and R2 mRNA have been found in pre-malignant and malignant
CC  tissues as compared to normal control tissue samples. The present
CC  antisense sequence is therefore useful for inhibiting tumourigenicity of
CC  neoplastic cells and inhibiting metastasis of tumour cells. It is also
CC  useful for increasing sensitivity of neoplastic cells to chemotherapeutic
CC  drugs, thus allowing chemotherapeutic treatments to be used in patients
CC  who have become resistant or less sensitive to chemotherapy. The sequence
CC  may be RNA or DNA and may comprise a modified backbone and/or nucleotide
CC  analogues
XX
SQ  Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY  4463 CTTTTTTTTTTTTTTT 4480
    |||||
    3 CGTTTTTTTTTCTTTT 20
XX
RESULT 3013
AAA66863
ID  AAA66863 standard; DNA; 20 BP.
XX
AC  AAA66863;
XX
DT  09-OCT-2000 (first entry)
XX
DE  Dog genomic marker oligonucleotide sequence SEQ ID NO:725.
XX
XX  Dog; genome; genomic marker; radiation hybrid map; identification;
XX  chromosome location; gene marker; polymorphic microsatellite marker;
XX  phenotype; behaviour; pedigree; ss.
XX
OS  Canis familiaris.
XX

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PN  WO200029615-A2.
XX
PD  25-MAY-2000.
XX
PF  15-NOV-1999; 99WO-IB001907.
XX
PR  13-NOV-1998; 98US-0108193P.
XX
PA  (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI  Galibert F, Andre C;
XX
DR  WPI; 2000-387821/33.
XX
FT  New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX  for e.g. identifying genes implicated in phenotypic and behavioral traits
XX  or in genetic diseases and for studying dog pedigrees.
XX
PS  Claim 1; Page 84; 87pp; English.
XX
CC  The present invention describes a radiation hybrid map of the dog (Canine
XX  familiaris) genome comprising the genome location of a marker selected
XX  from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX  identifying and localising dog genes, since it covers approximately 80 %
XX  of the dog genome and provides a dense map integrating different types
XX  (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX  (or complementary sequences) are especially useful to identify genes
XX  responsible for phenotypic and behavioural traits in dogs, to identify
XX  morbid genes, to analyse diseases and identify implicated genes in such
XX  diseases and their alleles, and to study dog pedigrees. They may also be
XX  useful for isolating corresponding human gene sequences e.g. genes
XX  involved in genetic diseases
XX
SQ  Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY  4273 CTGTCTGCACCTTTCT 4290
    |||||
    2 CTGTCTGCACCTTTCT 19
XX
Db
XX
RESULT 3014
AAA66923/C
ID  AAA66923 standard; DNA; 20 BP.
XX
AC  AAA66923;
XX
DT  09-OCT-2000 (first entry)
XX
DE  Dog genomic marker oligonucleotide sequence SEQ ID NO:785.
XX
XX  Dog; genome; genomic marker; radiation hybrid map; identification;
XX  chromosome location; gene marker; polymorphic microsatellite marker;
XX  phenotype; behaviour; pedigree; ss.
XX
OS  Canis familiaris.
XX
PN  WO200029615-A2.
XX
PD  25-MAY-2000.
XX
PF  15-NOV-1999; 99WO-IB001907.
XX
PR  13-NOV-1998; 98US-0108193P.
XX
PA  (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI  Galibert F, Andre C;
XX
DR  WPI; 2000-387821/33.
XX

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XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits
 PT or in genetic diseases and for studying dog pedigrees.
 XX
 PS Claim 1, Page 87, 87pp; English.
 CC The present invention describes a radiation hybrid map of the dog (Canine
 CC familiaris) genome comprising the genome location of a marker selected
 CC from AAG66139 to AAG66942. The radiation hybrid map is useful for
 CC identifying and localising dog genes, since it covers approximately 80 %
 CC of the dog genome and provides a dense map integrating different types
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
 CC (or complementary sequences) are especially useful to identify genes
 CC responsible for phenotypic and behavioural traits in dogs, to identify
 CC morbid genes, to analyse diseases and identify implicated genes in such
 CC diseases and their alleles, and to study dog pedigrees. They may also be
 CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases
 CC
 SQ Sequence 20 BP, 5 A; 8 C; 0 G; 7 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 3187 TTTGATGGGAAAGTGA 3204
 19 TTGAGATGGGAAAGTGTG 2
 RESULT 3015
 ID AAG91212 standard; DNA; 20 BP.
 AC AAG91212;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Antisense IGFBP-5 inhibitor #18.
 XX
 KM Insulin-like growth factor binding protein-5; IGFBP-5; human;
 KM antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
 KM breast cancer; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200105435-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 19-JUL-2000; 2000WO-CA000853.
 XX
 PR 19-JUL-1999; 99US-0144495P.
 XX
 PA (UVR-) UNIV BRITISH COLUMBIA.
 PA (MIYA/) MIYAKE H.
 XX
 PI Gleave M;
 XX
 DR WPI; 2001-168448/17.
 XX
 PT Composition for treating hormone-regulated cancer, e.g. breast and
 PT prostatic tumors, comprising an antisense oligonucleotide that inhibits
 PT expression of insulin like growth factor binding protein-5 by hormone-
 PT regulated tumor cells.
 XX
 PS Disclosure; Page 35; 45pp; English.
 CC This sequence represents an antisense oligonucleotide targeted against
 CC human insulin-like growth factor binding protein-5 (IGFBP-5). The
 CC invention relates to a composition for treatment of hormone-regulated
 CC cancer, comprising an antisense oligonucleotide (such as this sequence)

CC which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.
 CC The compositions is useful for delaying progression of hormone-regulated
 CC tumour cells such as prostatic cancer cells or breast cancer cells, to an
 CC androgen-independent state, by treating hormone sensitive tumour cells
 CC with the antisense sequence which inhibits expression of IGFBP-5 by the
 CC tumour cells. The composition can also be used for treating a hormone-
 CC responsive cancer in an individual, and administering the composition to
 CC the individual after intiation of hormone-withdrawal to induce apoptotic
 CC cell death of hormone-responsive tumour cells, and therefore delaying the
 CC progression of hormone-responsive cancer cells to a hormone-independent
 CC state in the individual. It can also be used for inhibiting or delaying
 CC metastatic bony progression of an IGF-1 sensitive tumour in a mammal, by
 CC administering the composition to inhibit the expression of IGFBP-5 by the
 CC hormone-responsive cancer cells, and therefore inhibiting or delaying
 CC metastatic bony progression of the tumour
 CC
 SQ Sequence 20 BP, 1 A; 1 C; 15 G; 3 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 3623 GGGTGGGGGTGGGAGG 3640
 1 GGCTGGGGGTGGGAGGCG 18
 RESULT 3016
 ID AAD06582/C
 ID AAD06582 standard; DNA; 20 BP.
 AC AAD06582;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human alpha1(I) collagen gene coding region amplifying SSCP 2REV primer.
 XX
 KM Human; alpha1(I) collagen; gelatin; cytostatic; viral infection;
 KM pharmaceutical; food industry; cosmetic; autoimmune disorder; vaccine;
 KM medical; arterial sealant; bone graft; dermal implant; haemostat; cancer;
 KM rheumatoid arthritis; beverage; photographic application; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200134647-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-US030792.
 XX
 PR 12-NOV-1999; 99US-00439058.
 PR 10-NOV-2000; 2000US-00709700.
 XX
 PA (FIBR-) FIBROGEN INC.
 PA
 PI Bell MP, Neff TB, Polarek JW, Seeley TW;
 XX
 DR WPI; 2001-335911/35.
 XX
 PT Novel isolated and purified bovine or porcine collagens and gelatins
 PT useful in medical, pharmaceutical, food and cosmetic industries, as
 PT vaccine, and for treating autoimmune disorders, infections and cancer.
 XX
 PS Example 1; Page 56; 168pp; English.
 CC The present sequence is a PCR primer used for amplifying the coding
 CC region of human alpha1(I) collagen gene. The present invention relates to
 CC recombinant synthesis of collagens and gelatins derived from animals.
 CC Collagen is useful in medical, pharmaceutical, food and cosmetic
 CC industries. Collagen is an important component of arterial sealants, bone
 CC grafts, drug delivery system, dermal implants, haemostats, and
 CC incontinence implants, and for treating autoimmune disorders such as
 CC rheumatoid arthritis. Collagen is useful in food products such as sausage

caseins, and in cosmetics or facial and skin products such as
moisturizers. Recombinant gelatin is useful in vaccine formulations for
treating viral infections, autoimmune diseases and cancer. Gelatin is
useful in the manufacture or as a component of various pharmaceutical and
medical devices and products, in food and beverage industries, in hair
care and skin care products, as a glue or adhesive in various
manufacturing processes, as a light-sensitive coating in various
electronic devices, as photorealist base in photolithographic processes,
in printing and photographic applications, in laboratory application, and
as a component in various gels used for biochemical and electrophoretic
analysis, including enzymographic gels

Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 263 TGCAGCAGTGTTCAGG 280
Db 20 TGCAGCTGTCTTCAGG 3

RESULT 3017
AAK95028/c
ID AAK95028 standard; DNA; 20 BP.

AAK95028;

06-NOV-2001 (first entry)

Human cDNA clone-specific primer, SEQ ID NO: 4273.

Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.

Homo sapiens.

EP1130094-A2.

05-SEP-2001.

07-JUL-2000; 2000EP-00114089.

08-JUL-1999; 98JP-00194486.

11-JAN-2000; 2000JP-00118774.

02-MAY-2000; 2000JP-00183765.

(HELI-) HELIX RES INST.

Ota T, Nishikawa T, Isogai T, Hayashi K, Ichii S, Kawai Y,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
WPI; 2001-524255/58.

WPI; 2001-524255/58.

830 Primers useful for synthesizing full length cDNA clones and their use
in genetic manipulation.

Example 18; Page 129; 1380pp + Sequence listing; English.

The invention relates to primers for synthesizing full length cDNA
clones. 830 cDNA molecules encoding a human protein have been isolated
and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
been determined. Primers for synthesizing the full length cDNA are useful
for clarifying the function of the protein encoded by the cDNA. The full
length clones were obtained by construction of full length enriched cDNA
libraries that were synthesised by the oligo-capping method. The primers
enable the production of the full length cDNA easily without any special
method. The present sequence is a primer used to amplify a human cDNA
clone provided in the invention

Sequence 20 BP; 8 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 898 ATTGATTCATGTGTGAG 915
Db 20 AATGATTCATGTGTG 3

RESULT 3018

AAF87023
ID AAF87023 standard; DNA; 20 BP.

AAF87023;

18-SEP-2001 (first entry)

Sequencing primer for Human CP2/LSF/LBP-1 ARNm sequence.

LBP-1; human; intron; Alzheimer's disease; diagnosis; ADN sequence;

CP2/LSF/LBP-1 gene; sequencing primer; ss.

Homo sapiens.

EP113081-A1.

04-JUL-2001.

28-DEC-1999; 99EP-00403304.

28-DEC-1999; 99EP-00403304.

(INSP) INST PASTEUR LILIE.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chartier-Harlin M, Amouyel P, Lambert J;

WPI; 2001-427121/46.

Predicting increased risk of human developing Alzheimer's disease,
PT comprises identifying polymorphisms located at untranslated regions of
CP2/LSF/LBP-1 gene.

Example 1; Page 10; 35pp; English.

This sequence is a sequencing primer for the human CP2/LSF/LBP-1 gene
cDNA. The invention relates to a method for predicting an increased risk
of a human subject of developing Alzheimer's disease, comprising assaying
for a mutation within the ADN sequence of the CP2/LSF/LBP-1 gene
including the region controlling the expression of the gene. The method
is useful for predicting an increased risk of a human subject of
developing Alzheimer's disease. Transgenic animals containing sequences
from the CP2/LSF/LBP-1 gene are useful for screening for drugs capable of
reducing or treating symptoms associated with Alzheimer's disease

Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3140 ACTCTGTAGCCCTGCAG 3157
Db 1 AATCTGTAGCCCTGCAG 18

RESULT 3019

AAD15632/c
ID AAD15632 standard; DNA; 20 BP.

AAD15632;

15-NOV-2001 (first entry)

```
DE Human Bcl-2 protein target DNA #6.
XX
XX Human; Bcl-2 protein; genetic disease; antisense target; therapeutic; ss.
XX
OS Homo sapiens.
XX WO200161030-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 14-FEB-2001; 2001WO-US004732.
XX
XX PR 14-FEB-2000; 2000US-00504653.
XX
XX PA (BOLT/) BOLLON A P.
XX PA (GRAY/) GRAY D M.
XX PA (JUSE/) JU-SEOG L.
XX
XX PI Bollon AP, Gray DM, Ju-Seog L;
XX
XX DR WPI; 2001-529916/58.
XX
XX PT Selecting optimal subsequence antisense targets for inhibition of mRNA
XX PT expression of target mRNA for the therapeutic treatment of genetic
XX PT disease.
XX
XX PS Example 9; Page 28; 87pp; English.
XX
XX CC The invention relates to a method for selecting optimal subsequence
XX CC antisense targets. The method involves preparing an antisense
XX CC oligonucleotide capable of inhibiting mRNA expression of target mRNA
XX CC sequences, as well as antisense oligonucleotides capable of binding DNA.
XX CC The antisense and antigen libraries are useful for preparing therapeutic
XX CC agents for the treatment of genetic disease. The present DNA sequence is
XX CC human Bcl-2 protein target DNA related to the invention. Note: The
XX CC present sequence is shown as DNA in the specification; however, in vivo,
XX CC this target sequence would be mRNA
XX
SQ Sequence 20 BP; 0 A; 10 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 40 AGGCTCGCGGCGGCGC 57
DB 20 AGGCCCGCGGCGGCGC 3

RESULT 3020
AAH28626
ID AAH28626 standard; DNA; 20 BP.
XX
XX AC AAH28626;
XX
XX DT 17-JUL-2001 (first entry)
XX
XX DE Human interleukin-13 coding sequence fragment PCR primer #1.
XX
XX KW Human; interleukin-13; IL13; single nucleotide polymorphism; SNP; cancer;
XX KW inflammation; immune disorder; cytokine; asthma; chromosome 5q31;
XX KW fibrosis; forensic; disease susceptibility; drug screening; PCR primer;
XX KW ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200123410-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 27-SEP-2000; 2000WO-US026556.
XX
XX PR 28-SEP-1999; 99US-0156489P.
XX
XX PS
```

```
XX
XX (GENA-) GENA1SSANCE PHARM INC.
XX
XX PI Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
XX DR WPI; 2001-343160/36.
XX
XX PT Novel polynucleotide comprising single nucleotide polymorphisms in human
XX PT interleukin-13 gene is useful for studying expression and function of
XX PT interleukin-13, as well as diagnosing and treating cancer, inflammatory,
XX PT and immune disorders.
XX
XX PS Example 1; Page 30; 85pp; English.
XX
XX CC The present invention provides the protein, cDNA and genomic sequences of
XX CC human interleukin-13 (IL13), and describes the single nucleotide
XX CC polymorphisms (SNPs) found within the gene, which is found on chromosome
XX CC 5q31. IL13 is a pro-inflammatory cytokine thought to be involved in the
XX CC pathogenesis of asthma and other immune and inflammatory diseases. The
XX CC IL13 sequences and the SNPs identified can be used in drug screening, to
XX CC determine an individual's susceptibility to disease, in forensic and
XX CC paternity testing, and to identify treatments for cancer, immune and
XX CC inflammatory diseases, including asthma and diseases characterised by
XX CC fibrosis. The present sequence is an IL13 fragment PCR primer
XX
SQ Sequence 20 BP; 6 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6866 CCGTGGCAGCGAGAGAGAG 6883
DB 3 CCGAGCAGCGCAGAGAGG 20

RESULT 3021
AAH28642
ID AAH28642 standard; DNA; 20 BP.
XX
XX AC AAH28642;
XX
XX DT 17-JUL-2001 (first entry)
XX
XX DE Human interleukin-13 coding sequence fragment PCR primer #17.
XX
XX KW Human; interleukin-13; IL13; single nucleotide polymorphism; SNP; cancer;
XX KW inflammation; immune disorder; cytokine; asthma; chromosome 5q31;
XX KW fibrosis; forensic; disease susceptibility; drug screening; PCR primer;
XX KW ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200123410-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 27-SEP-2000; 2000WO-US026556.
XX
XX PR 28-SEP-1999; 99US-0156489P.
XX
XX PA (GENA-) GENA1SSANCE PHARM INC.
XX
XX PI Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
XX DR WPI; 2001-343160/36.
XX
XX PT Novel polynucleotide comprising single nucleotide polymorphisms in human
XX PT interleukin-13 gene is useful for studying expression and function of
XX PT interleukin-13, as well as diagnosing and treating cancer, inflammatory,
XX PT and immune disorders.
XX
XX PS Example 1; Page 32; 85pp; English.
```

```
XX The present invention provides the protein, cDNA and genomic sequences of
CC human interleukin-13 (IL13), and describes the single nucleotide
CC polymorphisms (SNPs) found within the gene, which is found on chromosome
CC 5q31. IL13 is a pro-inflammatory cytokine thought to be involved in the
CC pathogenesis of asthma and other immune and inflammatory diseases. The
CC IL13 sequences and the SNPs identified can be used in drug screening, to
CC determine an individual's susceptibility to disease, in forensic and
CC paternity testing, and to identify treatments for cancer, immune and
CC inflammatory diseases, including asthma and diseases characterised by
CC fibrosis. The present sequence is an IL13 fragment PCR primer
XX
SQ Sequence 20 BP; 5 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 6866 CTTGGCAGGAGAGAGAGG 6883
Db 2 CTTGAGCAGGAGAGAGG 19
RESULT 3022
AAS03979/c
ID AAS03979 standard; DNA; 20 BP.
XX
AC AAS03979;
XX
DT 29-AUG-2001 (first entry)
XX
DE Biomarker UC band 201 primer #2 used in diagnosis/prognosis of cancer.
XX
KW prostate; breast; bladder; cancer; biomarker; probe; diagnostic;
KW benign prostatic hyperplasia; BPH; therapeutic; human; primer; ss.
XX
OS Homo sapiens.
XX
PN US6218529-B1.
XX
PD 17-APR-2001.
XX
PF 12-JUN-1998; 98US-00097199.
XX
PR 31-JUL-1995; 95US-0001655P.
PR 11-JAN-1996; 96US-0013611P.
PR 31-JUL-1996; 96US-00692787.
XX
PA (UROC-) UROCOR INC.
XX
PI An G, O'hara SM, Ralph D, Veltri R;
XX
DR WPI; 2001-289849/30.
XX
PT New nucleic acids as biomarkers and targets useful for detecting,
PT diagnosing, prognosing, and in developing treatments for prostate, breast
PT and bladder cancer.
XX
PS Example 4; Col 71; 78pp; English.
XX
The sequence represents nucleic acid biomarker UC band 201 primer #2,
CC used in detection of prostate, breast and bladder cancer. Biomarker
CC nucleic acid sequences can be used as hybridisation probes and primers
CC that specifically hybridise to prostate cancer, benign prostatic
CC hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins
CC encoded by the nucleic acid markers can be used to produce antibodies for
CC the detection of prostate, breast or bladder cancer. The nucleic acids
CC can be used as targets for therapeutic intervention in these diseases, in
CC the identification and isolation of full-length gene sequences, including
CC regulatory elements for gene expression, from genomic human DNA
CC libraries, as hybridisation probes for screening genomic human DNA
CC libraries. The kits comprising the nucleic acid sequences are useful for
CC detecting bladder, breast or prostate cancer cells in a biological sample
```

```
XX SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 3414 CTTATTCCTCTGTGCA 3431
Db 19 CATATTCCTCTGTGCA 2
RESULT 3023
AAF23272
ID AAF23272 standard; DNA; 20 BP.
XX
AC AAF23272;
XX
DT 19-MAR-2001 (first entry)
XX
DE Oligonucleotide for detection of Mycobacterium malmoeense.
XX
KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW Mycobacterium dermatit; PCR primer; probe; detection; ss.
XX
OS Mycobacterium malmoeense.
XX
PN WO200073436-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000MO-KR000477.
XX
PR 29-MAY-1999; 99KR-00019631.
PR 29-MAY-1999; 99KR-00019632.
PR 29-MAY-1999; 99KR-00019633.
PR 29-MAY-1999; 99KR-00019634.
PR 29-MAY-1999; 99KR-00019635.
PR 07-APR-2000; 2000KR-00018189.
XX
PA (SHTL-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
PI Kim CM, Park HK, Jang HJ;
XX
DR WPI; 2001-061527/07.
XX
PT Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
PS Claim 27; Page 65; 89pp; English.
XX
The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC dermatit genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
```

CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
SQ Sequence 20 BP; 2 A; 2 C; 3 G; 13 T; 0 U; 0 Other;
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 4644 TGTGATTTCTCTTTG 4661
3 TGTGATTTCTCTTTG 20
RESULT 3024
AAF91363/C
ID AAF91363 standard; DNA; 20 BP.
XX
AC AAF91363;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human E2F transcription factor 1 antisense oligonucleotide #69.
XX
KW Antisense; E2F transcription factor 1; human; infection; inflammation;
KM tumour; ss.
XX
OS Homo sapiens.
XX
PN US6187587-B1.
XX
PD 13-FEB-2001.
XX
PF 02-MAR-2000; 2000US-00517584.
XX
PR 02-MAR-2000; 2000US-00517584.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Popoff I, Brown-Driver VL, Cowsett LM;
XX
DR WPI; 2001-190981/19.
XX
PT Antisense compound capable of inhibiting the expression of E2F
XX transcription factor 1, useful for preventing or delaying infection,
PT inflammation or tumor formation.
XX
PS Example 15; Col 43; 40pp; English.
XX
CC The present invention relates to antisense compounds up to 30 nucleobases
CC in length targeted to a E2F transcription factor 1. The invention is
CC useful for inhibiting the expression of E2F transcription factor 1 in
CC cells or tissues. The antisense oligonucleotides may also be used as a
CC research agent and to prevent infection, inflammation or tumours
XX
SQ Sequence 20 BP; 4 A; 14 C; 0 G; 2 T; 0 U; 0 Other;
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2870 GGAGAGGGAGGTGGGT 2887
19 GGAGAGGGAGGTGGGT 2
RESULT 3025
ABL57890
ID ABL57890 standard; DNA; 20 BP.
XX
AC ABL57890;
XX
DT 11-SEP-2003 (revised)

DT 04-JUL-2002 (first entry)
XX
DE Hypersensitive reaction and pathogenicity, hrpC2, PCR primer Xcc2.4.
XX
KW PCR; primer; hypersensitive reaction and pathogenicity; hrpC2;
KM exo-polyasaccharide; xanthan gum; ss.
XX
OS Xanthomonas campestris; pv vesicatoria.
XX
FN WO200078967-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-FR001725.
XX
PR 22-JUN-1999; 99FR-00007963.
XX
PA (RHOD) RHODIA CHIM.
XX
PI Pierrard J, Simon J, Chevallereau P;
XX
DR WPI; 2001-102725/11.
XX
PT New Xanthomonas campestris bacteria strains for use in production of exo-
XX polyasaccharides are made non-virulent by inactivation of at least one
XX virulence gene.
XX
PS Example 1; Page 25; 33pp; French.
XX
CC The present invention relates to new Xanthomonas campestris bacteria
XX strains made non-virulent by inactivation of at least one virulence gene
CC but which have retained the capacity to produce exo-polyasaccharides
CC (preferably xanthan gum). One such virulence gene deleted to produce the
CC bacterial strains was the hrpC2 gene (Hypersensitive Reaction and
CC pathogenicity). The hrp genes are essential for pathogenicity in plants.
CC The present sequence is a PCR primer used to clone the hrpC2 gene in an
CC example from the invention. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2650 TACCACCTGGTGCACAG 2667
2 TTCACCTGGTGCACAG 19
RESULT 3026
AAH46127/C
ID AAH46127 standard; DNA; 20 BP.
XX
AC AAH46127;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human CLCA1 sequencing primer PR22, SEQ ID NO:29.
XX
KW Human CLCA1; goblet cell; mouse Gob-5 orthologue; drug screening;
XX expression inhibition; antisense therapy; gene therapy;
KW chronic obstructive pulmonary disease; bronchial asthma; antiasthmatic;
KW sequencing primer; ss.
XX
OS Homo sapiens.
XX
PN WO200038530-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-JP008232.
XX

```

PR 24-NOV-1999; 99JP-00333479.
PR 27-APR-2000; 2000JP-00127589.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Nakanishi A, Morita S;
XX
XX WPI, 2001-355935/37.
XX
XX New antisense nucleotide, useful for treatment and prevention of
XX bronchial asthma and chronic obstructive pulmonary disease.
XX
XX Example 5; Page 95; 104pp; Japanese.
XX
XX The invention relates to an antisense nucleotide targeted to the mouse
XX Gob-5 gene (coding sequence shown in AAH46101) or its human counterpart,
XX the CLCA1 gene (coding sequence shown in AAH46102). The invention also
XX relates to an antibody specific for the Gob-5 protein, medical and
XX diagnostic compositions containing the antisense nucleotide or the
XX antibody, and methods and kits for screening for compounds which inhibit
XX the protein. Gob-5 and CLCA1 are proteins expressed by goblet cells. The
XX antisense oligonucleotides and antibody are therefore useful for the
XX treatment and prevention of bronchial asthma and chronic obstructive
XX pulmonary disease. Sequences AAH46125-AAH46136 represent primers used in
XX an exemplification of the invention to sequence human CLCA1 cDNA
XX (AAH46124)
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;
XX Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
XX
XX Oy 1057 GTTACCCGTCGCCCTGCT 1074
XX ||||| ||||| |||||
XX 20 GTTACCACTGCCCATGCT 3
XX
XX Db
XX
XX RESULT 3027
XX AAH46128
XX ID AAH46128 standard; DNA; 20 BP.
XX
XX AC AAH46128;
XX
XX DT 11-SEP-2001 (first entry)
XX
XX DE Human CLCA1 sequencing primer PR23, SEQ ID NO:30.
XX
XX KW Human CLCA1; goblet cell; mouse Gob-5 orthologue; drug screening;
XX expression inhibition; antisense therapy; gene therapy;
XX KW chronic obstructive pulmonary disease; bronchial asthma; antiasthmatic;
XX sequencing primer; sg.
XX
XX OS Homo sapiens.
XX
XX PN WO200138530-A1.
XX
XX PD 31-MAY-2001.
XX
XX PF 22-NOV-2000; 2000WO-JP008232.
XX
XX PR 24-NOV-1999; 99JP-00333479.
XX PR 27-APR-2000; 2000JP-00127589.
XX
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX PI Nakanishi A, Morita S;
XX
XX DR WPI; 2001-355935/37.
XX
XX New antisense nucleotide, useful for treatment and prevention of
XX bronchial asthma and chronic obstructive pulmonary disease.
XX

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PS Example 5; Page 95; 104pp; Japanese.
XX
XX The invention relates to an antisense nucleotide targeted to the mouse
XX Gob-5 gene (coding sequence shown in AAH46101) or its human counterpart,
XX the CLCA1 gene (coding sequence shown in AAH46102). The invention also
XX relates to an antibody specific for the Gob-5 protein, medical and
XX diagnostic compositions containing the antisense nucleotide or the
XX antibody, and methods and kits for screening for compounds which inhibit
XX the protein. Gob-5 and CLCA1 are proteins expressed by goblet cells. The
XX antisense oligonucleotides and antibody are therefore useful for the
XX treatment and prevention of bronchial asthma and chronic obstructive
XX pulmonary disease. Sequences AAH46125-AAH46136 represent primers used in
XX an exemplification of the invention to sequence human CLCA1 cDNA
XX (AAH46124)
XX
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;
XX Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
XX
XX Oy 1057 GTTACCCGTCGCCCTGCT 1074
XX ||||| ||||| |||||
XX 1 GTTACCACTGCCCATGCT 18
XX
XX Db
XX
XX RESULT 3028
XX AAS00329
XX ID AAS00329 standard; DNA; 20 BP.
XX
XX AC AAS00329;
XX
XX DT 17-MAY-2001 (first entry)
XX
XX DE Primer c816F, used to sequence human RAD51 gene.
XX
XX KW Human; RAD51; breast cancer; BRCA1; BRCA2; primer; sg.
XX
XX OS Homo sapiens.
XX
XX PN WO200118254-A2.
XX
XX PD 15-MAR-2001.
XX
XX PF 08-SEP-2000; 2000WO-US024786.
XX
XX PR 10-SEP-1999; 99US-0153288P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Wang WW, Struwing JP;
XX
XX DR WPI; 2001-235217/24.
XX
XX PT New nucleic acids comprising a mutant of the RAD51 gene, useful for
XX diagnosing genetic predisposition or susceptibility to breast cancer.
XX
XX PS Example; Page 18; 42pp; English.
XX
XX The sequence represents primer c816F, used to sequence the human RAD51
XX gene. The nucleic acid is useful in diagnosing genetic predisposition or
XX susceptibility to breast cancer in an individual using the following
XX steps: (1) detecting a mutation in the RAD51 gene in a human subject,
XX comprising analysing a sample from the subject to detect the mutation;
XX (2) assessing the risk of developing breast cancer, comprising: (a)
XX analysing a sample from the subject for the presence of BRCA1 and/or
XX BRCA2 mutations; and (b) if (a) is positive, analysing the sample for a
XX mutation in the RAD51 gene, where the presence of the RAD51 mutation
XX indicates an increased risk in developing breast cancer in the subject as
XX compared to a subject having at least one of the BRCA mutations and a
XX wild-type RAD51 gene. Primers derived from the sequence can be used in a
XX kit for detecting a mutation in the RAD51 gene of a subject, which is
XX associated with a predisposition to breast cancer, comprising at least 2
XX

```


CC	nucleic acid primers derived from the RAD51 gene sequence
XX	
QQ	Sequence 20 BP; 8 A; 9 C; 2 G; 1 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	
Db	2954 CAAGACGACCACCGGCC 2971 CAACGACGACCACCGAC 19
RESULT 3029	
ID	AAH80771 standard; cDNA; 20 BP.
XX	
AC	AAH80771;
XX	
DT	11-SEP-2003 (revised)
DT	19-SEP-2001 (first entry)
XX	
DE	Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 735.
XX	
KW	Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KM	disease diagnosis; ss.
XX	
OS	Human immunodeficiency virus 1.
XX	
PN	US6251588-B1.
XX	
PD	26-JUN-2001.
XX	
PF	10-FEB-1998; 98US-00021701.
XX	
PR	10-FEB-1998; 98US-00021701.
XX	
PA	(AGIL-) AGILENT TECHNOLOGIES INC.
PI	Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
DR	WPI; 2001-424456/45.
XX	
PT	Predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence, useful for evaluating oligonucleotide probe sequences, by identifying a oligonucleotides based on the evaluation of parameters.
PT	
PS	Example 2; Col 71; 342pp; English.
XX	
CC	The present invention describes a method for predicting the potential of an oligonucleotide to hybridize to a (complementary) target nucleotide sequence, involving identifying a subset of oligonucleotides within the predetermined number of unique oligonucleotides based on the evaluation of the parameter. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridisable to the target nucleotide sequence. This is useful for evaluating oligonucleotide probe sequences. The present sequence of an oligonucleotide described in the exemplification of the invention. (Updated on 11-SEP-2003 to standardise OS field)
CC	
CC	
SQ	Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	
Db	5703 CCTTCCTTCTCCTTCT 5720 CCTTCCTTCTCCTTCT 19
RESULT 3030	

AB98541	AB98541 standard; DNA; 20 BP.
ID	AB98541
AC	AB98541;
XX	
DT	25-APR-2002 (first entry)
XX	
DE	Murine G protein-coupled receptor, IGPCR17, PCR primer #2.
XX	
XX	G protein-coupled receptor; IGPCR17; analgesic; neuroleptic;
XX	craniqluier; antiparkinsonian; neuroprotective; nootropic; murine;
KW	anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;
KW	antidiarrhetic; osteopathic; antisthmatic; antiallegic; antiarthritic;
KW	immunosuppressive; gene therapy; psychiatric disorder;
KW	central nervous system disorder; movement dysfunction; schizophrenia;
KW	multiple sclerosis; Alzheimer's disease; kidney disease; obesity;
KW	gastrointestinal disorder; osteoporosis; infection;
KW	gynecological disorder; PCR primer; ss.
XX	
OS	Mus musculus.
XX	
PN	WO200202599-A2.
XX	
PD	10-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP007532.
XX	
PR	30-JUN-2000; 2000US-0215759P.
XX	
PA	(INGE-) INGENIUM PHARM AG.
PI	Wattler F, Wattler S, Trommler P, Nehls MC;
XX	
DR	WPI; 2002-140080/18.
XX	
PT	New human or mouse G protein-coupled receptor protein, IGPCR17, useful
PT	for diagnosis, prevention, amelioration or treatment of central nervous
PT	system disorders such as Tourette's syndrome, Parkinson's disease and
PT	pain.
XX	
PS	Example 7; Page 40; 71pp; English.
XX	
CC	The present invention relates to human and murine G protein-coupled
CC	receptor (GPCR) protein, IGPCR17 (AAW48353 and AAW48354). The coding
CC	sequence for IGPCR17 is useful in gene therapy for prevention,
CC	amelioration or treatment of diseases characterised by aberrant
CC	expression or activity of IGPCR17, where the disease is a psychiatric or
CC	central nervous system (CNS) disorder associated with signal processing
CC	in CNS such as learning and memory disorders, movement dysfunctions,
CC	tics, tremor, Tourette's syndrome, Parkinson's disease, Huntington's
CC	disease, dyskinesias, dystonia, pain and spasms. In addition, IGPCR17 and
CC	its coding sequence are useful in diagnosis, prevention, amelioration or
CC	treatment of diseases associated with signal processing in CNS.
CC	Schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as
CC	obsessive compulsive disorder (COD), multiple sclerosis, Alzheimer's
CC	disease/dementia, anorexia, kidney diseases such as renal failure,
CC	obesity, gastrointestinal disorders such as irritable bowel syndrome
CC	(IBS), diarrhoea, motility disorders and conditions of delayed gastric
CC	emptying, osteoporosis, infections such as bacterial, fungal, protozoal
CC	and viral infections, asthma, allergy, arthritis, sepsis and
CC	gynecological disorders. The present sequence is a PCR primer for murine
CC	IGPCR17 coding sequence. This sequence was used along with the primer of
CC	AB98540 for tissue-specific expression analyses of IGPCR17 in an example
CC	from the invention. The resulting PCR product is given in AB98542
XX	
SQ	Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
0y	TCGGAACCTTAGGCTTAAC 6346

Db 3 TGGGAACTTTGGCTGAAC 20

RESULT 3031
ABK9487
ID ABR9487 standard; DNA; 20 BP.

AC ABR9487;
XX
DT 29-AUG-2002 (first entry)
XX
DE Fat regulated gene associated PCR primer #64.

XX Fatty acid regulated gene; polyunsaturated fatty acid disorder;
KM Fatty acid regulated gene; polyunsaturated fatty acid disorder;
KM dyslipidaemia; atherosclerosis; coronary artery disease;
KM dyslipidaemia; atherosclerosis; coronary artery disease;
KM cerebrovascular disease; peripheral vascular disease; inflammation;
KM sinusitis; asthma; pancreatitis; osteoarthritis; rheumatoid arthritis;
KM acne; body weight disorder; obesity; cachexia; anorexia;
KM psychiatric disorder; cancer; cystic fibrosis; pre-menstrual syndrome;
KM diabetes; diabetic complication; genetic polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200240666-A2.
XX
PD 23-MAY-2002.
XX
PF 19-NOV-2001; 2001WO-CA001632.
XX
PR 17-NOV-2000; 2000US-0248589P.
XX
PA (XENON-) XENON GENETICS INC.
PI Winther MD, Goldberg YP, Knickle LC, Haardt M, Allen SJ;
PI Ponton A, De Arbuena RJ, Jenkins DK, Nwaka SO;
XX
DR WPI; 2002-508327/54.

XX Novel isolated polypeptide segment encoded by fat regulated genes, useful
PT for diagnosing the presence of or a predisposition for a disorder
PT involving fatty acid regulated genes in a subject.
XX
PS Example 2; Page 81; 225pp; English.

XX The invention describes an isolated polypeptide segment (I) whose genes
CC are fat regulated. (I) or the polynucleotide encoding it (II) are useful
CC for diagnosing the presence of or a predisposition for a disorder
CC involving fatty acid regulated genes in a subject. A composition
CC containing (I) or (II) is useful for treating a disorder involving fatty
CC acid regulated genes, where the disorder is selected from a
CC polyunsaturated fatty acid (PUFA) disorder, eczema, cardiovascular
CC disorders (such as hypertriglyceridaemia, dyslipidaemia, atherosclerosis,
CC coronary artery disease, cerebrovascular disease or peripheral vascular
CC disease), inflammation (such as sinusitis, asthma, pancreatitis,
CC osteoarthritis, rheumatoid arthritis or acne), body weight disorders
CC (such as obesity, cachexia or anorexia), psychiatric disorders, cancer,
CC cystic fibrosis, pre-menstrual syndrome, diabetes, and diabetic
CC complications. (I) or (II) is useful as research agent and materials for
CC discovery of treatments and diagnostics for a disease, particularly human
CC disease. (II) is useful for constructing nucleotide probes and primers, of
CC for detecting genetic polymorphism, for detecting changes in the level of
CC expression of (II), and as a diagnostic tool. This sequence represents a
CC PCR primer used to isolate DNA encoding fat regulated genes
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3492 AGGCACTTTGGCACTTAG 3509
||||| |||||||

Db 2 AGGAGATGATGCACTTTG 19

RESULT 3032
AAS97790
ID AAS97790 standard; DNA; 20 BP.

AC AAS97790;
XX
DT 12-MAR-2002 (first entry)
XX
DE Murine SACL gene-specific oligonucleotide PCR primer #357.

XX Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
XX protein replacement therapy.
XX
OS Mus sp.
XX
PN WO200183749-A2.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013387.
XX
PR 28-APR-2000; 2000US-0200794P.
PR 28-JUL-2000; 2000US-0221419P.
PR 10-NOV-2000; 2000US-0247443P.
XX
PA (WARNER) WARNER LAMBERT CO.
PA (MONTELL) MONTELL CHEM SENSES CENT.
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PV, Li S, Li X;
PI Ohmen JD, Reed DR, Ross D, Tordoff MG;
XX
DR WPI; 2002-075162/10.

XX Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS Claim 14; Page 88; 239pp; English.

XX The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 544 GTCGACTTTGGAGTGAACA 561
||||| |||||||
Db 3 GTCGACATTTAGGTGAACA 20

```

RESULT 3033
AAS97594/c
ID AAS97594 standard; DNA; 20 BP.
XX
AC AAS97594;
XX
DE 12-MAR-2002 (first entry)
XX
DE Murine SACL gene-specific oligonucleotide PCR primer #199.
XX
XX Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KM protein replacement therapy.
XX
OS Mus sp.
XX
PN MO200183749-A2.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013387.
XX
PR 28-APR-2000; 2000US-0200794P.
PR 28-JUL-2000; 2000US-0221419P.
PR 10-NOV-2000; 2000US-0247443P.
XX
PA (WARN ) WARNER LAMBERT CO.
PA (MONE-) MONELL CHEM SENSES CENT.
XX
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohmen JD, Reed DR, Rose D, Tordoff MG;
XX
DR WPI; 2002-075162/10.
XX
PT Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS Claim 14; Page 81; 239pp; English.
XX
CC The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes
XX
SQ Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6069 TAAATCTGTCCTTTTC 6086
Db 18 TAAATCTGTCCTTTTC 1
RESULT 3034
AAS97784
ID AAS97784 standard; DNA; 20 BP.

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XX
AC AAS97784;
XX
DE 12-MAR-2002 (first entry)
XX
DE Murine SACL gene-specific oligonucleotide PCR primer #351.
XX
XX Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KM protein replacement therapy.
XX
OS Mus sp.
XX
PN MO200183749-A2.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013387.
XX
PR 28-APR-2000; 2000US-0200794P.
PR 28-JUL-2000; 2000US-0221419P.
PR 10-NOV-2000; 2000US-0247443P.
XX
PA (WARN ) WARNER LAMBERT CO.
PA (MONE-) MONELL CHEM SENSES CENT.
XX
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohmen JD, Reed DR, Rose D, Tordoff MG;
XX
DR WPI; 2002-075162/10.
XX
PT Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS Claim 14; Page 88; 239pp; English.
XX
CC The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 544 GTGACATTGAGGTGACA 561
Db 3 GTGACATTGAGGTGACA 20
RESULT 3035
AAS97786
ID AAS97786 standard; DNA; 20 BP.
AC AAS97786;
XX

```

DT 12-MAR-2002 (first entry)

XX Murine SACL gene-specific oligonucleotide PCR primer #353.

DE Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;

XX obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;

KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;

KW protein replacement therapy.

XX

OS Mus sp.

XX

XX WO200183749-A2.

XX

XX 08-NOV-2001.

XX

XX 25-APR-2001; 2001WO-US013387.

XX

XX 28-APR-2000; 2000US-0200794P.

PR 28-JUL-2000; 2000US-0221419P.

PR 10-NOV-2000; 2000US-0247443P.

XX

PA (WARN) WARNER LAMBERT CO.

PA (MONE-) MONELL CHEM SENSES CENT.

XX

XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong RJ, Li S, Li X;

PI Ohmen JD, Reed DR, Ross D, Tordoff MG,

XX

XX WPI; 2002-075162/10.

XX

PT Novel isolated polypeptide comprising variant form of mouse or human SACL

PT polypeptide, and is associated with altered preference for carbohydrates

PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

XX

XX Claim 14; Page 88; 239pp; English.

XX

CC The invention relates to an isolated polypeptide, comprising a variant

CC form of mouse or human SACL polypeptide. The variant form is associated

CC with altered preference for carbohydrates, other sweeteners or ethanol.

CC The polypeptide and its associated DNA sequence can be produced by

CC recombinant techniques and is useful for preventing obesity, diabetes or

CC alcoholism associated with SACL expression. The sequences are useful in

CC screening for drugs and sweeteners. Recombinant cell lines and transgenic

CC embryos may be used in screening for and identifying agents that induce

CC or repress function of SACL. Predisposition to diabetes, obesity or

CC alcoholism can be ascertained by testing any fluid or tissue of a human

CC (such as blood, pancreas or tongue) for sequence variations of the SACL

CC gene. A sequence variation of the SACL locus may indicate a

CC predisposition to diabetes, obesity and/or alcoholism and may provide a

CC diagnostic mark. The polynucleotide can be detected in a biological

CC sample by contacting the DNA with a probe to form a hybridisation complex

CC which is then detected. The sequences represent cDNA encoding human and

CC mouse SACL polypeptides and PCR primers specific for the SACL genes

XX

SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGACCTTGGAGGAC 561

DB 3 GTGACATTGAGTGACA 20

RESULT 3036

ID ABK37182/c

XX ABK37182 standard; DNA; 20 BP.

AC ABK37182;

XX

XX 08-MAY-2002 (first entry)

DT

XX Human lysophospholipase I gene, antisense oligonucleotide #134.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;

KW antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;

KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;

XX antisense gene therapy; primer; ss.

OS Homo sapiens.

OS Synthetic.

XX

XX WO200210185-A1.

XX

XX 07-FEB-2002.

XX

XX 20-JUL-2001; 2001WO-US022975.

XX

XX 31-JUL-2000; 2000US-00629645.

XX

XX (ISIS-) ISIS PHARM INC.

XX

XX Bennett CF, Wyatt JR;

XX

XX WPI; 2002-188720/24.

XX

XX

PT Novel antisense compound useful for treating inflammation,

PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and

PT myocardial ischemia, inhibits lysophospholipase I.

XX

XX Claim 3; Page 83; 131pp; English.

XX

CC The invention relates to an antisense compound (I) 8-30 nucleobases in

CC length targeted to a nucleic acid molecule encoding lysophospholipase I

CC (II), where (I) specifically hybridises with and inhibits the expression

CC of (II). (I) is useful for inhibiting the expression of (II) in cells or

CC tissues, and for treating a human having a disease or condition

CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,

CC and cardiovascular disorders such as atherosclerosis and myocardial

CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also

CC useful for distinguishing functions of various members of a biological

CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191

CC represent lysophospholipase I coding sequences, antisense

CC oligonucleotides and related PCR primers of the invention. Note:

CC Antisense oligonucleotides are modified such that bases 1-5 and 16-20 are

CC 2'-methoxyethyl (2'-MOE) nucleotides, all bases have phosphorothioate

CC linkages, and all cytidines are 5-methyl cytidines

XX

SQ Sequence 20 BP; 13 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6464 CTTTCTTTCTGTTGT 6481

DB 18 CTGTATTTCTCTTGT 1

RESULT 3037

ID ABN83847/c

XX ABN83847 standard; DNA; 20 BP.

XX

XX ABN83847;

XX

XX 10-SEP-2002 (first entry)

XX

XX Insulin gene -2221 MspI polymorphism PCR primer INS56.

DE

XX Non-insulin dependent diabetes; type II diabetes; obesity; human;

KW diagnosis; prognosis; linkage disequilibrium; polymorphism; marker;

KW insulin; PCR; primer; ss.

XX

XX Homo sapiens.

XX

XX WO200236820-A2.

XX PD 10-MAY-2002.
 XX PF 31-OCT-2001; 2001WO-IB002747.
 XX PR 02-NOV-2000; 2000US-0245493P.
 XX PA (BOUG/) BOUGNERS P.
 XX DR WPI; 2002-519258/55.
 XX PT Determining risk of developing non-insulin dependent diabetes mellitus,
 PT comprises determining the identity of polymorphic bases of a marker in
 PT linkage disequilibrium with the insulin HphI locus.
 XX PS
 XX Example 2; Page 57; 74pp; English.
 CC The present invention provides methods for determining the risk of
 CC development of non-insulin dependent diabetes mellitus (NIDDM or type II
 CC diabetes) in a subject. It results from the discovery that homozygotes of
 CC the HphI locus of the insulin gene along with body fat measurement serve
 CC as an excellent indicator of NIDDM susceptibility. Thus, obese
 CC individuals with HphI(+/+) or (-/-) genotypes are significantly more
 CC likely to develop NIDDM than obese individuals with HphI(+/-) genotypes.
 CC A method of determining the risk of developing NIDDM in an individual
 CC involves genotyping at least one marker in linkage disequilibrium with
 CC the insulin HphI locus. The marker is especially -4217 bp, -2221 MspI,
 CC -23 HphI, +1428 FokI, +1100 AluI and +32000 ApaI. In an example, new
 CC polymorphisms were screened to determine whether they altered a
 CC restriction site. These sites were then amplified in a panel of random
 CC diabetes and controls, and a subset of polymorphisms was amplified using
 CC the primers given in ABN83845-56. The present primer, INSS56, was used
 CC with primer INSS7 to amplify the -2221 MspI site. PCR products were
 CC digested with MspI and gel electrophoresed to determine genotype.
 CC Products of digestion were 108 and 78 bp for +/+, 186, 108 and 78 bp for
 CC +/-, and 186 bp for -/- genotypes, where (+) indicates the restriction
 CC enzyme cut the sequence, and (-) indicates a cut was not made. The
 CC invention provides methods for diagnosing a subtype of NIDDM, for
 CC estimating the frequency of a haplotype for a set of genetic markers in a
 CC population suffering from juvenile obesity (claimed), and methods to
 CC facilitate therapy and maintenance of NIDDM patients
 CC XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4729 CTTGAGGCCAGCTGAG 4746
 Db 18 CTTAGAGCCAGCTGTC 1
 RESULT 3038
 AB874284/c
 ID AB874284 standard; DNA; 20 BP.
 XX
 AC AB874284;
 XX
 DT 09-DEC-2002 (first entry)
 XX
 DE Human calcium channel alpha2delta SSCP PCR primer #8.
 XX
 XX Human; sea primer; calcium channel alpha2delta; splice isoform; CACNA2D2;
 KM gene therapy; Lambert-Eaton myasthenic syndrome; LEMS; PCR;
 KM autoimmune disease; epilepsy; migraine; episodic ataxia; cancer; stroke;
 KM brain trauma; Alzheimer's disease; multifactor dementia; convulsion;
 KM Korsakoff's disease; amyotrophic lateral sclerosis; seizure;
 KM Huntington's disease; amnesia; cardiac arrhythmia; angina pectoris;
 KM hypoxia; ischemia; myocardial infarction; congestive heart failure;
 KM muscular dystrophy; hypertension; chromosome 3p21.3; lung cancer;
 KM breast cancer; preneoplastic lesion; hyperplasia; dysplasia; carcinoma;
 KM SSCP; single strand change polymorphism.

XX OS Homo sapiens.
 XX XX US6441156-B1.
 XX EN
 XX PD 27-AUG-2002.
 XX PF 22-DEC-1999; 99US-00470443.
 XX PR 30-DEC-1998; 98US-0114359P.
 XX XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX XX
 XX PI Lerman MI, Latic F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;
 XX DR WPI; 2002-730574/79.
 XX PT Novel purified nucleic acid sequence encoding human calcium channel
 PT alpha2delta subunit protein, useful for detecting, preventing and
 PT treating cancer, stroke, brain trauma, Huntington's disease, myocardial
 PT infarction.
 XX PS
 XX Example 7; Col 46; 77pp; English.
 CC The invention relates to a purified nucleic acid sequence (referred as
 CC CACNA2D2 gene which encodes human calcium channel alpha2delta-2 subunit
 CC protein) comprising a fully defined alpha2delta splice isoform 1, 2 or 3
 CC nucleic acid sequence, or its complement and the encoded proteins. Also
 CC include are: (1) a method of producing a calcium channel protein which
 CC involves introducing a recombinant expression vector comprising the
 CC CACNA2D2 nucleic acid and encoding the calcium channel protein, into a
 CC cultured host cell under conditions such that the host cell expresses the
 CC amino acid sequences; and (2) a method for co-expressing calcium channel
 CC proteins, comprising carrying out the method of (1), but with one or more
 CC than one expression vector comprising one or more nucleic acid sequences
 CC encoding the splice variants. CACNA2D2 nucleic acid is useful for
 CC producing a calcium channel protein. The recombinantly expressed
 CC polypeptide (LEMS) (an autoimmune disease) and for identifying compounds
 CC useful for treating other diseases associated with abnormal calcium
 CC channel protein activity (e.g. epilepsy, migraine, episodic ataxia,
 CC cancer, stroke, brain trauma, Alzheimer's disease, multifactor dementia,
 CC Korsakoff's disease, amyotrophic lateral sclerosis, convulsions,
 CC seizures, Huntington's disease, amnesia, cardiac arrhythmia, angina
 CC pectoris, hypoxic damage to the cardiovascular system, ischemic heart
 CC to the cardiovascular system, myocardial infarction, congestive heart
 CC failure, muscular dystrophy and hypertension) CACNA2D2 nucleic acid is
 CC useful as primers and probes for detecting presence of nucleic acid
 CC sequence encoding at least a portion of calcium channel protein, in
 CC detection, identification and isolation of alpha2delta sequences
 CC diagnosing and typing of preneoplasias and cancers, since genetic
 CC disruption of 3p21.3 region (in which the alpha2delta gene is located)
 CC is common in cancer (e.g. lung cancer and breast cancer) and
 CC preneoplastic lesion (e.g. hyperplasia, dysplasia, carcinoma in situ).
 CC The present is an SSCP (single strand change polymorphism) PCR primer
 CC used to detect polymorphisms in sequences encoding a human calcium
 CC channel alpha2delta splice isoform protein
 CC XX
 SQ Sequence 20 BP; 1 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 5287 CAGCCTCTACTCCACGA 5304
 Db 20 CAGCCGCGACTCCACGA 3
 RESULT 3039
 ABA90030/c
 ID ABA90030 standard; DNA; 20 BP.
 XX


```
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
XX the obtained data.
PS Example 6; Page 18; 34pp; Japanese.
XX
PS This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 14 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6682 TTTATTTTATATATAT 6699
DB 18 TTTTATATATATATAT 1
RESULT 3042
ABA97650/C
ID ABA97650 standard; DNA; 20 BP.
XX
AC ABA97650;
XX
DT 11-APR-2002 (first entry)
XX
DE probe u.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS unidentified.
XX
PN JP2001286300-A.
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
XX the obtained data.
```

```
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6682 TTTATTTTATATATAT 6699
DB 18 TTTTATATATATATAT 1
RESULT 3043
AAS16663
ID AAS16663 standard; DNA; 20 BP.
XX
AC AAS16663;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Inhibitor of DNA binding-1, antisense oligonucleotide ISIS #124761.
XX
KW Human; inhibitor of DNA binding-1; Id-1; cytostatic; antiinflammatory;
KW immunosuppressive; antisense therapy; antisense oligonucleotide;
KW hyperproliferative disorder; immune disorder; muscular disorder; ss;
KW vascular disorder; pancreatic disorder; infection; inflammation; tumour.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT 1..20
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone. Also, all cytidine
FT residues are 5-methyl cytidines"
FT 1..5
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT 16..20
FT modified_base /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
WO200183513-A2.
08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013209.
XX
PR 28-APR-2000; 2000US-00561497.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Bennett CF, Wyatt JR;
XX WPI; 2002-041477/05.
XX
DR Novel antisense compound, specifically hybridizing to and inhibiting the
XX expression of inhibitor of DNA binding-1, useful for treating
XX hyperproliferative, immune, muscular, vascular or pancreatic disorder.
XX Example 15; Page 82; 105pp; English.
XX
PT The invention relates to novel antisense compounds (I) 8-30 nucleobases
CC
```


in length targeted to a nucleic acid molecule encoding inhibitor of DNA binding-1, where (i) specifically hybridises with and inhibits the expression of inhibitor of DNA binding-1. Antisense inhibition of human oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a deoxy gap was tested. A series of oligonucleotides were designed to target different regions of the human inhibitor of DNA binding-1 RNA. The compounds were analysed for their effect on human inhibitor of DNA binding-1 mRNA levels by quantitative real-time polymerase chain reaction (PCR). The result showed that the oligonucleotides showed at least 25% inhibition of human inhibitor of DNA binding-1 expression. (i) is useful for inhibiting the expression of inhibitor of DNA binding-1 in cells or tissues by contacting the cells or tissues with (i). (i) is also useful for treating a human having a disease or condition associated with inhibitor of DNA binding-1 by administering a therapeutically or prophylactically effective amount of (i), where the disease or condition is a hyperproliferative disorder, immune disorder, muscular disorder, vascular disorder or pancreatic disorder. (i) may also be used for diagnostics, therapeutics, prophylaxis (e.g., to prevent or delay infection, inflammation or tumour formation), and as research reagents and kits. (i) may be safely and effectively administered to humans. The present sequence represents a human inhibitor of DNA binding-1, antisense oligonucleotide used in the method of the invention

Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3270 ATTTGTTAAGAGAGAAA 3287
|||||
3 ATTGTTAATTAACAAAA 20

RESULT 3044
ABL94386/C
ID ABL94386 standard; DNA; 20 BP.
AC ABL94386;
XX
DT 29-JUN-2002 (first entry)
XX
DB Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:152.
XX
KW Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;
KW LAP; TCF5; CRP2; NF16; IL6BP; NF-M; AGP/EBP; Apc/EBP;
KW transcription factor; tissue development; cellular function;
KW proliferation; differentiation; hormone responsiveness;
KW oxidative stress response; IL-6 signalling mediator; interleukin-6;
KW carbohydrate metabolism; immunity; Th1 response; female fertility;
KW gluconeogenesis; ovarian; cancer; tumour formation; type II; diabetes;
KW infection; inflammation; expression inhibition; phosphorothioate;
KW antisense oligonucleotide; ss.
XX
OS Mus musculus.
XX
FH Key location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
XX

US6271030-B1.
07-AUG-2001.
14-JUN-2000; 2000US-00593711.
14-JUN-2000; 2000US-00593711.
14-JUN-2000; 2000US-00593711.
(ISIS-) ISIS PHARM INC.
Monia BP, Butler MM, Wyatt J;
WPI; 2002-214451/27.
Novel antisense compound targeted to nucleic acids encoding human or mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for inhibiting expression of human or mouse C/EBP beta in cells/tissues.
Example 17; Col 49-50; 69pp; English.
Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha) gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human and/or mouse C/EBP alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels by quantitative real-time PCR. The C/EBP family of proteins are a family of transcription factors which regulate the expression of a wide range of genes that control normal tissue development, cellular function, cellular proliferation and functional differentiation. C/EBP beta (also known as C/EBP2, LAP, TCF5, CRP2, NF16, IL6BP, NF-M, AGP/EBP and Apc/EBP) primarily regulates hormone responsiveness and oxidative stress responses and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is thought to be involved in carbohydrate metabolism, immunity, the Th1 response, female fertility and gluconeogenic pathways. C/EBP beta is expressed in the liver, lung, spleen, kidney, brain, and testis, with the highest expression found in the lung. It is also expressed at a higher level in malignant ovarian tissue compared with normal ovarian tissue, and its expression in pancreas is upregulated in response to chronically elevated levels of glucose, indicating that it is involved in the impairment of insulin secretion in type II diabetes. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with C/EBP beta expression, such as cancer (particularly ovarian cancer), tumour formation, diabetes (particularly type II diabetes), infection, or inflammation

Sequence 20 BP; 0 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

7414 AGCAGCAGCAGCAGCAGC 7431
|||||
18 AGCGCAGCAGCAGCGCAGC 1

RESULT 3045
ABI93710
ID ABI93710 standard; DNA; 20 BP.
AC ABI93710;
XX
DT 16-FEB-2002 (first entry)
XX
DB Capture oligonucleotide zip ID#797 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.

PN	XX	WO200179548-A2.
XX	XX	
PD	XX	25-OCT-2001.
XX	XX	
PF	XX	04-APR-2001; 2001WO-US010958.
XX	XX	
PR	XX	14-APR-2000; 2000US-0197271P.
XX	XX	
PA	XX	(CORR) CORNELL RES FOUND INC.
XX	XX	
PI	XX	Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
XX	XX	
DR	XX	WPI, 2002-034366/04.
XX	XX	
PT	XX	Designing capture oligonucleotide probes for use on a support to which
XX	XX	complementary oligonucleotides hybridize with little mismatch.
PS	XX	Example 5; Fig 29; 300pp; English.
XX	XX	
CC	XX	The present invention describes a method (M1) for designing capture
CC	XX	oligonucleotide probes (I) for use on a support to which complementary
CC	XX	oligonucleotide probes (II) will hybridize with little mismatch, where
CC	XX	(I) have melting temperatures within a narrow range. The method is useful
CC	XX	for detecting infectious diseases caused by bacterial infectious agents
CC	XX	e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC	XX	infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC	XX	Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC	XX	Epsstein-Barr virus and polio virus, and parasitic infectious agents
CC	XX	selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC	XX	medicinis. The method is also useful for detecting genetic diseases such
CC	XX	as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC	XX	Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC	XX	involved in DNA amplification, replication, recombination or repair, the
CC	XX	cancer is specifically associated with a gene selected from BRCA1 gene,
CC	XX	p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC	XX	method is also used for environmental monitoring, forensics and the food
CC	XX	and feed industry, detecting comprises scanning (using e.g. a scanning
CC	XX	electron microscope and infrared microscope) the support at the
CC	XX	particular sites and identifying if ligation of the oligonucleotide probe
CC	XX	sets occurred and correlating (using a computer) identified ligation to a
CC	XX	presence or absence of the target nucleotide sequences. AB187074 to
CC	XX	AB197546 represent oligonucleotide sequences used in the exemplification
CC	XX	of the present invention
SQ	XX	Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
XX	XX	
Query Match	0.2%;	Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%;	Pred. No.2e+03;
Matches 16; Conservative	0;	Mismatches 2; Indels 0; Gaps 0
OY	6403	CCACCTGCTAGTACCTT 6420
DB	3	CCACCTGCAGATGCTT 20
RESULT 3046		
AB194356		
ID	AB194356	standard; DNA; 20 BP.
AC	AB194356;	
DT	16-FEB-2002	(first entry)
DE	Capture oligonucleotide zip ID#1443	oligo #5.
XX		
XX	Human; K-ras; PCR primer; probe; capture probe; mutation detection;	
KW	ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;	
KW	infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;	
KW	oncogene; tumour suppressor; human papillomavirus; forensic;	
KW	environmental monitoring; food industry; feed industry; 88.	
XX		
XX	Synthetic.	

XX	PN	WO200179548-A2.
XX	PD	25-OCT-2001.
XX	PF	04-APR-2001; 2001WO-US010958.
XX	PR	14-APR-2000; 2000US-0197272P.
XX	PA	(CORR) CORNELL RES FOUND INC.
XX	P1	Barany F, Zivvi M, Gerry NP, Favie R, Klman R;
XX	DR	WPI; 2002-034366/04.
XX	PT	Designing capture oligonucleotide probes for use on a support to which
XX	PS	complementary oligonucleotides hybridize with little mismatch.
XX		Example 5; Fig 29; 300pp; English.
CC		The present invention describes a method (M1) for designing capture
CC		oligonucleotide probes (I) for use on a support to which complementary
CC		oligonucleotide probes (II) will hybridise with little mismatch, where
CC		(I) have melting temperatures within a narrow range. The method is useful
CC		for detecting infectious diseases caused by bacterial infectious agents
CC		e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC		infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC		Aspergillus fumigatus, viruses e.g. T-cell lymphocyctotropic virus,
CC		Epsilon-Barr virus and polio virus, and parasitic infectious agents
CC		selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC		medinisii. The method is also useful for detecting genetic diseases such
CC		as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC		Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC		involved in DNA amplification, replication, recombination or repair, the
CC		cancer is specifically associated with a gene selected from BRCA1 gene,
CC		p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC		method is also used for environmental monitoring, forensics and the food
CC		and feed industry, detecting comprises scanning (using e.g. a scanning
CC		electron microscope and infrared microscope) the support at the
CC		particular sites and identifying if ligation of the oligonucleotide probe
CC		sees occurred and correlating (using a computer) identified ligation to a
CC		presence or absence of the target nucleotide sequences. ABI82074 to
CC		ABI97546 represent oligonucleotide sequences used in the exemplification
CC		of the present invention .
SQ		Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
		Query March 0.2%; Score 14.8; DB 1; Length 20;
		Best Local Similarity 88.9%; Pred. No. 2e+03; Indels 0; Gaps 0
		Matches 16; Conservative 0; Mismatches 2;
OY		3117 TGCTTGACAGCTTGTGTA 3124
Db		3 TGCTTGACGCGTTGGCA 20
RESULT 3047		
ID	ABK28754	standard; DNA; 20 BP.
XX	AC	ABK28754;
XX	DT	09-APR-2002 (first entry)
XX	DE	Human CDC14 gene donor splice site #14.
XX	KW	Human; de; cell-cycle control; CDC14A; cancer; splice site;
XX	KW	prostate cancer; breast cancer; tumour; lymph node metastasis;
XX	KW	malignant mesothelioma; chromosome 1p21; dual specificity phosphatase;
XX	KW	gene therapy; protein replacement therapy.
OS	Homo sapiens.	

PN US6331614-B1.
 XX 18-DEC-2001.
 PD 22-DEC-1999; 99US-00468872.
 XX 23-DEC-1998; 98US-0113833P.
 PR (MYRI-) MYRIAD GENETICS INC.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA Wong AKC, Teng DHF, Tavtigian SV;
 DR WPI; 2002-129551/17.
 XX Nucleic acid encoding mutated form of human dual-specificity phosphatase
 PT CDC14A polypeptide, useful to diagnose and treat cancers.
 XX
 PS Example 2; Col 43-44; 41pp; English.
 CC The invention relates to an isolated nucleic acid encoding a CDC14A
 CC polypeptide (cell-cycle control protein 14A, a dual specificity
 CC phosphatase), its complement or RNA molecule corresponding to it. Also
 CC included are an expression vector comprising the nucleic acid and a host
 CC cell transformed with the vector. The gene for CDC14A is located on human
 CC chromosome 1p21. The nucleic acid and protein are useful to diagnose and
 CC treat human cancers (e.g. breast cancer, prostate cancer) and tumours
 CC (e.g. lymph node metastasis, malignant mesothelioma) which have a
 CC mutation in the CDC14A gene, by gene therapy, protein replacement therapy
 CC or protein mimetics. They can also be used to screen for drugs to treat
 CC cancer. The present sequence is a splice donor or splice acceptor
 CC sequence from the CDC14A gene
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5479 TGTAAAGATGATATTTT 5496
 DB 2 TGTAAAGAGTAAATTTT 19
 RESULT 3048
 ABL56505/C
 ID ABL56505 standard; DNA, 20 BP.
 AC ABL56505;
 XX
 XX 22-JUL-2002 (first entry)
 DT
 XX PCR primer Cx30-S3 used to amplify a fragment of the human GJB6 gene.
 DE
 XX GJB6 gene; connexin-30; Cx-30; Clouston syndrome; alopecia; hair loss;
 KW hydrotic ectodermal dysplasia; hair growth; hair disorder; PCR; primer;
 KM ss.
 XX
 OS Homo sapiens.
 OS
 XX WO200226976-A1.
 PN
 XX 04-APR-2002.
 PD
 XX 27-SEP-2001; 2001WO-FR002997.
 PF
 XX 29-SEP-2000; 2000FR-00012473.
 PR
 XX (GENE-) GENETHON III.
 PA (UYDE-) UNIV DEVRV VAL DESSONNE.
 XX Waksman G, Lamartine J;
 PI WPI; 2002-340014/37.
 DR

XX New mutant forms of connexin-30 nucleic acid, useful for the diagnosis
 PT and treatment of Clouston syndrome and other forms of alopecia.
 PT
 XX Example 1; Page 19; 44pp; French.
 PS
 CC PCR primers ABL56504-07 were used to amplify fragments of the human GJB6
 CC gene. The GJB6 gene encodes connexin-30 (Cx-30). A G to A mutation at
 CC position 31 and/or a C to T mutation at position 263 causes Clouston
 CC syndrome (hydrotic ectodermal dysplasia). Nucleic acids encoding Cx-30,
 CC antisense oligonucleotides and vectors containing them, are used to treat
 CC Clouston syndrome and other forms of alopecia with a genetic component.
 CC They are also used to reduce growth of hair and/or promote hair loss.
 CC They may also be used for (cosmetic) treatment and/or prevention of
 CC disorders of the hair. Transgenic animals/cells that contain Cx-30 are
 CC used to screen for agents that are potentially useful for treating some
 CC forms of alopecia. Primers derived from GJB6 gene are useful in
 CC amplification assays for diagnosis of Clouston syndrome
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5714 CTCTTCTCTTTCCTG 5731
 DB 20 CTCTTCTCTCTCCGCTG 3
 RESULT 3049
 ABQ87739/C
 ID ABQ87739 standard; DNA, 20 BP.
 AC ABQ87739;
 XX
 XX 18-SEP-2002 (first entry)
 DT
 XX Human ESR1 exon 8.18 sequencing PCR primer ERLx8.18er3_54048.
 DE
 XX Human; oestrogen; receptor; oestrogen receptor alpha; cytostatic;
 KW osteopathic; cardiatic; cancer; osteoporosis; cardiovascular disorder;
 KM ESR-alpha; ESR1; sequencing; PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX WO200234945-A2.
 PN
 XX 02-MAY-2002.
 PD
 XX 21-AUG-2001; 2001WO-US025990.
 PF
 XX 20-OCT-2000; 2000US-00692414.
 PR 24-JAN-2001; 2001US-00768184.
 PR 13-MAR-2001; 2001US-00804076.
 PR 05-APR-2001; 2001US-00826314.
 XX
 PA (APPL-) APPLERA CORP.
 PA
 XX Kalush F, Casel MJ, Hwang SS, Winn_deen ES;
 PI WPI; 2002-479722/51.
 DR
 XX Peptide of estrogen receptor alpha genes variant or its fragment for use
 PT in identifying modulators for treating disorders e.g. a susceptibility to
 PT cancer, osteoporosis, cardiovascular disorder.
 XX
 XX Example 1; Fig 2E; 352pp; English.
 PS
 XX The invention relates to novel human oestrogen receptor variant peptides,
 CC and the polynucleotides encoding them. The peptides of the invention have
 CC cytosolic, osteopathic and cardiatic activity. The peptides of the
 CC invention are useful to mediate or modulate a variety of disorders such

CC as a susceptibility to cancer, osteoporosis, cardiovascular disorder, etc., and hence are useful in the treatment of the disorders. The CC sequences shown in AB087720-AB087746 represent PCR primers used in the CC invention to sequence individual exons of the human oestrogen receptor alpha (ESR-alpha or ESR1) gene

CC alpha (ESR-alpha or ESR1) gene

XX

SO Sequence 20 BP; 10 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4842 TATCCAGTTCGTCT 4859
DB 19 TATGCCAGTTCTCTCT 2

RESULT 3050
AAL47461
ID AAL47461 standard; DNA; 20 BP.
XX
AC AAL47461;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human MTHFR gene probe.
XX
KM Human; MTHFR; sequencing; single nucleotide polymorphism; SNP; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "modified by FITC"
XX
PN DE10058915-A1.
XX
PD 06-JUN-2002..
XX
PF 20-NOV-2000; 2000DB-01058915.
XX
PR 20-NOV-2000; 2000DB-01058915.
XX
PA (ATTO-) ATTOMOL GMBH MOLEKULARE DIAGNOSTIKA.
XX
DR WPI; 2002-520952/56.
XX
PT Determining nucleic acid sequence, useful for characterizing single-
PT nucleotide polymorphisms, by incubating with probe in presence of
PT phosphorothioate nucleotide and exonuclease.
XX
PS Example 1; Page 6; 12pp; German.
XX
CC The present invention relates to a method of determining a nucleic acid
CC sequence, involving incubating with a probe, adding at least one
CC phosphorothioate nucleotide in presence of an enzyme that synthesises a
CC complementary sequence on the 3'-end of the probe, and adding a second
CC enzyme that degrades the phosphorothioate-free complement. The method can
CC be used to determine very short (up to 10 base pair) sequences,
CC especially for characterisation of single-nucleotide polymorphisms. The
CC present sequence is a probe for the human MTHFR gene which was used to
CC demonstrate the method of the invention
XX
SO Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5816 CTATGATGATGAATC 5833
XX

DB 2 CTGCGATGATGAATC 19

RESULT 3051
ID AAL49188/c
ID AAL49188 standard; DNA; 20 BP.
XX
AC AAL49188;
XX
DT 30-OCT-2002 (first entry)
XX
DE Porcine CD 151 coding sequence PCR primer #12.
XX
KM CD 151; porcine reproductive and respiratory syndrome virus; PRRSV; pig;
KM selective breeding; xenotransplant; anti-RNA entry protein; anti-RBP;
KM anti-viral; vaccine; PCR; primer; ss.
XX
OS Sus scrofa.
XX
PN WO200260924-A2.
XX
PD 08-AUG-2002.
XX
PF 29-JAN-2002; 2002WO-US002868.
XX
PR 29-JAN-2001; 2001US-00772044.
PR 28-JAN-2002; 2002US-00772044.
XX
PA (UNITV) UNITV KANSAS STATE RES FOUND.
XX
PI Kapil S, Shammukhappa K;
XX
DR WPI; 2002-619225/66.
XX
PT Determining susceptibility and resistance to porcine reproductive and
PT respiratory syndrome virus (PRRSV), useful for improving swine breeding,
PT by assaying for CD 151 in a sample of cellular material of known origin
PT from the animal.
XX
PS Example 17; Page 35; 77pp + Sequence Listing; English.
XX
CC The present invention relates to a method of determining the
CC susceptibility or resistance of an animal to porcine reproductive and
CC respiratory syndrome virus (PRRSV). This involves assaying for CD 151 in
CC a sample of cellular material of known origin from the animal. In
CC addition, coding sequences of CD 151 are described, and anti-viral
CC compounds designated anti-RNA entry proteins (anti-REPs). The method is
CC useful for determining susceptibility and resistance to PRRSV in an
CC animal. This is particularly useful for improving swine breeding or for
CC screening different pig breeding lines. The method is also useful for
CC developing non-simian recombinant cell lines for propagating the virus,
CC for producing anti-viral compounds or vaccines for inducing immunity
CC against PRRSV, and for diagnosing PRRSV infection in a swine. The present
CC sequence is a PCR primer used to isolate the porcine CD 151 coding
CC sequence. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SO Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CAAGGCTTGAGTGA 1010
DB 19 CAAGAGCTGAGCTGA 2

RESULT 3052
ID AB292414
ID AB292414 standard; DNA; 20 BP.
XX

AC AB292414;
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002MO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7656; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3226 AGCAGGAGGAGATTGTTT 3243
|||
Db 1 AGCAGGAGGAGATTGTTT 18

RESULT 3053
AB292635/C
ID AB292635 standard; DNA; 20 BP.
XX

AC AB292635;
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002MO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7877; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6795 TTCTAAGCAGATGGGAA 6812
|||
Db 19 TTCTAAGCAGATGGGAA 2

RESULT 3054
AB288435
ID AB288435 standard; DNA; 20 BP.
XX

AC AB287286;
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 2528; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 10 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3385 CTCCCCAGTCGCCACC 3402
DB 3 CTCCCCAGTCGCCACC 20

RESULT 3057
AB287732/C
ID AB287732 standard; DNA; 20 BP.
XX

AC AB287732;
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 2974; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 1 C; 15 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2999 CCCCACCCCTCACCCT 3016
DB 19 CCCCACCCCTCACCCT 2

RESULT 3058
AB293605/C
ID AB293605 standard; DNA; 20 BP.
XX

AC AB293605;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 8847; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 DB Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 564 CCTGGGAGGAGGA 581
 19 CCTGGGAGGAGGA 2
 RESULT 3059
 AB297793
 ID AB297793 standard; DNA; 20 BP.
 XX

AC AB297793;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human CCR3 oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 13035; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 DB Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2405 GGACCAAGTGACCA 2422
 1 GGCCCAAGTGACCA 18
 RESULT 3060
 AB293220/c
 ID AB293220 standard; DNA; 20 BP.
 XX

AC ABZ93220;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN W0200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002MO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8462; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 11 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 5709 TTTCTCTCTCTCTCTT 5726
DB 19 TTTCCTCTCTCTCTT 2

RESULT 3061
ABZ86063/C
ID ABZ86063 standard; DNA; 20 BP.
XX

AC ABZ86063;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN W0200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002MO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1305; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 7415 GCAGCAGCAGCAGCAGCA 7432
DB 18 GCAGCAGCAGCAGCAGCA 1

RESULT 3062
ABZ90434
ID ABZ90434 standard; DNA; 20 BP.
XX


```
AC AB290434;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5676; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1341 GATCAGTCGCTGATGAA 1358
Db 1 GATCGTCCTGATGAA 18
RESULT 3063
AB290042
ID AB290042 standard; DNA; 20 BP.
XX
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AC AB290042;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5284; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3955 TCTTATGTTTCATTAATT 3972
Db 1 TCTTATGTTTCATTAATT 18
RESULT 3064
AB285315/c
ID AB285315 standard; DNA; 20 BP.
XX
```

AC ABZ5315;
XX
DT 17-OCT-2003 (first entry)
DE
DE Human oligonucleotide sequence.
XX
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 557; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 12 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6461 ATACTTTTTCGT 6478
| | | | | | | | | | | | | | | | | | | | | |
DB 19 AACTTTTTCGTCTT 2

RESULT 3065
ABZ93982/C
ID ABZ93982 standard; DNA; 20 BP.
XX

AC ABZ93982;
XX
DT 17-OCT-2003 (first entry)
DE
DE Human oligonucleotide sequence.
XX
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PE 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 9224; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 7 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3302 AGATCATATTTTGGAT 3319
| | | | | | | | | | | | | | | | | | | | | |
DB 20 AGATTAAGATTTTAGAT 3

RESULT 3066
ABZ98928/C
ID ABZ98928 standard; DNA; 20 BP.
XX

AC ABZ98928;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human PDE4A oligonucleotide sequence.
 XX
 KW Human; antiseense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiallathmic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KW antiseense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPig-) EPIGENESIS PHARM INC.
 XX
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antiseense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 14170; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antiseense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiallathmic, hypotensive,
 CC immunosuppressive, and cyostatic activity. The composition may have a
 CC use in antiseense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Db Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6406 CCTGCTAGATGCTTCTC 6423
 Db 19 CCTGCTAGATAACTACTC 2
 RESULT 3067
 ABZ88693/C
 ID ABZ88693 standard; DNA; 20 BP.
 XX

AC ABZ88693;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antiseense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiallathmic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KW antiseense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPig-) EPIGENESIS PHARM INC.
 XX
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antiseense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3935; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antiseense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiallathmic, hypotensive,
 CC immunosuppressive, and cyostatic activity. The composition may have a
 CC use in antiseense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 12 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Db Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5473 TTTTGTGTAATAAGATA 5490
 Db 18 TTTTGTGTAATAAGATA 1
 RESULT 3068
 ABZ91491/C
 ID ABZ91491 standard; DNA; 20 BP.
 XX

AC	ABZ91491;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.
XX	
KM	Human; antisense; lung dysfunction; nasal airway dysfunction;
KM	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
PF	23-APR-2002; 2002WO-US013135.
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIC-) EPIGENESIS PHARM INC.
P1	Nyce JM, Li Y, Sandraagra A, Katz B, Pabalan J, Aguilar D;
P1	Miller S, Tang L, Shahabuddin S,
PT	WPI, 2003-229219/22.
DR	
XX	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 6733; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, cytostatic, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung irritant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
	Query Match 0.2%; Score 14.8; DB 1; Length 20;
	Best Local Similarity 88.9%; Pred. No.2e+03;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	3385 CTCGCCAGCTGCGCACCC 3402
DB	19 CTCTGCAGCTGCGCACCC 2
	RESULT 3069
ID	ABZ93213/C
XX	ABZ93213 standard; DNA; 20 BP.

AC	ABZ93213;
XX	
DT	I ¹⁷ -OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.
XX	
KM	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KX	antiaschematic; hypocoensive; immunosuppressive; cyostatic; gene therapy;
KV	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPFG-) EPIGENESIS PHARM INC.
XX	
P1	Nyze JM, Li Y, Sandrasagra A, Katz B, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 8455; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiaschematic, hypocoensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 11 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	6463 ACTTTTTCGTTTG 6480
DB	18 ACCTTCCTTCGTTTG 1
XX	
RESULF 3070	
ABZ92117	
ID	ABZ92117 standard; DNA; 20 BP.
XX	

AC AB292117;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Noyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
XX
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7359; 872bp; English.
XX
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4301 TCTTTTCCTTCCCTGG 4318
|||
Db 2 TCTTTTCCTTCCCTGG 19

RESULT 3071
ACC62225/c
ID ACC62225 standard; DNA; 20 BP.
XX

AC ACC62225;
XX
DT 20-JUN-2003 (first entry)
XX
DE Mouse alphaoprotein B antisense oligonucleotide SEQ ID NO: 114.
XX
KW alphaoprotein B; Apob; antilipemic; antiatherosclerotic; antidiabetic;
XX anorectic; cardiovascular; gene therapy; lipid metabolism;
XX cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
XX type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
XX glucose; antisense oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO2003011887-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002WO-US024247.
XX
PR 01-AUG-2001; 2001US-00920033.
PR 30-APR-2002; 2002US-00135985.
PR 13-MAY-2002; 2002US-00147196.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
PI WPI; 2003-268105/26.
XX
XX
PT New antisense oligonucleotides for modulating apolipoprotein B,
PT especially for preventing or treating atherosclerosis, hyperlipidaemia or
PT diabetes, or for modulating glucose, cholesterol, lipoprotein or
PT triglyceride levels.
XX
XX
XX Example 17; Page 100; 160bp; English.
XX
XX
CC The invention relates to a novel compound that is 8-50 nucleotides in
CC length that is targeted to a nucleic acid molecule encoding
CC apolipoprotein B (Apob), and specifically hybridises with and inhibits
CC the expression of a nucleic acid molecule encoding Apob; or which
CC specifically hybridises with at least an 8-nucleotide portion of an
CC active site on a nucleic acid molecule encoding Apob. A compound of the
CC invention has antilipemic, antiatherosclerotic, antidiabetic,
CC anorectic, and cardiovascular activity. The compound may have a use in
CC gene therapy. The antisense oligonucleotide is useful for treating an
CC animal having a disease or conditions associated with Apob, e.g. a
CC condition involving abnormal lipid metabolism, a condition involving
CC abnormal cholesterol metabolism, atherosclerosis, or a condition
CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
CC (specifically Type 2 diabetes), obesity, atherosclerosis or
CC cardiovascular disease). The new compound or the antisense
CC oligonucleotide is also useful for modulating glucose levels
CC (particularly plasma or serum glucose levels) in a human or diabetic
CC animal, or for modulating serum cholesterol levels, lipoprotein levels
CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,
CC particularly in a human. The antisense compound is also useful for
CC preventing or delaying the onset of a disease or condition associated
CC with Apob, or the onset of an increase in glucose levels in the animal or
CC human. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6291 ACACTGGCTTCAGGAT 6308
|||
Db 19 ACACTGGCTTCAGGAT 2

RESULT 3072
AB277000
ID AB277000 standard; DNA; 20 BP.
XX
XX
AC
XX
AB277000;
XX
DT 07-MAY-2003 (first entry)
XX
DE Bovine DGAT PCR primer #36.
XX
XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
KW milk; meat marbling; low fat; polymorphic; SNP;
KM single nucleotide polymorphism; PCR primer; ss.
XX
OS Bos taurus.
XX Synthetic.
XX
PN MO2003004630-A2.
XX
PD 16-JAN-2003.
XX
PF 05-JUL-2002; 2002MO-EP007520. --
XX
PR 06-JUL-2001; 2001EP-00116412.
XX 13-MAY-2002; 2002OS-0379412P.
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
XX
PI Fries H, Winter A;
XX
DR WPI; 2003-239205/23.
XX
PT New nucleic acid molecule comprising a sequence of an allele of a
PT polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for
PT testing a mammal for its predisposition for fat content of milk and for
PT meat marbling.
XX
XX
XX Example 1: Page 36; 91pp; English.
XX
XX The present invention describes a nucleic acid molecule (NA) (I) encoding
XX a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or
XX indicative for low fat content of milk and to low meat marbling
XX (intramuscular fat content). Human DGAT is located to chromosome 8, and
XX bovine DGAT is located to chromosome 14. (I) is useful for testing a
XX mammal for its predisposition for fat content of milk and/or its
XX predisposition for meat marbling. The method comprises analyzing the gene
XX encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
XX polymorphisms (SNPs)) which are connected with the predisposition. The
XX nucleotide polymorphisms are located in the coding region of the DGAT
XX gene and result in substitution, deletion and/or addition of an amino
XX acid sequence of the polypeptide which is encoded by the gene. The
XX nucleic acid molecule has at the position 10433 and 10434 of the DGAT
XX gene a guanine and a cytosine residue, at position 3343 a cytosine or
XX guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
XX thymine, which correlate with a predisposition for low fat content of
XX milk and low meat marbling. The nucleic acid molecule has at the position
XX corresponding to position 10433 and 10434 of the DGAT gene two adenine
XX residues which correlate with a predisposition for high content of milk
XX and high meat marbling. The nucleotide polymorphisms are located in a
XX region which is responsible for the regulation of the expression of the
XX product of the gene encoding DGAT. AB276924 to AB277045 and AB276935 to
XX AB276946 represent sequences used in the exemplification of the present
XX invention
XX
XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX
XX 1095 ACAAGTGGAGAGTGGACA 1112
XX |||||
XX 1 ACAAGTGGAGAGTGGAGACA 18

4. RESULT 3073
ABZ76933
ID ABZ76933 standard; DNA, 20 BP.
XX
XX ABZ76933;
AC
XX 07-MAY-2003 (first entry)
DT
XX
XX
DE Bovine DGAT BAC-DNA sequencing primer #6.
KW Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
KW milk; meat marbling; low fat; polymorphic; SNP;
KW single nucleotide polymorphism; PCR primer; ss.
XX
XX Bos taurus.
OS Synthetic.
XX
XX WO2003004630-A2.
PN
XX
XX 16-JAN-2003.
PD
XX
XX 05-JUL-2002; 2002WO-EP007520.
PF
XX
XX 06-JUL-2001; 2001EP-00116412.
PR 13-MAY-2002; 2002US-0379412P.
XX
XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
PA
XX
XX Fries H, Winter A;
PI
XX
XX WPI; 2003-239205/23.
DR
XX
XX
PT New nucleic acid molecule comprising a sequence of an allele of a
PT polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for
PT testing a mammal for its predisposition for fat content of milk and for
PT meat marbling.
XX
XX
PS Example 1; Page 35; 91pp; English.
XX
XX The present invention describes a nucleic acid molecule (NA) (1) encoding
XX a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or
XX indicative for low fat content of milk and to low meat marbling
XX (intramuscular fat content). Human DGAT is located to chromosome 8, and
XX bovine DGAT is located to chromosome 14. (1) is useful for testing a
XX mammal for its predisposition for fat content of milk and/or its
XX predisposition for meat marbling. The method comprises analysing the gene
XX encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
XX polymorphisms (SNPs)) which are connected with the predisposition. The
XX nucleotide polymorphisms are located in the coding region of the DGAT
XX gene and result in substitution, deletion and/or addition of an amino
XX acid sequence of the polypeptide which is encoded by the gene. The
XX nucleic acid molecule has at the position 10433 and 10434 of the DGAT
XX gene a guanine and a cytosine residue, at position 3343 a cytosine or
XX guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
XX thymine, which correlate with a predisposition for low fat content of
XX milk and low meat marbling. The nucleic acid molecule has at the position
XX corresponding to position 10433 and 10434 of the DGAT gene two adenine
XX residues which correlate with a predisposition for high content of milk
XX and high meat marbling. The nucleotide polymorphisms are located in a
XX region which is responsible for the regulation of the expression of the
XX product of the gene encoding DGAT. ABZ75924 to ABZ77045 and ABP96035 to
XX ABP96046 represent sequences used in the exemplification of the present
XX invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Fred. No. 2e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1095 ACAGCTGAGAGTGAGCA 1112

Db 1 ACAGCTGAGTGAAGACA 18

RESULT 3074
ABT34193/c
ID ABT34193 standard; DNA; 20 BP.

XX ABT34193;

XX 12-JUN-2003 (first entry)

XX Mouse short heterodimer partner-1 expression oligo SEQ ID No 68.

XX Antiartherosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
XX antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
XX short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
XX cardiovascular disease; infection; inflammation; tumour formation; mouse;
XX antisense; ds.

XX Unidentified.

XX WO2003012033-A2.

XX 13-FEB-2003.

XX 17-JUL-2002; 2002WO-US023245.

XX 31-JUL-2001; 2001US-00919197.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

XX WPI; 2003-248161/24.

XX New antisense oligonucleotide targeted to a nucleic acid encoding short
PT heterodimer partner-1, useful for treating diseases involving abnormal
PT lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
PT diseases.

XX Example 16; Page 95; 121pp; English.

XX The invention relates to a novel compound of 8 - 50 nucleobases in length
CC targeted to a nucleic acid molecule encoding a short heterodimer partner-
CC 1. The novel compound specifically hybridizes with a nucleic acid
CC molecule encoding the short heterodimer partner-1, and inhibits the
CC expression of the nucleic acid molecule. The compound, and a composition
CC comprising it are useful for treating a disease or condition associated
CC with the short heterodimer partner-1, particularly a condition involving
CC abnormal lipid or cholesterol metabolism such as atherosclerosis or a
CC cardiovascular disease. They are also useful in research and diagnostics
CC for modulating the expression of short heterodimer partner-1. They can
CC also be useful prophylactically in preventing or delaying infection,
CC inflammation or tumour formation. This polynucleotide sequence represents
CC a mouse antisense oligo relating to the heterodimer partner-1 of the
CC invention

XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 860 ATGCTCAGCCACTGCCT 877
DB 18 ATCTCAGCCACTGCCT 1

RESULT 3075
AB270582/c
ID AB270582 standard; DNA; 20 BP.

AC AB270582;
XX 23-MAY-2003 (first entry)

XX Insulin gene VNTR allele genotyping primer INS56.

XX Insulin; genotyping; obesity; variable number of tandem repeats; VNTR;
XX human; PCR; primer; ss.

XX Homo sapiens.

XX WO2003012139-A2.

XX 13-FEB-2003.

XX 31-JUL-2002; 2002WO-IB003347.

XX 31-JUL-2001; 2001US-0309235P.

XX 21-AUG-2001; 2001US-0316830P.

XX (BOUG/) BOUGNERES P.

XX Bougneres P;

XX WPI; 2003-248167/24.

XX Determining the risk of developing obesity for treating or reducing the
PT risk of developing obesity by determining a paternal insulin variable
PT number of tandem repeats allele in the individual.
XX Disclosure; Page 16; 62pp; English.

XX The invention provides methods for determining the risk of development of
CC obesity in a subject by examining the paternal insulin variable number of
CC tandem repeats (VNTR) class. The presence of a paternal insulin VNTR
CC class I allele indicates that the subject has an approximately 2-fold
CC increase in risk of developing obesity compared with a subject carrying a
CC paternal insulin VNTR class II allele. Methods are provided to facilitate
CC rational therapy and maintenance of individuals predisposed to obesity.
CC The insulin VNTR allele may be genotyped by determining the identity of a
CC nucleotide at an insulin-related genetic marker that is in linkage
CC disequilibrium with the insulin HphI locus. This includes any marker that
CC is a surrogate for the VNTR in the insulin gene. The -2221 MspI marker is
CC an example of a genetic marker associated with the insulin gene, and can
CC be detected by PCR using primers INS56 (present sequence) and INS57 (see
CC AB270583)

XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4729 CTTGAGGCCAGCTGGAG 4746
DB 18 CTTGAGGCCAGCTGGAG 1

RESULT 3076
ACC47290/c
ID ACC47290 standard; DNA; 20 BP.

XX ACC47290;

XX 11-AUG-2003 (first entry)

XX Human apolipoprotein(a) mRNA inhibiting antisense oligo ISIS 144373.

XX Apolipoprotein(a); antiarteriosclerotic; cardiact; gene therapy; human;
XX antisense; ss.

XX Synthetic.
XX Homo sapiens.


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XX WO2003014307-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024920.
XX
XX 07-AUG-2001; 2001US-00923515.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ;
XX
XX WPI; 2003-255656/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease.
XX
XX Claim 3; Page 87; 120pp; English.
XX
XX The invention relates to a new compound, 8-50 nucleobases in length
XX targeted to a nucleic acid molecule encoding human apolipoprotein(a),
XX specifically hybridizes with and inhibits the expression of human
XX apolipoprotein(a). The antisense compounds are useful for preparing a
XX composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. Sequences ACC47284-318
XX represent specific examples of chimeric antisense phosphorothioate
XX oligonucleotides having 2'-MOE wings and a deoxy gap targeting human
XX apolipoprotein(a) mRNA
XX
XX Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1752 GCAGCTCATTTATGTCAT 1769
DB 18 GCAGCTCCTTATTTTAT 1
RESULT 3077
ABX04329/C
ID ABX04329 standard; DNA; 20 BP.
XX
XX ABX04329;
XX
XX 13-JAN-2003 (first entry)
XX
XX Mouse Interleukin 5 antisense oligonucleotide ISIS 17981.
XX
XX Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor; antiasthmatic;
XX immunosuppressant; eosinophilic syndrome; asthma.
XX
XX Mus musculus.
XX Synthetic.
XX
XX US2002128216-A1.
XX
XX 12-SEP-2002.
XX
XX 07-MAR-2001; 2001US-00800629.
XX
XX 26-MAR-1999; 99US-00280799.
XX
XX 17-MAR-2000; 2000WO-US007318.
XX
XX (DEAN/) DEAN N M.
XX (KARR/) KARRAS J G.
XX (MCKA/) MCKAY R.
XX (MANO/) MANOHARAN M.
XX
XX Dean NM, Karras JG, McKay R, Manoharan M;
```

```
XX WPI; 2003-039602/03.
XX
XX Novel antisense compound for treating disease/condition e.g. eosinophilic
XX syndrome or asthma associated with interleukin-5 or IL-5 receptor
XX expression or IL-5 signal transduction, modulates IL-5 signal
XX transduction.
XX
XX Example 14; Page 16; 77pp; English.
XX
XX The invention relates to an antisense compound of 8-30 nucleobases in
XX length, which modulates interleukin (IL)-5 signal transduction. Also
XX include are a pharmaceutical composition comprising the antisense
XX oligonucleotide and a pharmaceutically acceptable carrier or diluent, and
XX a diagnostic kit for detecting the expression level of the membrane form
XX versus soluble form of IL-5 receptor a. The antisense compound is useful
XX for modulating IL-5 signal transduction, modulating expression of
XX mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,
XX in cells or tissues, for altering the ratio of the isoforms of mammalian
XX IL-5 receptor a in mammalian cells or tissues, treating a mammalian
XX having a disease or condition associated with IL-5 signal transduction,
XX IL-5 expression or IL-5 receptor a expression, where the disease or
XX condition include eosinophilic syndrome or asthma. An antisense compound
XX which alters splicing of an RNA encoding IL-5 receptor a is also useful
XX for treating a mammal having a disease or condition. The present sequence
XX is an antisense oligonucleotide targeting mouse IL5
XX
XX Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5272 ATACGAGCAGGTGGCAG 5289
DB 20 AGACGAGCAGGTGGCAG 3
RESULT 3078
ABX17722
ID ABX17722 standard; DNA; 20 BP.
XX
XX ABX17722;
XX
XX 05-FEB-2003 (first entry)
XX
XX Human urokinase plasminogen activator antisense oligonucleotide #27.
XX
XX Urokinase plasminogen activator; gene therapy; cancer;
XX hyperproliferative disorder; cancer; breast cancer; colon cancer;
XX bone cancer; brain cancer; ovary cancer; cervix cancer;
XX endometrium cancer; stomach cancer; kidney cancer; tumor metastasis;
XX antisense oligonucleotide; ss.
XX
XX Synthetic.
XX
XX WO200279515-A1.
XX
XX 10-OCT-2002.
XX
XX 18-MAR-2002; 2002WO-US008112.
XX
XX 30-MAR-2001; 2001US-00821972.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Freiler SM, Watt AT;
XX
XX WPI; 2003-058441/05.
XX
XX New antisense compound, useful for preparing a composition for treating
XX hyperproliferative disorders, cancer e.g., breast, colon, bone, brain,
XX ovary, cervix, endometrium, stomach or kidney cancer, or tumor
```



```

PT metastasis.
XX
PS Example 15; Page 91; 153bp; English.
XX
CC A new compound, which is 8-50 nucleobases in length targeted to a nucleic
CC acid molecule encoding urokinase plasminogen activator, specifically
CC hybridizes with and inhibits the expression of urokinase plasminogen
CC activator. The compound is useful for preparing a composition for
CC treating (e.g. by gene therapy) hyperproliferative disorder, cancer e.g.,
CC breast, colon, bone, brain, ovary, cervix, endometrium, stomach or kidney
CC cancer, or tumour metastasis. This sequence represents an antisense
CC oligonucleotide used to modulate expression of urokinase plasminogen
CC activator
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1965 TTTTCAACAGCCAGTGAT 1982
DB 2 TTTTCCAAAGCCAGTGAT 19
RESULT 3079
AADS3839/c
ID AAD53839 standard; DNA; 20 BP.
XX
AC AAD53839;
XX
DT 28-MAY-2003 (first entry)
XX
DE BMPRIA exon 8 specific PCR primer, AKK3-8b.
XX
KM Juvenile polyposis; JP; colorectal carcinoma; BMPRIA; gene therapy;
XX
OS Unidentified.
XX
PN WO200294084-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US016053.
XX
PR 21-MAY-2001; 2001US-0292691P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Howe JR;
XX
DR WPI; 2003-120737/11.
XX
PT Diagnosing or treating juvenile polyposis or colorectal carcinoma,
PT comprises obtaining a tissue or fluid sample from a subject and
PT determining the loss or alteration of a functional BMPRIA gene in cells
PT of the sample.
XX
PS Example 1; Page 74; 108bp; English.
XX
CC The invention relates to a method of diagnosing juvenile polyposis (JP)
CC or colorectal carcinoma. The method involves obtaining a sample from a
CC subject and determining the loss or alteration of a functional BMPRIA
CC gene in cells of the sample. The method is useful in diagnosing or
CC treating JP or colorectal carcinoma. The invention is also useful in gene
CC therapy. The present sequence is BMPRIA exon specific PCR primer, used to
CC illustrate the method of the invention
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;

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```

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5685 CTTTGACCACTGTTTG 5702
DB 20 CTTTGCCCACTGTTTG 3
RESULT 3080
AADS3846
ID AAD53846 standard; DNA; 20 BP.
XX
AC AAD53846;
XX
DT 28-MAY-2003 (first entry)
XX
DE PCR primer #3 used in BMPRIA exon mutation analysis.
XX
KM Juvenile polyposis; JP; colorectal carcinoma; BMPRIA; gene therapy;
XX
OS Unidentified.
XX
PN WO200294084-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US016053.
XX
PR 21-MAY-2001; 2001US-0292691P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Howe JR;
XX
DR WPI; 2003-120737/11.
XX
PT Diagnosing or treating juvenile polyposis or colorectal carcinoma,
PT comprises obtaining a tissue or fluid sample from a subject and
PT determining the loss or alteration of a functional BMPRIA gene in cells
PT of the sample.
XX
PS Example 1; Page 74; 108bp; English.
XX
CC The invention relates to a method of diagnosing juvenile polyposis (JP)
CC or colorectal carcinoma. The method involves obtaining a sample from a
CC subject and determining the loss or alteration of a functional BMPRIA
CC gene in cells of the sample. The method is useful in diagnosing or
CC treating JP or colorectal carcinoma. The invention is also useful in gene
CC therapy. The present sequence is a PCR primer used in BMPRIA exon
CC mutation analysis. This primer is used to illustrate the method of the
CC invention
XX
SQ Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7246 AGCATGATGGGAATG 7263
DB 2 AGTATGATGGGCAATG 19
RESULT 3081
ACC86760/c
ID ACC86760 standard; DNA; 20 BP.
XX
AC ACC86760;
XX
DT 04-AUG-2003 (first entry)
XX
DE Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:55.
XX

```


AC	AA61734,
XX	(First entry)
DZ	22-SEP-2003
DE	Human PCTAIR protein kinase 1 antisense oligo, ISIS 204171.
XX	
KM	Human; PCTAIR protein kinase 1; PCTAIR-1; sideroblastic anaemia;
KW	hyperproliferative disease; neurological disease; thrombocytopenia;
KW	retinitis pigmentosa; X-linked Charcot-Marie-Tooth disease; therapy;
KW	mental retardation; Wiskott-Aldrich syndrome; dysontia; Parkinsonism;
KM	PCTK1; crf5; incontinentia pigmenti; phosphorichioate backbone;
XX	antisense; ss.
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorichioate backbone; All cytidines are 5-
FT	methylcytidines"
FT	1..5
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "2'methoxyethyl nucleotides"
FT	16..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2'methoxyethyl nucleotides"
XX	
PN	WO2003049691-A2.
PD	19-JUN-2003.
XX	
PF	06-DEC-2002; 2002WO-US039138.
XX	
PR	07-DEC-2001; 2001US-00017621.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Freier SM, Roach MP;
DR	WPI; 2003-577271/54.
XX	
PT	New antisense oligonucleotides for modulating PCTAIR protein kinase 1
PT	gene expression, particularly useful for treating hyperproliferative or
PT	neurological disorders for example, mental retardation, or
PT	thrombocytopenia.
XX	
PS	Claim 3; Page 74; 104pp; English.
XX	
CC	The invention relates to antisense compounds, compositions and methods
CC	for modulating the expression of PCTAIR protein kinase 1 (also known as
CC	PCTAIR-1, PTK1 and crf5). The antisense oligonucleotide is useful for
CC	treating an animal having a disease or condition associated with PCTAIR
CC	protein kinase 1, particularly a hyperproliferative disease or a
CC	neurological disease. These diseases include thrombocytopenia, mental
CC	retardation, Wiskott-Aldrich syndrome, retinitis pigmentosa, dysontia
CC	with Parkinsonism, sideroblastic anaemia, X-linked Charcot-Marie-Tooth
CC	disease, or incontinentia pigmenti. The antisense oligonucleotide is
CC	particularly useful for inhibiting the expression of PCTAIR protein
CC	kinase 1 in cells or tissues. It is useful for diagnostics, prophylaxis,
CC	or as research reagents or kits. The present sequence is an antisense
CC	oligonucleotide targeted to human PCTAIR protein kinase 1 DNA. This
CC	sequence is used to illustrate the method of the invention
XX	
SO	Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Fred.No.2e+03;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0

1412 AGGATGACATGACGGAGG 1429
 |||||
 2 AGGCTGACACGACGGAGG 19
 Db

RESULT 3084
 ACD25682/C
 ID ACD25682 standard; DNA; 20 BP.
 XX
 AC ACD25682;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Human calcium channel alpha2delta SSCP primer c163ER.
 KW Human; ss; PCR; calcium channel alpha2delta; chromosome 3p21.3; primer;
 KW transgenic; cancer; lung cancer; small cell carcinoma; epilepsy; stroke;
 KW non-small cell carcinoma; breast cancer; nasopharyngeal cancer;
 KW cervical cancer; head and neck cancer; neurological disease;
 KW brain trauma; Alzheimer's disease; multiinfarct dementia; seizure;
 KW amyotrophic lateral sclerosis; convulsions; Huntington's disease;
 KW amnesia; cardiovascular disease; cardiac arrhythmia; angina pectoris;
 KW hypoxic damage; ischaemia; myocardial infarction; SSCP;
 KW congestive heart failure; Lambert-Eaton myasthenic syndrome;
 KW single strand conformation polymorphism.
 KM
 KM
 KM
 OS Homo sapiens.
 XX
 PN US2003044911-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 05-APR-2002; 2002US-00116949.
 XX
 PR 30-DEC-1998; 98US-0114359P.
 XX
 PR 22-DEC-1999; 99US-0047044J.
 PR
 PA (LERN/) LERMAN M I.
 PA (LATI/) LATIF F.
 PA (WEIM/) WEI M.
 PA (DUHF/) DUH F.
 PA (MINN/) MINNA J D.
 PA (SEKI/) SEKIDO Y.
 PA (GAOB/) GAO B.
 XX
 XX
 PI Lerman MI, Latif F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;
 WP1; 2003-492262/46.
 XX
 XX
 XX
 PT New substantially pure human calcium channel alpha2delta subunit splice
 PT isoform 1, 2 and 3 sequence useful in preventing, treating and diagnosing
 PT cancer, neurological disorders and cardiovascular disease.
 PT
 XX
 PS Example 7, Page 25, 79pp; English.
 XX
 XX
 XX The invention relates to a substantially purified amino acid sequence
 CC comprising at least a portion of human calcium channel alpha2delta
 CC subunit splice isoform 1, splice isoform 2 sequence or splice isoform 3,
 CC or their variants, and their encoding nucleic acids (or their
 CC complements, variants, or homologues). Also included are screening a test
 CC compound for modulating calcium channel activity, an antibody which binds
 CC to the calcium channel or its variants and producing a transgenic non-
 CC human animal (where the animal expresses a reduced level of calcium
 CC channel alpha 2delta subunit relative to a corresponding wild-type
 CC animal. The calcium channel proteins are useful for generating an
 CC antibody (which is useful for detecting the proteins or their portions).
 CC The transgenic animal (preferably a rodent e.g. mouse) is useful for
 CC identifying a therapeutic compound for treating a transgenic animal
 CC having cancer, especially lung cancer (small cell carcinoma or non-small
 CC cell carcinoma), breast cancer, nasopharyngeal cancer, cervical cancer,
 CC head and neck cancer, a neurological disease, especially epilepsy,
 CC stroke, brain trauma, Alzheimer's disease, multiinfarct dementia,
 CC amyotrophic lateral sclerosis, convulsions, seizures, Huntington's

CC disease, and amnesia, a cardiovascular disease, especially cardiac
 CC arrhythmia, angina pectoris, hypoxic damage to the cardiovascular system,
 CC ischemic damage to the cardiovascular system, myocardial infarction, and
 CC congestive heart failure; or Lambert-Baton myasthenic syndrome. The
 CC proteins and nucleic acids are useful in the diagnosis, prevention and
 CC treatment of the above mentioned diseases. The human gene for the calcium
 CC channel is located on chromosome 3p21.3. The present sequence is an SSCP
 CC (single strand conformation polymorphism) primer used to detect
 CC polymorphisms in the calcium channel alpha2delta subunit gene
 XX

Sequence 20 BP; 1 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5287 CAGCCTTACTCTCCAGCA 5304
 DB 20 CAGCCGCGACTCCAGCA 3

RESULT 3085
 ABT44169/C
 ID ABT44169 standard; DNA; 20 BP.
 AC ABT44169;
 XX
 DT 06-NOV-2003 (first entry)
 DE Chimeric antisense oligonucleotide ISIS 199165 to inhibit human NOD1.
 XX
 KW Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;
 KW caspase associated recruitment domain 4; programmed cell death; cancer;
 KW apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;
 KW viral infection; human; chimeric.
 XX
 OS Chimeric - Homo sapiens.
 XX
 EN WO2003050246-A2.
 XX
 PD 19-JUN-2003.
 XX
 PE 04-DEC-2002; 2002WO-US038606.
 XX
 PR 05-DEC-2001; 2001US-00006883.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dobie KW, Roach MP;
 XX
 DR WPI; 2003-577293/54.
 XX
 PT New compound, comprising a sequence targeted to a nucleic acid encoding
 PT nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing
 PT a composition for treating hyperproliferative disease, e.g., cancer.
 XX
 PS Example 15; Page 75; 138pp; English.
 XX
 CC This invention relates to novel chimeric antisense oligonucleotides that
 CC specifically hybridize to and inhibit the expression of the nucleotide
 CC binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4
 CC (caspase associated recruitment domain 4) is a domain that is involved in
 CC the elimination of cells via programmed cell death and in the host
 CC defence against pathogens, i.e., it works to regulate apoptosis. Apoptosis
 CC is a naturally occurring process, however, if it becomes overstimulated
 CC it can lead to cell loss and neurodegenerative conditions including
 CC Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis
 CC pigmentosa and blood cell disorders. Conversely, insufficient apoptosis
 CC can contribute to the development of cancer, autoimmune disorders and
 CC viral infections. The present invention describes antisense
 CC oligonucleotides that can modulate NOD1 expression (and variants
 CC thereof), such that these compounds, via gene therapy, can be used to

CC treat various human diseases caused by aberrant apoptosis. This
 CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit
 CC expression of human NOD1, the aim of the invention. Note that it has two
 CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a
 CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate
 CC throughout
 XX

Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2093 TGGCGGTACAGCGACAC 2110
 DB 18 TGGCGGGGACGACGACAC 1

RESULT 3086
 AAD56488/C
 ID AAD56488 standard; DNA; 20 BP.
 AC AAD56488;
 XX
 DT 27-AUG-2003 (first entry)
 DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 11.
 XX
 KW EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;
 KW epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;
 KW Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;
 KW memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;
 KW amyotrophic lateral sclerosis; attention deficit disorder; depression;
 KW injury; human; RT; reverse transcription; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 EN WO2003040304-A2.
 XX
 PD 15-MAY-2003.
 XX
 PE 11-NOV-2002; 2002WO-IB004930.
 XX
 PR 09-NOV-2001; 2001US-0345206P.
 XX
 PR 02-JUN-2002; 2002US-0393272P.
 XX
 PA (NEUR-) NEURONOVA AB.
 XX
 PI Holmberg J, Friksen J;
 XX
 DR WPI; 2003-441543/41.
 XX
 PT Alleviating a symptom of a disease or disorder of the nervous system by
 PT administering a modulator of neural stem or neural progenitor cell
 PT activity in vivo to a patient.
 XX
 PS Example 6; Page 54; 93pp; English.
 XX
 CC The invention relates to a method for alleviating a symptom of a disease
 CC or disorder of nervous system which involves administering a modulator to
 CC modulate an activity of a neural stem cell or a neural progenitor cell in
 CC vivo to a patient suffering from the disease or disorder of the nervous
 CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5
 CC or an interaction between EphA7 and ephrin-A2). The method is useful for
 CC alleviating a symptom of a disease or disorder of the nervous system,
 CC e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,
 CC neural stem cell, neural progenitor, ischaemic, affective,
 CC neuropsychiatric or learning and memory disorders, such as Parkinson's
 CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,
 CC amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or
 CC cancer-related brain/spinal cord injury, schizophrenia, psychoses,
 CC depression, bipolar depression/disorder, anxiety syndromes/disorders,
 CC phobias, stress and related syndromes, cognitive function disorders,

CC aggression, obsessive compulsive behaviour syndromes, multi-infarct
CC dementia, seasonal mood disorder, Lewy body dementia, borderline
CC personality disorder, cerebral palsy, age related/geriatric dementia,
CC epilepsy and injury related to epilepsy, spinal cord injury, brain
CC injury, trauma related brain/spinal cord injury, anticancer treatment
CC related brain/spinal cord tissue injury, infection and inflammation
CC related brain/spinal cord injury, environmental toxin related brain/
CC spinal cord injury, multiple sclerosis, autism, attention deficit
CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
CC to the retina or sleep disorders. The invention is also used in gene
CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
CC illustrate the method of the invention

XX SQ Sequence 20 BP, 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7408 AACATCGACGACGACG 7425
Db 19 AACGACGACGACGACG 2

RESULT 3087
AAD56486/c
ID AAD56486 standard; DNA; 20 BP.
XX AC AAD56486;
XX 27-AUG-2003 (first entry)

DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 9.

XX BphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;
XX epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;
XX Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;
XX memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;
XX amyotrophic lateral sclerosis; attention deficit disorder; depression;
XX injury; human; RT; reverse transcription; PCR; primer; ss.

XX OS Homo sapiens.
XX PN WO2003040304-A2.
XX PD 15-MAY-2003.
XX PF 11-NOV-2002; 2002WO-1B004930.
XX PR 09-NOV-2001; 2001US-0345206P.
XX PR 02-JUL-2002; 2002US-0393272P.

XX PA (NEUR-) NEURONOVA AB.
XX PI Holmberg J, Erlsen J;
XX WPI; 2003-441543/41.

PT Alleviating a symptom of a disease or disorder of the nervous system by
PT administering a modulator of neural stem or neural progenitor cell
PT activity in vivo to a patient.

XX Example 6; Page 54; 93pp; English.

XX The invention relates to a method for alleviating a symptom of a disease
CC or disorder of nervous system which involves administering a modulator to
CC modulate an activity of a neural stem cell or a neural progenitor cell in
CC vivo to a patient suffering from the disease or disorder of the nervous
CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5
CC or an interaction between EphA7 and ephrin-A2). The method is useful for
CC alleviating a symptom of a disease or disorder of the nervous system,
CC e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,

CC neural stem cell, neural progenitor, ischaemic, affective,
CC neuropsychiatric or learning and memory disorders, such as Parkinson's
CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,
CC amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or
CC cancer-related brain/spinal cord injury, schizophrenia, psychosis,
CC depression, bipolar depression/disorder, anxiety syndromes/disorders,
CC phobias, stress and related syndromes, cognitive function disorders,
CC aggression, obsessive compulsive behaviour syndromes, multi-infarct
CC dementia, seasonal mood disorder, Lewy body dementia, borderline
CC personality disorder, cerebral palsy, age related/geriatric dementia,
CC epilepsy and injury related to epilepsy, spinal cord injury, brain
CC injury, trauma related brain/spinal cord injury, anticancer treatment
CC related brain/spinal cord tissue injury, infection and inflammation
CC related brain/spinal cord injury, environmental toxin related brain/
CC spinal cord injury, multiple sclerosis, autism, attention deficit
CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
CC to the retina or sleep disorders. The invention is also used in gene
CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
CC illustrate the method of the invention

XX SQ Sequence 20 BP, 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7408 AACATCGACGACGACG 7425
Db 19 AACGACGACGACGACG 2

RESULT 3088
ACF36185
ID ACF36185 standard; DNA; 20 BP.
XX AC ACF36185;
XX 04-DEC-2003 (first entry)

DE Delta constant region specific forward primer Delta1F.

XX KM Embryonic stem cell; transgene; chimeric chicken; avian; transgenic; PCR;
XX primer; ss.

XX OS Synthetic.
XX PN WO2003064627-A2.
XX PD 07-AUG-2003.
XX PF 03-FEB-2003; 2003WO-US003235.
XX PR 01-FEB-2002; 2002US-00067148.

XX PA (ORIG-) ORIGIN THERAPEUTICS.
XX PI Etches RJ, Van De Lavoie M, Heyer B, Diamond J, Mather C;
XX Beemer K, Myers H;
XX WPI; 2003-646148/61.

PT New compositions comprising sustained chicken embryonic stem (ES) cell
PT culture having a transgene integrated into genome of ES cell progenies,
PT useful in producing engineered chickens for avian transgenics, e.g.
PT protein production.

XX Example 4; Page 18; 46pp; English.

XX The invention relates to a composition comprising a sustained culture of
CC chicken embryonic stem cells with a transgene stably integrated into the
CC genome of substantially all of the progeny of the embryonic stem cells.
CC The embryonic stem cell progeny contribute to a somatic tissue of a

CC chimeric chicken produced by the injection of the chicken embryonic cells
CC into a chicken embryo. Compositions comprising cultures of embryonic
CC chicken embryonic stem cells are useful in producing engineered chickens
CC for avian transgenics, including protein production for pharmaceutical
CC industry, production of chickens that deposit human antibodies in their
CC eggs, and site-specific modification of the avian genome for other
CC applications. The cultures may be used in the selection of desirable
CC phenotypes in chimeric animals and modifications to the genome of chicken
CC embryonic cells to introduce exogenous DNA into a chimeric offspring.
CC Sequences AC936177-186 represent primers used in a PCR analysis of
CC transgenes for the presence of an unrearranged human heavy chain locus
XX
SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6223 GGGAGAGGAGGAGGACTGT 6240
Db 3 GGGAGAGGAGGAGGAGGACTGT 20

RESULT 3089
ADC37131
ID ADC37131 standard; DNA; 20 BP.
XX
AC ADC37131;
XX
DT 18-DEC-2003 (first entry)
XX
DE CK19 forward primer #2.
XX
KM directly amplifying nucleic acid; inhibit; breakdown; cancer metastasis;
KW PCR; primer; ss; CK19.
XX
OS unidentified.
XX
PN WO2003060116-A1.
XX
PD 24-JUL-2003.
XX
PF 08-JAN-2003; 2003WO-JP000060.
XX
PR 09-JAN-2002; 2002JP-00002046.
PR 13-NOV-2002; 2002JP-00329958.
XX
PA (SYSM-) SYSMEX CORP.
XX
PI Tada S, Yoshida T, Shohmi K, Nishida M, Nakabayashi K;
PI Yamagata K;
XX
DR WPI; 2003-587284/55.
XX
PT Directly amplifying nucleic acids in a sample by inhibiting nucleic acid
PT breakdown.
XX
PT Example 7; SEQ ID NO 20; 56pp; Japanese.
XX
PS The invention relates to a novel method for directly amplifying nucleic
CC acids in a sample without having to isolate it. The method comprises a
CC step to inhibit the breakdown of nucleic acids. The invention further
CC comprises: a solution for treating the nucleic acid sample; a method for
CC treating the sample; a reagent for detecting nucleic acids; a nucleic
CC acid detection system; and a method for detecting cancer metastasis. This
CC polynucleotide represents a PCR primer used in the exemplification of the
CC invention.
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 AGATCAAGGCGCTGAAG 1006
Db 2 AGATCAAGGCGCTGAAG 19

RESULT 3090
ADD20586
ID ADD20586 standard; DNA; 20 BP.
XX
AC ADD20586;
XX
DT 15-JAN-2004 (first entry)
XX
DE Oreochromis niloticus microsatellite primer SEQ ID NO:1221.
XX
KM single nucleotide polymorphism; SNP; fish; Salmo salar;
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KM detection; primer; ss.
XX
OS Synthetic.
OS Oreochromis niloticus.
XX
PN WO2003060160-A2.
XX
PD 24-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-IB000112.
XX
PR 18-JAN-2002; 2002US-0349950P.
PR 16-AUG-2002; 2002US-0404200P.
XX
PA (GENO-) GENOMAR ASA.
XX
PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX
DR WPI; 2003-627388/59.
XX
PT Novel isolated nucleic acid molecule comprising single nucleotide
PT polymorphism associated with fish, useful for forming PCR primers which
PT are used for detecting single nucleotide polymorphisms in fish nucleic
PT acids.
XX
PS Claim 18; SEQ ID NO 1221; 233pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) comprising a
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC (i), or its complement under highly stringent hybridisation conditions.
CC Also described: (1) an isolated oligonucleotide (II) comprising at least
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites; and determining (MI) the
CC origin of fish sample comprising providing a parentage genotype database
CC comprising a collection of candidate parent genotypes, where each of the
CC candidate parent genotype represents a distinct origin, and comparing a
CC sample genotype to the parentage genotype database, where a match between
CC the sample genotype and one of the candidate parent genotype identifies
CC to the origin of the sample. (MI) is useful for determining the origin of
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC detecting nucleic acid molecule comprising SNP in a sample, which
CC involves contacting the sample containing nucleic acids with one or more
CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC useful for detecting nucleic acid molecule comprising a polymorphic
CC sequence in a sample, comprising contacting the sample containing nucleic

CC acids with one or more (ii) which is derived from O. niloticus
 CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
 CC sites or seabase polymorphic sites, and identifying a nucleic acid that
 CC hybridizes to (ii). (iii) is useful for detecting nucleic acid molecule
 CC comprising a microsatellite sequence in sample. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7021 ACAGAGGAAATAGGAAA 7038
 DB 2 ACAGCGGACAAATAGGAAA 19

RESULT 3091
 AAD62234/C
 ID AAD62234 standard; DNA; 20 BP.

XX
 AC AAD62234;
 XX
 DT 15-JAN-2004 (first entry)

XX Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150789.
 XX
 KM Haematopoietic cell; tyrosine kinase; hyperproliferative disorder;
 KM cancer; therapy; inflammation; diabetes; viral infection; inflammation;
 KM tumour; cytostatic; virucide; antisense therapy; antisense; human;
 KM phosphorothioate backbone; ss.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidines are 5-
 FT methyl cytidines"
 FT 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"

XX
 FN US2003125275-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 04-DEC-2001; 2001US-00007010.
 XX
 PR 04-DEC-2001; 2001US-00007010.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Borchers AH, Dobie KM;
 XX
 DR WPI; 2003-811000/76.
 XX
 PT New antisense oligonucleotides targeted to nucleic acids encoding
 PT haematopoietic cell protein tyrosine kinase, useful for diagnosing or
 PT treating cancer (e.g. leukemia), inflammation, diabetes or viral
 PT infections.
 XX
 PS Example 15; Page 27; 59pp; English.
 XX
 CC The invention relates to a compound targeted to a nucleic acid molecule

CC encoding haematopoietic cell protein tyrosine kinase. The compound
 CC inhibits the expression of haematopoietic cell protein tyrosine kinase
 CC and it specifically hybridizes with the nucleic acid molecule encoding
 CC the tyrosine kinase or with at least an 8-nucleobase portion of an active
 CC site on the nucleic acid molecule encoding the tyrosine kinase. The
 CC antisense compounds are useful for modulating the expression of
 CC haematopoietic cell protein tyrosine kinase and treating diseases or
 CC conditions associated with the expression of the tyrosine kinase, such as
 CC hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a
 CC viral infection. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits and in
 CC distinguishing between functions of various members of a biological
 CC pathway. The present sequence is human haematopoietic cell tyrosine
 CC kinase antisense oligonucleotide

XX
 SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7140 CCAGCCTAATGATATGT 7157
 DB 19 CCAGCCTAATGATATGT 2

RESULT 3092
 ADD42189
 ID ADD42189 standard; DNA; 20 BP.

XX
 AC ADD42189;
 XX
 DT 15-JAN-2004 (first entry)

XX Human infertility associated primer SEQ ID 50.
 XX
 KM primer; male infertility; infertility-associated mutation;
 KM azoospermia factor; Y-chromosome;
 KM cystic fibrosis transmembrane conductance regulator; CFTR;
 KM Kallmann syndrome; KAL1; androgen resistance; steroid 21-hydroxylase;
 KM CYP21; microarray; quantitative trait locus; in vitro fertilization;
 KM oligospermia; ss.

XX
 OS Homo sapiens.
 OS
 PN WO2003050299-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2002; 2002WO-EP013995.
 XX
 PR 10-DEC-2001; 2001DE-01060563.
 XX
 PA (OGHA-) OGHAM GMBH.
 XX
 PI Cullen P, Seedorf U;
 XX
 DR WPI; 2003-505402/47.
 XX
 PT Investigating male genetic infertility, useful for diagnosis e.g. for
 PT assessing suitability for in vitro fertilization, based on multifactorial
 PT analysis of infertility-related mutations.
 XX
 PS Claim 13; SEQ ID NO 50; 110pp; German.
 XX
 CC This invention describes a novel method for investigating genetic
 CC infertility or predisposition in males. The method involves selecting at
 CC least two infertility-associated mutations which are recessive or
 CC intermediate that are associated with infertility in the heterozygous
 CC state and/or only in the homozygous state. Preferably at least one
 CC azoospermia factor is detected which may be lost by microdeletions in
 CC intervals 5 or 6 of the Y-chromosome. Also any of several hundred

CC mutations, listed, present in the cystic fibrosis transmembrane
 CC conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen
 CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.
 CC Probes for the mutated genes and/or native nucleic acid, or their
 CC complementary strands, are fixed to a carrier, particularly as a
 CC microarray, then tested for hybridization with oligonucleotides from or
 CC synthesized from, a patient sample and hybridization detected.
 CC Multiaxial analysis is by standard statistical methods, particularly
 CC the quantitative trait locus method. The method is used to diagnose
 CC inherited male infertility or predisposition to its, especially in
 CC conjunction with in vitro fertilization programs, e.g. for assessing
 CC subjects with oligospermia for possible application of the
 CC intracytoplasmic sperm injection method. Analysis of many mutations
 CC improves diagnosis of the genetic basis of male infertility, including
 CC polygenic origins (complex interactions between different heterozygotic
 CC mutations). A chip for analyzing genetic infertility in males comprises
 CC oligonucleotides that represent known mutations (nonsense or missense,
 CC insertions, allelic variants deletions or rearrangements) in the cystic
 CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen
 CC resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent
 CC oligonucleotides used in the microarray described in the method of the
 CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the
 CC SEQ ID list of the specification.

SO Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2275 GCGTCATCAACTGGAA 2292
 DB 1 GCCTTCATCACCTGGAA 18
 |||||

RESULT 3093
 ADD81662
 ID ADD81662 standard; DNA; 20 BP.
 XX
 AC ADD81662;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE HIV PRT antisense derived probe #591.
 XX
 KM ss; oligonucleotide hybridisation potential; efficient hybridisation;
 KM large array; minimum oligonucleotide synthesis; probe.
 XX
 OS Human immunodeficiency virus.
 XX
 PN US2003054346-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 15-FEB-2001; 2001US-00784674.
 XX
 PR 10-FEB-1998; 98US-00021701.
 XX
 PA (SHAN/) SHANNON K W.
 PA (WOLBER/) WOLBER P K.
 PA (DELENSTARR/) DELENSTARR G C.
 PA (WEBB/) WEBB P G.
 PA (KINCAID/) KINCAID R H.
 XX
 PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 XX
 DR WPI; 2003-743746/70.
 XX
 PT Predicting potential of oligonucleotides to hybridize to target
 PT nucleotide sequence comprises determining and evaluating for each
 PT oligonucleotide a parameter predictive of the oligonucleotides ability to
 PT hybridize with target.

PS Example 2; SEQ ID NO 735; 423bp; English.
 XX
 CC The invention relates to a method of predicting the potential of
 CC oligonucleotides to hybridize to target nucleotide sequences. The method
 CC is useful for predicting the potential of an oligonucleotide to hybridize
 CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
 CC contains chemically modified nucleotides. The method is also useful for
 CC predicting the potential of the oligonucleotides to hybridize to a
 CC complementary target nucleotide sequence. The method is useful to predict
 CC efficient hybridisation oligonucleotides for each of multiple target
 CC sequences therefore very large arrays may be constructed and tested with
 CC minimum synthesis of oligonucleotides. The present sequence represents a
 CC HIV PRT antisense derived probe.

SO Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5703 CCTTCCTTTTCCTTCT 5720
 DB 2 CCTTCCTTTTCCTTCT 19
 |||||

RESULT 3094
 ADE39777/c
 ID ADE39777 standard; DNA; 20 BP.
 XX
 AC ADE39777;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Porcine CD 151 related PCR primer seq id 13.
 XX
 KM porcine reproductive and respiratory syndrome virus; PRRSV;
 KM susceptibility; CD 151; susceptibility standard; PRRSV infection;
 KM vaccine; vaccine virus stock; non-simian vaccine; xenotransplantation;
 KM non-simian cell line; drug testing; transformed cell line; porcine; pig;
 KM PCR; primer; ss.
 XX
 OS Sus sp.
 XX
 PN US2003186236-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 28-JAN-2002; 2002US-00058597.
 XX
 PR 29-JAN-2001; 2001US-00772044.
 XX
 PA (KAPIL/) KAPIL S.
 PA (SHAN/) SHANMUKHAPPA K.
 XX
 PI Kapil S, Shanmukhappa K;
 XX
 DR WPI; 2003-811729/76.
 XX
 PT Determination of susceptibility to porcine reproductive and respiratory
 PT syndrome virus non-invasively useful e.g. to breed pigs with low
 PT susceptibility or classify infection resistance in an animal, by assaying
 PT for CD 151.
 XX
 PS Example 17; SEQ ID NO 13; 45bp; English.
 XX
 CC The invention describes a method to identify susceptibility to porcine
 CC reproductive and respiratory syndrome virus (PRRSV) in an animal by
 CC assaying a cellular material sample from known origin in the animal for
 CC CD 151. The method is useful to determine the susceptibility of animals
 CC (especially pigs) to PRRSV and to compare susceptibility to a known
 CC susceptibility standard, especially for material of the same cellular
 CC origin. It can be used to determine if an animal is resistant to PRRSV
 CC infection, by determining presence/absence of CD 151, and to classify

CC resistance levels. It is especially useful to select animals for
CC breeding by selecting animals with CD 151 levels lower (especially a
CC least 50 % lower) than a known standard (especially for material of the
CC same cellular origin). Polynucleotides encoding CD 151 are useful to
CC produce vaccines and to modify PRSV production in cells susceptible to
CC PRSV infection, especially to increase PRSV production e.g. in vaccine
CC virus stock. They are especially useful to produce non-simian vaccines,
CC avoiding possible introduction of primate viruses into organs
CC xenotransplanted from pigs to humans. They may be used to determine the
CC effect of single nucleotide polymorphisms on PRSV susceptibility, and to
CC compare PRSV susceptibility factors between individual swine. They can
CC also be used to modulate viral RNA (especially PRSV RNA) entry into
CC cells by altering CD 151 amounts in cells. Polynucleotides may be
CC included in plasmids useful to render a cell line susceptible to PRSV
CC infection, useful to produce non-simian lines for drug testing. They may
CC be included in vectors and used to integrate CD 151 into a chromosome.
CC They can also be used to produce transformed cell lines, useful e.g. to
CC diagnose PRSV infection in swine herds or produce vaccines for inducing
CC immunity against PRSV. This sequence represents a primer used to
CC determine sequence of a porcine CD 151 intron in order to determine the
CC entire sequence of porcine CD 151.

XX Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CAAGGCGCTGAAGGTGA 1010

Db 19 CAAGAGCTGAGAGCTGA 2

RESULT 3095

ADe40361

ID ADE40361 standard; DNA; 20 BP.

XX ADE40361;

DT 29-JAN-2004 (first entry)

XX Reverse Ag4809 RT-PCR primer used to amplify human NOV RNA.

XX NOX; cardiact; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

KM antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;

KM antiparkinsonian; antisthmatic; gynaecological; cardiomyopathy;

KM atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

KM multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;

KM asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;

XX tissue typing; human; NOV; ss; primer; PCR; RT-PCR.

OS Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

PF 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 07-AUG-2001; 2001US-0310544P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 16-AUG-2001; 2001US-0312892P.

PR 17-AUG-2001; 2001US-0313201P.

PR 17-AUG-2001; 2001US-0313415P.

PR 20-AUG-2001; 2001US-0313643P.

PR 20-AUG-2001; 2001US-0313702P.

PR 21-AUG-2001; 2001US-0314031P.

PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323949P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-MAR-2002; 2002US-035478P.
PR 19-APR-2002; 2002US-0373814P.
PR 19-APR-2002; 2002US-0373825P.
PR 19-APR-2002; 2002US-0373989P.
PR 23-APR-2002; 2002US-0374632P.
PR 07-JUN-2002; 2002US-038671P.
PR 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

XX Kekuda R, Miller CE, Raturajan M, Pena CE, Rieger DK;
PI Shlmeitz RA, Zernusen BD, Li L, Ji W, Padigaru M, Casman SJ;
PI Voss E, Boldog FL, Gotman L, Leite MW, Vernet CAM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjalte T, Raetelli L, Spytek KA;
PI Edinger SR, Ellerman K, Malyanar UM, MacDougall JR, Stone DJ;
PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
PI Smithson G;

DR WPI; 2003-663472/62.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX Example C; SEQ ID NO 267; 560bp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiact, antiarteriosclerotic, hypotensive,
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antisthmatic and
CC gynaecological activities and may be useful in diagnosing, treating or
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the RT-PCR primer of the invention which was used to amplify human NOV
CC RNA.

XX Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CCATCACACCCGCTTTT 2354

Db 1 CCATCACACCGCCATTT 18

RESULT 3096

AAQ50784

ID AAQ50784 standard; RNA; 21 BP.

XX AAQ50784;

DT 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX HBV target sequence 10.

XX RNA, enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; hnRNA;

KM picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;

KM papilloma virus; HPV; Epstein-Barr virus; EBV; TCV;

KM T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus;


```
XX 20-JAN-1994.
PD
XX 30-JUN-1993; 93WO-AU000320.
XX
XX 03-JUL-1992; 92AU-00003330.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Scott NS, Thomas MR;
XX
XX WPI; 1994-035083/04.
XX
PT Novel ribosome DNA probe sequences - for the accurate identification of
PT grape cultivars.
XX
XX Claim 14; Page 22; 55pp; English.
XX
XX The sequences given in AA055251-56 are primers which were used in a
CC method for the analysis of nucleic acid derived from ribosomes of the
CC grapevine genus Vitis. The amplified sequences represent the 5S region of
CC the ribosomal (r)DNA repeat and contain polymorphisms. These
CC polymorphisms may be used in a method for the identification of different
CC grape cultivars. The amplified clones contain simple repeat sequences and
CC may be identified in a genomic library of grapevine DNA using simple di-
CC tri- or tetra- nucleotide repeats such as (AT)8, (GT)10, (GGT)10 and such
CC like as probes. See also AA055231-50. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5197 TGGATACATTTTGGGGCT 5214
DB 19 TGGATACATTTTACGGGCT 2
XX
RESULT 3099
AA16749/c
ID AA16749 standard; RNA; 21 BP.
XX
XX AA16749;
AC
XX
XX 09-OCT-1996 (first entry)
DT
XX
XX E.coli tRNA(Pro) anticodon stem-loop used for generating analogues.
DE
XX
XX Analogue; ligand binding; 16S rRNA; parental molecule; conformation;
KM stem-loop structure; stable; helix; nucleotide clamp; decoding region;
KM tRNA; tRNA; A site; ribosome; protein synthesis; assay; antibiotics;
KM tRNA; aminoglycoside protection assay; ss.
XX
XX Synthetic.
OS
XX
XX WO9606106-A1.
XX
XX 29-FEB-1996.
PD
XX
XX 23-AUG-1995; 95WO-US010721.
PF
XX
XX 23-AUG-1994; 94US-00294450.
PR
XX 05-JUL-1995; 95US-00498402.
PR
XX
XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
PA
XX
XX Stern S, Purohit P;
PT
XX
XX WPI; 1996-151324/15.
XX
XX Oligo:ribonucleotide analogue for identifying new antibiotics - have same
```

```
PT binding pattern as parental RNA derivative, and assays for detecting
PT therapeutic activity of cpd.
XX
XX Disclosure; Page 18; 57pp; English.
XX
XX Novel analogues able to assume the same conformation as the parent mol.
CC are generated from two sections, the first section corresp. to sequences
CC in the parental RNA mol., whilst the second section consists of an
CC artificial nucleotide structure (i.e. not found in the parental RNA) that
CC can combine with the first section to stabilise the analogue. The second
CC structure also contains a stem-loop structure and a second nucleic
CC structure able to form a stable base-paired helix, designated the
CC nucleotide clamp. The analogues pref. contain the complete sequence of
CC the 16S rRNA decoding region (the decoding region being the region which
CC correctly aligns the mRNA with the tRNA in the "A site" of the ribosome
CC during protein synthesis). The sequences AA16748-52 were used to
CC generate analogues of the invention esp. for aminoglycoside protection
CC assays. The analogues can be used in assays to detect potential ligands
CC e.g. new antibiotics or anti-viral agents, that could bind to the parent
CC molecule
XX
SQ Sequence 21 BP; 3 A; 4 C; 8 G; 0 T; 6 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4187 GGTATCGCCCAAGATG 4204
DB 21 GGTCATCACCCCAAGATG 4
XX
RESULT 3100
AA11723
ID AA11723 standard; DNA; 21 BP.
XX
XX AA11723;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 18-JUL-1996 (first entry)
DT
XX
XX Polycystic kidney disease 1 gene antisense primer, KGB-R27.
DE
XX
XX Polycystic kidney disease; PKD; autosomal dominant; ADPKD; mutation;
KM exon; short arm; chromosome 16; repeated region; alternative splicing;
KM extracellular matrix proteins; antibody; detection; diagnosis;
KM mini gene therapy; single strand conformational polymorphism analysis;
KM SSCP; primer; amplify; ss.
XX
XX Synthetic.
OS
XX
XX WO9534573-A1.
XX
XX 21-DEC-1995.
PD
XX
XX 02-JUN-1995; 95WO-US007079.
PF
XX
XX 03-JUN-1994; 94US-00253524.
PR
XX 30-MAR-1995; 95US-00413580.
PR
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (MILL-) MILLENITUM PHARM INC.
XX
XX Reeders S, Schneider M, Glucksmann S;
XX
XX WPI; 1996-049618/05.
XX
XX DNA encoding poly-cytic kidney disease gene product - for use in gene
PT therapy of ADPKD, and in the evaluation of treatment for PKD.
XX
XX Example; Page 68; 126pp; English.
XX
XX The sequences given in AA11709-29 are primers which were used in single-
```



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XX AAV20817;
XX
XX 16-JUL-1998 (first entry)
XX
XX
XX DE Primer for Human haematopoietic stem cell growth factor.
XX
XX Haematopoietic stem cell growth factor, SCGF, burst-promoting activity;
XX BPA; granulocyte macrophage colony stimulating activity; gene therapy;
XX GPA; haematopoietic cell disorder; bone marrow inhibition; human;
XX PCR primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX MO9808869-A1.
XX
XX 05-MAR-1998.
XX
XX 27-AUG-1997; 97MO-JP002985.
XX
XX 27-AUG-1996; 96JP-00262252.
XX 24-MAR-1997; 97JP-00087242.
XX 07-JUL-1997; 97MO-JP002349.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hiraoka A, Sugimura A, Mio H;
XX
XX WPI; 1998-179383/16.
XX
XX Haematopoietic stem cell growth factor - useful for, e.g. treatment and
XX diagnosis of haematopoietic cell abnormalities and bone marrow
XX inhibition.
XX
XX Example 21; Page 49; 85pp; Japanese.
XX
XX This sequence is a primer for DNA encoding the human haematopoietic stem
XX cell growth factor (SCGF) of the invention. The polypeptide of the
XX invention is of mammalian origin and has haematopoietic stem cell growth
XX factor SCGF activity, including burst-promoting activity (BPA) and
XX granulocyte macrophage colony stimulating activity (GPA). The products
XX can be used for treatment, diagnosis and analysis of haematopoietic cell
XX disorders and bone marrow inhibition, e.g. by cytotoxic anticancer agents
XX such as 5-fluorouracil. The products can also be used for amplification
XX of haematopoietic cells in vitro, e.g. for use in marrow grafting and
XX gene therapy by insertion of SCGF gene using a suitable therapeutic
XX vector
XX
XX Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2274 TGCCTGCATCAACTGGA 2291
XX 21 TGCCTGCATTAAGCTGGA 4
XX
XX
XX RESULT 3104
XX AA226119
XX ID AA226119 standard; DNA; 21 BP.
XX
XX AA226119;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 308.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX

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XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
XX
XX MO9841648-A2.
XX
XX 24-SEP-1998.
XX
XX 19-MAR-1998; 98MO-US005419.
XX
XX 20-MAR-1997; 97US-0041057P.
XX
XX (VAR-) VARIAGENICS INC.
XX
XX Housman D, Ledley FD, Stanton VP;
XX
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AA225812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 6 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4198 CAAGATGGGTCACAGCT 4215
XX 1 CAAGAAAGGAGCACAGGCT 18
XX
XX
XX RESULT 3105
XX AA226693
XX ID AA226693 standard; DNA; 21 BP.
XX
XX AA226693;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 882.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX

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OS Homo sapiens.
XX
XX WO9841648-A2.
XX
XX 24-SEP-1998.
XX
XX 19-MAR-1998; 98WO-US005419.
XX
XX 20-MAR-1997; 97US-0041057P.
XX
XX (VARI-) VARIAGENICS INC.
XX
XX Housman D, Ledley FD, Stanton VP;
XX
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumors, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AA25812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 10 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 5420 AAAAGCAAGACATCAGC 5437
XX |||||
XX 3 AAAAGCAAGATCAGC 20
XX
XX RESULT 3106
XX AAX35653
XX ID AAX35653 standard; DNA; 21 BP.
XX
XX AAX35653;
XX
XX 09-JUL-1999 (first entry)
XX
XX PCR primer used to amplify human heparanase cDNA.
XX
XX Heparanase; hpa; modulator; heparin-binding growth factor;
XX cellular response; cytokine; cell interaction; plasma lipoprotein;
XX cellular susceptibility; infection; disintegration;
XX neurodegenerative plaque; wound healing; angiogenesis; restenosis;
XX atherosclerosis; inflammation; neurodegenerative disease; neuritis;
XX plasma heparin; micrometastasis; autoimmune lesion; renal failure;
XX PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9911798-A1.
XX
XX

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XX
XX 11-MAR-1999.
XX
XX 31-AUG-1998; 98WO-US017954.
XX
XX 02-SEP-1997; 97US-00922170.
XX
XX 02-JUL-1998; 98US-00109386.
XX
XX (INST-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
XX
XX Pecker I, Vlodevsky I, Feinstein E;
XX
XX WPI; 1999-302255/25.
XX
XX New human polynucleotide useful for treating angiogenesis, restenosis,
XX and inflammation.
XX
XX Example 7; Page 30; 63pp; English.
XX
XX The specification describes a polypeptide having heparanase (hpa)
XX activity. The recombinant protein is used as a modulator of heparin-
XX binding growth factors, cellular responses to heparin-binding growth
XX factors and cytokines, cell interaction with plasma lipoproteins,
XX cellular susceptibility to viral, protozoal and bacterial infections or
XX disintegration of neurodegenerative plaques. Heparanase may be useful for
XX conditions such as wound healing, angiogenesis, restenosis,
XX atherosclerosis, inflammation, neurodegenerative diseases, and viral
XX infections. Mammalian heparanase can be used to neutralize plasma
XX heparin, and anti-heparanase antibodies may be applied for
XX immunodetection and diagnosis of micrometastases, autoimmune lesions, and
XX renal failure in biopsy specimens, plasma samples, and body fluids. The
XX present PCR primer was used to amplify hpa cDNA, in the course of the
XX invention
XX
XX Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 7413 CAGCAGCAGCAGCAGCAG 7430
XX |||||
XX 4 CAGCAGCAGCAGCATCAG 21
XX
XX RESULT 3107
XX AAX18314
XX ID AAX18314 standard; DNA; 21 BP.
XX
XX AAX18314;
XX
XX 26-JUL-1999 (first entry)
XX
XX PCR primer for telomerase coding sequence.
XX
XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukemia;
XX neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
XX smooth muscle cell hyperplasia; stem cell proliferation; Wilms tumor;
XX stem cell differentiation; organ regeneration; organ differentiation;
XX PCR primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9901560-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US013835.
XX
XX 01-JUL-1997; 97US-0051410P.
XX
XX

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PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
XX Killian A, Bowtell D;
XX WPI; 1999-106060/09.
XX
XX New isolated vertebrate telomerase genes - used to develop products for
XX treating cancers or for organ regeneration, nerve cell or brain cell
XX growth following injury or bone marrow transplantation.
XX
XX Example 1; Page 42; 134pp; English.
XX
CC This sequence is a PCR primer for DNA encoding a truncated human
CC telomerase of the invention. Primers that amplify the telomerase coding
CC sequence can be used in a method for diagnosing cancer in a patient. The
CC telomerase can be used for detection, diagnosis and drug screening.
CC Inhibitors of telomerase activity can be used to treat cancers such as
CC melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon
CC carcinomas, leukemias, lymphomas, osteosarcomas or smooth muscle cell
CC hyperplasias or skin growths. Enhancers of telomerase may be used to
CC stimulate stem cell proliferation and differentiation (expansion of
CC hematopoietic stem cells could be administered in the bone marrow
CC transplant context). As well, many tissues have stem cells. Proliferation
CC of these cells may be useful in wound healing, hair growth, treatment of
CC disease such as Wilm's tumour, organ regeneration or differentiation
CC after injury or diseases, nerve cell or brain cell growth following
CC injury
XX
XX Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7335 TGAAGCTGTACTTGTCTCA 7352
Db 4 TGAGCTGTACTTGTCTCA 21
RESULT 3108
AAZ79141/C
ID AAZ79141 standard; DNA; 21 BP.
XX
XX AAZ79141;
AC
XX 17-AUG-1999 (first entry)
DT
XX
XX Primer NGAL107-L for A.thaliana SLP marker.
DE
XX
XX MSH6; Muts homologue; plant; DNA mismatch repair; genetic variation;
KM characteristic; microsatellite; primer; PCR; amplification; SLP; ss;
KM sample sequence length polymorphism.
XX
XX Synthetic.
OS
XX Arabidopsis thaliana.
OS
XX WO9919492-A2.
PN
XX
XX 22-APR-1999.
PD
XX
XX 09-OCT-1998; 98WO-EP006977.
PF
XX 10-OCT-1997; 97AU-00009745.
PR
XX (RHON) RHON-POULENC AGROCHIMIE.
PA
XX
XX Doutriaux M, Betzner AS, Freysinet G, Perez P;
PI
XX

```

```

DR WPI; 1999-277644/23.
XX
XX DNA encoding protein functionally involved in the DNA mismatch repair
XX system of a plant.
PT
XX
XX Example 3; Page 28; 117pp; English.
XX
XX The invention relates to the isolation of the Arabidopsis thaliana MSH3
XX (AAZ79066) and MSH6 (AAZ79067) genes. These genes are Muts homologues
XX (MSH) from plants and are involved in DNA mismatch repair. The DNA
XX sequence can be used in processes for at least partially inactivating a
XX DNA mismatch repair system of a plant, for increasing genetic variation
XX in a plant, and for obtaining a plant with a desired characteristic.
XX Primers AAZ79105-X79160 represent 28 primer pairs used to amplify short
XX allelic repeat fragments designated Simple Sequence Length Polymorphisms
XX (SSLP). These fragments can be used as markers in the analysis of
XX homologous recombination between genomes of A.thaliana subspecies
XX
XX Sequence 21 BP; 14 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4459 TGAAGCTTTTGTCTTTT 4476
Db 21 TGAGTTTTTTGTCTTTT 4
RESULT 3109
AAZ28937/C
ID AAZ28937 standard; DNA; 21 BP.
XX
XX AAZ28937;
AC
XX 07-FEB-2000 (first entry)
DT
XX
XX Reverse primer cmar8 for amplification of paraplegin gene exon.
DE
XX
XX Reverse primer cmar8; paraplegin; human; hereditary spastic paraplegia;
KM HSP; mutation; diagnosis; treatment; neurodegenerative condition;
KM Amyotrophic Lateral Sclerosis; ALS; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO9958556-A2.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 06-MAY-1999; 99WO-EP003112.
PF
XX 08-MAY-1998; 98IT-MI001003.
PR
XX
XX (TELE-) FOND TELETHON.
PA
XX
XX Ballabio A, Cabari G;
PI
XX
XX WPI; 2000-039065/03.
DR
XX
XX A novel protein associated to hereditary spastic paraplegia used for the
XX diagnosis of neurodegenerative conditions.
PT
XX
XX Claim 4; Fig 3; 53pp; English.
PS
XX
XX The present sequence is a reverse primer cmar8 used for amplification and
XX detection of mutations in paraplegin gene exon from hereditary spastic
XX paraplegia (HSP) patients. Detection of mutations in paraplegin gene
XX helps in the diagnosis and treatment of various forms of HSP or other
XX neurodegenerative conditions, such as Amyotrophic Lateral Sclerosis
XX
XX Sequence 21 BP; 8 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
SQ

```

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5350 AGTTGGTTTCAGCTGGG 5367

DB 18 AGTTGCTTTTCAGCTGAG 1

RESULT 3110

AAA75055

ID AAA75055 standard; DNA; 21 BP.

AC AAA75055;

DE 15-JAN-2001 (first entry)

XX PCR primer hpl-629 used to amplify human cDNA encoding heparanase.

XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;

XX heparin-binding growth factor; cytokine; neurodegenerative plaque;

XX wound healing; infection; burn; angiogenesis; restenosis;

XX atherosclerosis; inflammation; neurodegenerative disease;

XX Gerstmann-Strausser Syndrome; Creutzfeldt-Jakob disease; PCR primer; ss.

OS Homo sapiens.

XX WO200052178-A1.

XX 14-FEB-2000; 2000WO-US003542.

XX 01-MAR-1999; 99US-00258892.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX (PRIE/) FRIEDMAN M M.

XX Pecker I, Vlodavsky I, Feinstein E;

XX WPI; 2000-579289/54.

XX New polynucleotides encoding a polypeptide having heparanase activity.

XX PT useful in wound healing and in gene therapy, particularly in treating

XX tumor, inflammation, autoimmunity, neurodegenerative diseases.

XX Example 6; Page 53; 152pp; English.

XX The present PCR primer was used to amplify a human cDNA sequence, which

XX encoded a protein with heparanase catalytic activity. The heparanase

XX (hpa) polynucleotide is useful in gene therapy, particularly in treating

XX tumour, inflammation or autoimmunity. Particularly, the polynucleotide is

XX useful in modulating the bioavailability of heparin-binding growth

XX factors, cellular responses to heparin-binding growth factors (e.g. bFGF)

XX and cytokines (e.g. interleukin (IL)-8), cell interaction with plasma

XX lipoproteins, cellular susceptibility to certain viral and some bacterial

XX CC and protozoa infections, or disintegration of neurodegenerative plaques.

XX CC The polynucleotide is also useful in wound healing (e.g. thermal,

XX CC chemical or radiation burns), and in the treatment of angiogenesis,

XX CC restenosis, atherosclerosis, inflammation, neurodegenerative diseases

XX CC (Gerstmann-Strausser Syndrome or Creutzfeldt-Jakob disease), and some

XX CC viral, bacterial or protozoa infections

XX SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 21;

XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAG 7430

DB 4 CAGCAGCAGCAGCAGCAG 21

RESULT 3111

ID AA272700 standard; DNA; 21 BP.

AC AA272700;

DE 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:7056.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation;

XX amplification; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

OS Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

XX Claim 9; Page 1735; 2745pp; English.

XX AA265654 to AA269578 represent human biallelic markers from the present

XX invention, which contain a polymorphic base at position 24 of their

XX nucleotide sequences. AA269579 to AA27440 represent amplification

XX primers for the biallelic markers. The biallelic markers of the invention

XX have a variety of uses: they can be used for high density mapping of the

XX human genome, and in complex association studies and haplotyping studies

XX which are useful in determining the genetic basis for disease states.

XX CC Compositions and methods of the invention can also be useful for the

XX identification of the targets for the development of pharmaceutical

XX agents and diagnostic methods, as well as the characterisation of the

XX CC differential efficacious responses to and side effects from

XX CC pharmaceutical agents acting on a disease as well as other treatment.

XX CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

XX CC 3367, are not actually given a sequence in the Sequence Listing from the

XX CC present invention

XX SQ Sequence 21 BP; 9 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 21;

XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4028 GAGAAAACAAATGTTAT 4045

DB 1 GAGAAAATAAATGTTAT 18

RESULT 3112

AAA63845/c

ID AAA63845 standard; DNA; 21 BP.

XX AAA63845;

XX


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DT 04-DEC-2000 (first entry)
XX
XX PCR primer used to amplify cDNA encoding full length human DAGKbeta.
DE
XX Human; diacylglycerol kinase beta; DAGKbeta; diacylglycerol; DAG;
XX phosphatidic acid; DAG-dependent protein kinase C activation;
KM mood disorder; epilepsy; neurodegenerative disorder; anxiety;
KM schizophrenia; migraine; drug dependence; stroke; Alzheimer's dementia;
KM Parkinson's disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200047723-A2.
PN
XX 17-AUG-2000.
PD
XX 23-DEC-1999; 99WO-GB004421.
PF
XX 15-FEB-1999; 99GB-00003430.
PR (GLAX ) GLAXO GROUP LTD.
PA
XX Caricasole A, Caldara F, Sala CF;
PI
XX WPI; 2000-506093/45.
XX
XX New human diacylglycerol kinase beta (hDAGKbeta) protein and its
PT modulating compounds, useful for treatment of neurodegenerative and mood
PT disorders.
XX
XX Disclosure; Page 15; 57pp; English.
XX
XX PCR primers AAA63845-46 were used to amplify cDNA encoding full length
CC human diacylglycerol kinase beta (DAGKbeta). DAGK converts diacylglycerol
CC (DAG) to phosphatidic acid and attenuates DAG-dependent protein kinase C
CC activation. Compounds that modulate the activity of DAGKbeta may be
CC administered to a human patient for the treatment or prophylaxis of a
CC disorder that is responsive to modulation of DAGK activity. The disorder
CC may be a mood disorder, epilepsy, a neurodegenerative disorder, anxiety,
CC schizophrenia, migraine, drug dependence, stroke, Alzheimer's dementia or
CC Parkinson's disease
CC
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4418 ATTTTCCTGCTGCCA 4435
DB 19 ATTTTCCTGCTGTCGA 2
RESULT 3113
AAA63843/c
ID AAA63843 standard; DNA; 21 BP.
XX
XX AAA63843;
AC
XX
XX 04-DEC-2000 (first entry)
DT
XX
XX PCR primer used to amplify cDNA encoding full length human DAGKbeta.
DE
XX Human; diacylglycerol kinase beta; DAGKbeta; diacylglycerol; DAG;
XX phosphatidic acid; DAG-dependent protein kinase C activation;
KM mood disorder; epilepsy; neurodegenerative disorder; anxiety;
KM schizophrenia; migraine; drug dependence; stroke; Alzheimer's dementia;
KM Parkinson's disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200047723-A2.
PN
XX
XX

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PD 17-AUG-2000.
XX
XX 23-DEC-1999; 99WO-GB004421.
PF
XX 15-FEB-1999; 99GB-00003430.
PR (GLAX ) GLAXO GROUP LTD.
PA
XX Caricasole A, Caldara F, Sala CF;
PI
XX WPI; 2000-506093/45.
XX
XX New human diacylglycerol kinase beta (hDAGKbeta) protein and its
PT modulating compounds, useful for treatment of neurodegenerative and mood
PT disorders.
XX
XX Disclosure; Page 15; 57pp; English.
XX
XX PCR primers AAA63843-44 were used to amplify cDNA encoding full length
CC human diacylglycerol kinase beta (DAGKbeta). DAGK converts diacylglycerol
CC (DAG) to phosphatidic acid and attenuates DAG-dependent protein kinase C
CC activation. Compounds that modulate the activity of DAGKbeta may be
CC administered to a human patient for the treatment or prophylaxis of a
CC disorder that is responsive to modulation of DAGK activity. The disorder
CC may be a mood disorder, epilepsy, a neurodegenerative disorder, anxiety,
CC schizophrenia, migraine, drug dependence, stroke, Alzheimer's dementia or
CC Parkinson's disease
CC
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4418 ATTTTCCTGCTGCCA 4435
DB 19 ATTTTCCTGCTGTCGA 2
RESULT 3114
AAF95448
ID AAF95448 standard; DNA; 21 BP.
XX
XX AAF95448;
AC
XX
XX 06-JUN-2001 (first entry)
DT
XX
XX Human gene single nucleotide polymorphism #209.
DE
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM polymorphism; vascular disease; coronary artery disease; forensics;
KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM pulmonary embolism; paternity test; db.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
PN
XX
XX 15-MAR-2001.
PD
XX
XX 07-SEP-2000; 2000WO-US024503.
PF
XX 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
XX (WHEE ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX

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XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JI;
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.
XX PS Example; Page 63; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX SQ Sequence 21 BP; 5 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7194 GACTACTCTGCTTTTAC 7211
DB 3 GACTACTCTGCTTTTAC 20

RESULT 3115
AAF96689
ID AAF96689 standard; DNA; 21 BP.
AC AAF96689;
XX 06-JUN-2001 (first entry)
DT
DE Human gene single nucleotide polymorphism #1450.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,T)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX WO200118250-A2.
XX PN 15-MAR-2001.
XX PD 07-SEP-2000; 2000WO-US024503.
XX PF
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JI;
XX DR WPI; 2001-226749/23.
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```
XX PT 'Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.
XX PS Example; Page 146; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5069 CCTAAGAGAGTGATGCT 5086
DB 2 CCTAAGAGAGTGATGCT 19

RESULT 3116
AAF96584
ID AAF96584 standard; DNA; 21 BP.
AC AAF96584;
XX 06-JUN-2001 (first entry)
DT
DE Human gene single nucleotide polymorphism #1345.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,T)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX WO200118250-A2.
XX PN 15-MAR-2001.
XX PD 07-SEP-2000; 2000WO-US024503.
XX PF
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JI;
XX DR WPI; 2001-226749/23.
XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
```

PT atherosclerosis.
 XX
 PS Example, Page 141; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 CC
 SQ Sequence 21 BP; 6 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4509 CTTCAGAGCTGAGAG 4526
 DB 2 CTGACAGAGCTGAGAG 19
 RESULT 3117
 AAF96360
 ID AAF96360 standard; DNA; 21 BP.
 XX
 AC AAF96360;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #1121.
 XX
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation /tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN W0200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PP 07-SEP-2000; 2000MO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX WPI; 2001-226749/23.
 DR
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 PS Example; Page 129; 242pp; English.
 XX

CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 CC
 SQ Sequence 21 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 1 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 896 TGATTGATTCATGTCAG 915
 DB 2 TGCTGATTCATGTCAG 21
 RESULT 3118
 AAF95480
 ID AAF95480 standard; DNA; 21 BP.
 XX
 AC AAF95480;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #241.
 XX
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation /tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN W0200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PP 07-SEP-2000; 2000MO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX WPI; 2001-226749/23.
 DR
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 PS Example; Page 66; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided

CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification

XX Sequence 21 BP; 11 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032
DB 4 ATGAGAAAGTAGAGAGAA 21

RESULT 3119

AAH28472
ID AAH28472 standard; DNA; 21 BP.

XX AAH28472;
XX 17-SEP-2001 (first entry)

DE PCR primer for cDNA encoding human slit polypeptide Zslit3.

XX Slit protein; Zslit3; neurite growth; cellular proliferation;
KW immune response; stroke; brain damage; paralysis; Huntington's disease;
KW neurodegenerative disease; amyotrophic lateral sclerosis;
KW Alzheimer's disease; Parkinson's disease; peripheral neuropathy;
KW demyelinating disease; multiple sclerosis; lung organogenesis;
KW pulmonary disease; respiration; circulation; cystic fibrosis; asthma;
KW immunosuppression; autoimmune disease; insulin dependent diabetes;
KW rheumatoid arthritis; PCR primer; ss.

XX Homo sapiens.

XX WO200146418-A1.

XX 28-JUN-2001.

XX 14-DEC-2000; 2000WO-US034230.

XX 21-DEC-1999; 99US-00469847.

XX (ZYMO) ZYMOGENETICS INC.

XX Holloway JL, Chandrasekhar VA;

XX WPI; 2001-441677/47.

XX Novel human slit polypeptide, ZSLIT3, useful for treating and diagnosing
PT cystic fibrosis, insulin dependent diabetes and multiple sclerosis.
XX Example 2; Page 123; 125pp; English.

CC PCR primers AAH28472-73 were used to amplify DNA encoding a human slit
CC protein polypeptide, designated Zslit3. Zslit is a neurite growth and
CC development modulator, and an cellular proliferation and differentiation
CC and immune response modulator. Zslit3 polypeptides and polynucleotides
CC are useful for regenerating and directing neurite outgrowth following
CC strokes, brain damage caused by head injuries, paralysis caused by spinal
CC injuries, and for treating neurodegenerative diseases such as amyotrophic
CC lateral sclerosis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease and peripheral neuropathies, or demyelinating diseases e.g.
CC multiple sclerosis. They are useful for lung organogenesis and repair,
CC and thus useful for diagnosing and treating pulmonary diseases such as
CC respiration and circulation, cystic fibrosis and asthma. They also act as
CC a mediator of immunosuppression, and thus are useful for diagnosing and
CC treating autoimmune diseases such as insulin dependent diabetes and

CC rheumatoid arthritis

XX Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2530 ACACGACATGAGCTCCAG 2547
DB 4 ACAGAAAGATGTGCTCCAG 21

RESULT 3120

AAH78643
ID AAH78643 standard; DNA; 21 BP.

XX AAH78643;

XX 10-DEC-2001 (first entry)

DE PCR primer for mechanically sensitive potassium channel gene fragment.

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;
KW polysaturated fatty acid; arachidonic acid; hTRPAK; chromosome 11q13;
KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;
KW hormone secretion; cardiac disease; vascular disease; ischemia;
KW nervous system disorder; endocrinal disease; muscle disease;
KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration;
KW PCR primer; ss.

XX Homo sapiens.

XX WO200168670-A2.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-FR000758.

XX 14-MAR-2000; 2000FR-00003264.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Maingret F;

XX WPI; 2001-590037/66.

XX New mechanically sensitive potassium channel, useful for treating
PT cardiovascular diseases and in drug screening, is activated by
PT polysaturated fatty acids.

XX Disclosure; Page 15; 37pp; French.

CC PCR primers AAH78642-43 were used to amplify a gene fragment of the human
CC mechanically sensitive potassium channel gene. The channel is activated
CC by polysaturated fatty acids (particularly arachidonic acid (AA)) and
CC by riluzole. The polypeptide is designated human TWICK-related (AA-
CC activated potassium channel (hTRPAK). The hTRPAK gene is located on
CC chromosome 11q13. hTRPAK is involved in regulation of neuronal and muscle
CC excitation, cardiac rhythm and secretion of hormones. Cells that express
CC hTRPAK, designated to screen for modulators of hTRPAK activity. Such
CC modulators are potentially useful for prevention or treatment, in humans
CC and animals, of cardiac and/or vascular disease; nervous system
CC disorders associated with ischemia and anoxia; endocrinal diseases
CC associated with anomalous hormone secretion or muscle diseases; and
CC retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and
CC neurodegeneration

XX Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 GCCCGCGCGGATCCCG 129
 ID AAH78640
 DB 4 GCCCGCGCGGATCTTG 21

RESULT 3121

AAH78640
 ID AAH78640 standard; DNA; 21 BP.

AC AAH78640;

DT 10-DEC-2001 (first entry)

XX PCR primer for mechanically sensitive potassium channel gene fragment.

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;
 KW polyunsaturated fatty acid; arachidonic acid; hTRPAK; chromosome 11q13;
 KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;
 KW hormone secretion; cardiac disease; vascular disease; ischemia;
 KW nervous system disorder; endocrinal disease; muscle disease;
 KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration;
 KW PCR primer; ss.

XX Homo sapiens.

OS WO200168670-A2.

XX 20-SEP-2001.

PD 14-MAR-2001; 2001WO-FR000758.

PF 14-MAR-2000; 2000FR-00003264.

PR 14-MAR-2000; 2000FR-00003264.

PA (CNRS) CNRS CENT NAT RECH SCT.

PI Lazdunski M, Lesage F, Maingret F;

XX WPI; 2001-590037/66.

PT New mechanically sensitive potassium channel, useful for treating

XX PT cardiovascular diseases and in drug screening, is activated by

XX PT polyunsaturated fatty acids.

PS Disclosure; Page 15; 37pp; French.

XX PCR primers AAH78639-40 were used to amplify a gene fragment of the human
 CC mechanically sensitive potassium channel gene. The channel is activated
 CC by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and
 CC by riluzole. The polypeptide is designated human TWICK-related A-
 CC activated potassium channel (hTRPAK). The hTRPAK gene is located on
 CC chromosome 11q13. hTRPAK is involved in regulation of neuronal and muscle
 CC excitation, cardiac rhythm and secretion of hormones. Cells that express
 CC hTRPAK, designated to screen for modulators of hTRPAK activity. Such
 CC modulators are potentially useful for prevention or treatment, in humans
 CC and animals, of: cardiac and/or vascular disease; nervous system
 CC disorders associated with ischemia and anoxia; endocrinal diseases
 CC associated with anomalous hormone secretion or muscle diseases; and
 CC retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and
 CC neurodegeneration

XX Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 GCCCGCGCGGATCCCG 129

DB 4 GCCCGCGCGGATCTTG 21

RESULT 3122

AAH62114
 ID AAH62114 standard; DNA; 21 BP.
 AC AAH62114;

DT 12-SEP-2001 (first entry)

XX CACNA2D2 polymorphism containing DNA fragment #15.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 KW heart disease; paternity testing; forensic science; de.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH replace(11,A)
 FT Variation /tag= a
 FT /standard_name= "single nucleotide polymorphism"

XX WO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US031639.

XX 24-NOV-1999; 99US-0167334P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-36705/38.

XX New nucleic acid segments of the human genome, particularly from genes
 PT including polymorphic sites, for phenotype correlation, forensics,
 PT paternity testing, medicine and genetic analysis.

PS Claim 1, Page 29; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 CC diseases, diseases of the cardiovascular system, and infection by
 CC microorganisms. The oligonucleotides are also useful in the manufacture
 CC of a medicament for the treatment or prophylaxis of the diseases, and as
 CC a pharmaceutical. SNP containing oligonucleotides are useful in
 CC applications such as phenotype correlation, forensics, paternity testing,
 CC medicine and genetic analysis

XX Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3582 GCTGCAGAACTGCACCT 3599

DB 1 GCTGCAGAACTGCACAT 18

RESULT 3123

AAH62539
 ID AAH62539 standard; DNA; 21 BP.

AC AAH62539;

DT 12-SEP-2001 (first entry)

XX Arachidonate 12-lipoxygenase polymorphism containing DNA fragment #440.

KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 KW heart disease; paternity testing; forensic science; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation /tag=a
 FT /standard_name="single nucleotide polymorphism"
 XX
 EN WO200138576-A2.
 XX
 PD 31-MAY-2001.
 XX
 PE 17-NOV-2000; 2000WO-US031639.
 XX
 PR 24-NOV-1999; 99US-0167334P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-367705/38.
 XX
 PT New nucleic acid segments of the human genome, particularly from genes
 PT including polymorphic sites, for phenotype correlation, forensics,
 PT paternity testing, medicine and genetic analysis.
 XX
 PS Claim 1; Page 64; 80pp; English.
 XX
 CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 CC diseases, diseases of the cardiovascular system, and infection by
 CC microorganisms. The oligonucleotides are also useful in the manufacture
 CC of a medicament for the treatment or prophylaxis of the diseases, and as
 CC a pharmaceutical. SNP containing oligonucleotides are useful in
 CC applications such as phenotype correlation, forensics, paternity testing,
 CC medicine and genetic analysis
 XX
 SO Sequence 21 BP; 10 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred.No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 6216 AAAAGCTGGGAAAGGAGA 6233
 Db 4 AAAAGCTGGGAAAGGAGA 21
 RESULT 3124
 AAF64065
 ID AAF64065 standard; DNA; 21 BP.
 XX
 AC AAF64065;
 XX
 DT 06-APR-2001 (first entry)
 XX
 DE Primer #9.
 XX
 KW Human; lipoprotein lipase; LPL; stenosis; ss.
 KW
 OS Homo sapiens.
 XX
 EN WO200102606-A2.
 XX
 PD 11-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US018308.

XX
 PR 102-JUL-1999; 99US-00347114.
 XX
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX
 PI Taylor KD, Scheuner M, Rotter J, Yang H;
 XX
 DR WPI; 2001-138155/14.
 XX
 PT Genetic testing for determining non-responsiveness to statin drug in
 PT patients of a coronary artery disease, involves analyzing amplification
 PT products for homozygosity for a variant allele in the human lipoprotein
 PT lipase gene.
 XX
 PS Claim 11; Page 17; 74pp; English.
 XX
 CC The present invention relates to detecting a genetic predisposition in a
 CC human subject for non-responsiveness to statin drug treatment, involving
 CC amplifying nucleic acids including a non-coding or untranslated region
 CC within the 3' end of the human lipoprotein lipase (LPL) gene from a
 CC tissue sample. The method is useful for determining which patients
 CC suffering from coronary artery disease, or which coronary artery bypass
 CC graft (CABG) patients, will likely not respond positively to statin drug
 CC treatment with respect to stenosis of a coronary artery or bypass graft
 XX
 SO Sequence 21 BP; 3 A; 3 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred.No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4280 GCACCTCTTCTTGCAAGT 4297
 Db 4 GCACCTGTTCTTGTAAGT 21
 RESULT 3125
 AAH78090/C
 ID AAH78090 standard; DNA; 21 BP.
 XX
 AC AAH78090;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Primer for breast amplified G protein coupled receptor (BCA-GPCR)-2.
 XX
 KW Breast amplified G protein coupled receptor; BCA-GPCR; breast cancer;
 KW chromosome 1q44; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3; BCA-GPCR-4;
 KW signal transduction; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 EN WO200168704-A2.
 XX
 PD 20-SEP-2001.
 XX
 PR 13-MAR-2001; 2001WO-US008020.
 XX
 PR 14-MAR-2000; 2000US-00524730.
 PR 11-APR-2000; 2000US-00546986.
 XX
 PA (TULA-) TULARIK INC.
 PA (POWER/) POWERS S.
 PA (YANG/) YANG J.
 PA (CUTLER/) CUTLER G.
 XX
 PI Powers S, Yang J, Cutler G;
 XX
 DR WPI; 2001-570865/64.
 XX
 PT Four nucleic acids encoding breast amplified G protein coupled receptors
 PT (BCA-GPCRs) useful for identifying modulators of G-protein coupled
 PT receptor signal transduction which can be used in the treatment of cancer

PT such as breast cancer.
XX
XX Claim 7; Page 54; 68pp; English.
XX
XX PCR primers AAH78089-90 were used to amplify cDNA or DNA encoding breast
CC amplified G protein coupled receptor (BCA-GPCR)-2. BCA-GPCRs are
CC amplified and/or overexpressed in breast cancer cells. The BCA-GPCRs are
CC located at chromosome 1q44, in the following orientation (starting from
CC the centromere end): BCA-GPCR-1 (3'-5' orientation), BCA-GPCR-2 (5'-3'
CC orientation), BCA-GPCR-3 (3'-5' orientation), and BCA-GPCR-4 (5'-3'
CC orientation). The G protein coupled receptors are useful for assaying and
CC identifying modulators of G-protein coupled receptor signal transduction.
CC The modulators and antibodies against the G protein coupled receptors are
CC useful for pharmacological modulation of signalling pathways, e.g. in
CC cancer cells such as breast cancer
XX
XX
SQ Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3894 CTGAGTTACTTTCATAG 3911
DB 18 CTGAGTTACTTCTTAG 1
RESULT 3126
AAH89072
ID AAH89072 standard; DNA; 21 BP.
XX
XX AAH89072;
DT 27-FEB-2002 (first entry)
XX
XX Human polymorphic oligonucleotide L21952 fragment.
DE
XX Human, single nucleotide polymorphic; SNP; forensic science;
KM paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation /*tag= a
FT /standard_name= "single nucleotide polymorphism"
PN WO200134840-A2.
XX
XX 17-MAY-2001.
PD
XX 10-NOV-2000; 2000MO-US030766.
PF
XX 10-NOV-1999; 99US-0164596P.
PR
XX (GLAXO) GLAXO GROUP LTD.
PA (AFY-) AFFYMETRIX INC.
XX
XX Au K, Chen J, Patil N, Thomas D;
PI
XX WPI; 2001-335945/35.
DR
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.
XX
XX Claim 82; Page 13; 43pp; English.
XX
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with

CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX
XX
SQ Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7408 AACATAGCAGCAGCAGC 7425
DB 2 AACATAGCAGCAGCAGC 19
RESULT 3127
AAF89455
ID AAF89455 standard; DNA; 21 BP.
XX
XX AAF89455;
AC
XX 14-AUG-2001 (first entry)
DT
DE Human genetic marker PCR primer SEQ ID NO: 44.
XX
XX Genetic marker; genetic disease diagnosis; cystic fibrosis; haemophilia;
KM sickle cell disease; muscular dystrophy; Huntington's disease;
KW retinoblastoma; PCR primer; ss.
XX
XX
XX Homo sapiens.
OS
XX WO200134839-A1.
PN
XX 17-MAY-2001.
PD
XX 03-NOV-2000; 2000MO-US030493.
PF
XX 12-NOV-1999; 99US-0165301P.
PR
XX (DUNL/) DUNLOP C L M.
PA (WEIS/) WEISEL J M.
XX
XX Dunlop CLM, Weisel JM;
PI
XX WPI; 2001-329096/34.
DR
XX
XX
PT Detecting multiple genetic markers in one assay, useful to simultaneously
PT detect a number of genetic disorders, comprises generating extension
PT products and separating them on the basis of melting behavior is.
XX
XX Claim 44; Page 36; 40pp; English.
XX
XX The present invention describes a method of identifying the presence of a
CC plurality of genetic markers in a subject, involving generating extension
CC products using PCR primers flanking the plurality of markers, separating
CC the extension products depending on their melting temperatures, and
CC analysing them to determine the presence or absence of each genetic
CC marker. This can be used in the diagnosis of genetic diseases, including
CC familial hypercholesterolaemia, cystic fibrosis, Tay-Sachs, thalassemia,
CC sickle cell disease, phenylketonuria, galactosaemia, fragile X syndrome,
CC haemophilia A, myotonic dystrophy, medium chain acyl-CoA dehydrogenase,
CC maturity onset diabetes, cystinuria, methylmalonic acidemia, urea cycle
CC disorders, hereditary fructose intolerance, hereditary haemochromatosis,
CC neonatal thrombocytopenia, Gaucher's disease, tyrosinaemia, Wilson's
CC disease, acropnuria, hypolactasia, Baker's disease, argininaemia,
CC adenomatous polyposis coli, hereditary nonpolyposis colorectal cancer,
CC Huntington's disease, adult polycystic kidney disease, alpha-1-
CC antitrypsin deficiency, Duchenne muscular dystrophy, Marfan's syndrome,
CC neurofibromatosis, osteogenesis imperfecta, retinoblastoma, Friedreich's
CC ataxia, haemoglobinopathies, Leber's hereditary optic neuropathy, MCAD,
CC Canavan's disease, retinitis pigmentosa, Bloom syndrome, Fanconi anaemia
CC or Neuman Pick disease. The present sequence is one of the PCR primers
XX of the invention

SQ Sequence 21 BP; 5 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 597 CTCGATCAAGTGCTAGC 614

Db 4 CTCGATCAAGTGCTAGC 21

RESULT 3128

AAS12385/C

ID AAS12385 standard; RNA; 21 BP.

AC AAS12385;

XX 21-NOV-2001 (first entry)

DE Class VII ribozyme, substrate domain.

KM Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;

KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.

OS Synthetic.

PN WO200159102-A2.

XX 16-AUG-2001.

PF 08-FEB-2001; 2001WO-US004223.

XX 08-FEB-2000; 2000US-0181360P.

PR 31-MAR-2000; 2000US-0193646P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (UYVA) UNIV YALE.

XX Breaker R, Beigelman L, Emlisson G;

DR WPI; 2001-536526/59.

PT New nucleic acids with endonuclease activity, such as ribozymes and

PT nucleozymes, for modulating gene expression in a plant, mammalian,

PT bacterial or fungal cell.

PS Example 1; Fig 9; 96pp; English.

XX The invention relates to nucleic acid molecules with endonuclease

CC activity, which are particularly useful for cleavage of RNA or DNA. The

CC nucleic acids are used in a pharmaceutical composition and are used to

CC modulate expression of a gene in a plant, mammalian, bacterial or fungal

CC cell. They are used to cleave a separate nucleic acid, preferably RNA.

CC The nucleic acids are used to inhibit gene expression and/or cell

CC proliferation, and can be used to treat a disease or condition. More than

CC one nucleic acid can be independently targeted to the same or different

CC sites in a cell. The nucleic acids may be used to study DNA. The

CC modifications to the nucleic acids optimises their catalytic activity and

CC can maintain or enhance their activity. They exhibit a high degree of

CC specificity for RNA. The present sequence represents the Class VII

CC ribozyme, substrate domain, used in an example which demonstrates the

CC method of the invention

XX Sequence 21 BP; 4 A; 6 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4911 TGGAGAAAGCATCAGAC 4928

Db 18 TGGAGTAACATCAGAC 1

RESULT 3129

AAS12374/C

ID AAS12374 standard; RNA; 21 BP.

AC AAS12374;

XX 21-NOV-2001 (first entry)

DE Class I-XII ribozyme substrate.

KM Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;

KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.

OS Synthetic.

PN Key

XX misc_binding

FT 1. .8

FT /note= "Forms double-stranded region with bases 46 to 39

FT of AAS12375"

FT 1. .8

FT /note= "Forms double-stranded region with bases 20 to 28

FT of AAS12383"

FT 1. .8

FT /note= "Forms double-stranded region with bases 30 to 23

FT of AAS12394"

FT 1. .5

FT /note= "Forms double-stranded region with bases 42 to 38

FT of AAS12377"

FT 1. .5

FT /note= "Forms double-stranded region with bases 43 to 39

FT of AAS12379"

FT 1. .5

FT /note= "Forms double-stranded region with bases 29 to 25

FT of AAS12381"

FT 1. .5

FT /note= "Forms double-stranded region with bases 49 to 45

FT of AAS12388"

FT 1. .4

FT /note= "Forms double-stranded region with bases 49 to 46

FT of AAS12392"

FT 1. .4

FT /note= "Forms double-stranded region with bases 35 to 32

FT of AAS12396"

FT 8. .15

FT /note= "Forms double-stranded region with bases 8 to 1 of

FT AAS12377"

FT 8. .15

FT /note= "Forms double-stranded region with bases 8 to 1 of

FT AAS12379"

FT 8. .15

FT /note= "Forms double-stranded region with bases 8 to 1 of

FT AAS12381"

FT 8. .13

FT /note= "Forms double-stranded region with bases 14 to 9

FT of AAS12388"

FT 8. .12

FT /note= "Forms double-stranded region with bases 36 to 32

FT of AAS12390"


```

AAD29834/C
ID   AAD29834 standard; DNA; 21 BP.
XX
XX   AAD29834;
AC
XX
XX   17-MAY-2002 (first entry)
DT
XX
DE   Arabidopsis NADPH dependent trx reductase gene amplifying primer, STR2B.
XX
XX   Transgenic plant; thioredoxin reductase; starch; protein; grain;
KM   milling process; enzyme; PCR primer; ss.
XX
XX   Arabidopsis sp.
OS
XX   WO200198509-A2.
PN
XX
XX   27-DEC-2001.
PD
XX
XX   19-JUN-2001; 2001WO-EP006918.
PF
XX   21-JUN-2000; 2000US-0058747.
PR
XX
XX   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX   lanahan MB, Desai NM, Gasdaaka PY;
PI
XX
XX   WPI; 2002-179557/23.
DR
XX
PT   Transgenic plant coding for eukaryotic thioredoxin reductase at elevated
PT   levels useful for separating the starch and protein components of grain
PT   in a milling process.
XX
XX   Example 4; Page 52; 86pp; English.
XX
XX   The present invention relates to a transgenic plant comprising
CC   heterologous DNA coding for eukaryotic thioredoxin reductase integrated
CC   into its nuclear or plastid genome and use of thioredoxin reductase for
CC   separating the starch and protein components of grain in a milling
CC   process. Transgenic plant is used for separating the starch and protein
CC   components of grain in a milling process. Transgenic plant may be used to
CC   produce thioredoxin reductase at elevated levels. Delivery of thioredoxin
CC   reductase eliminates the need to develop exogenous sources for addition
CC   during processing. Secondly, physical disruption of seed integrity is not
CC   necessary to bring the enzyme in contact with the storage or matrix
CC   proteins of the seed prior to processing or as an extra processing step.
CC   The present sequence is Arabidopsis NADPH dependent trx reductase gene
CC   (NTR) amplifying PCR primer
XX
XX   Sequence 21 BP; 3 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
SQ
XX
XX   Query Match          0.2%; Score 14.8; DB 1; Length 21;
XX   Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX   Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY   351 CATCCCTAAGATCGACGT 368
DB   19 CAACCCGAGATCGACGT 2

```

```

XX
XX   JP2002017187-A.
XX
XX   22-JAN-2002.
XX
XX   07-JUL-2000; 2000JP-00207230.
XX
XX   07-JUL-2000; 2000JP-00207230.
XX
XX   07-JUL-2000; 2000JP-00207230.
XX
XX   (NICH-) JAPAN CHEM RES CO LTD.
XX
XX   WPI; 2002-263239/31.
DR
XX
XX   Plant with incorporated human interferon gene.
XX
XX   Example; Page 4; 22pp; Japanese.
XX
XX   The present invention describes a true grass plant in which a base
CC   sequence encoding a human interferon protein, with a base sequence
CC   encoding a signal amino acid sequence causing accumulation of the stored
CC   protein of albumen to the protein body connected upstream, is recombined
CC   expressably to a genomic DNA. The grass plant can be used for the
CC   creation of a useful application of tea. The present sequence represents
CC   a PCR primer which is used in an example from the present invention
XX
XX   Sequence 21 BP; 5 A; 2 C; 8 G; 6 T; 0 U; 0 Other;
SQ
XX
XX   Query Match          0.2%; Score 14.8; DB 1; Length 21;
XX   Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX   Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY   6317 GGCTACTGTTGCTGGGAA 6334
DB   4 GGCTAATGTTGTCGGGAA 21

```

```

RESULT 3132
ABL49744
ID   ABL49744 standard; DNA; 21 BP.
XX
XX   ABL49744;
AC
XX
XX   29-MAY-2002 (first entry)
DT
XX
XX   Rice PCR primer SEQ ID NO:6.
DE
XX
XX   Human; interferon alpha; interferon omega; prolamin; fusion protein;
KM   plant; grass plant; tea; PCR primer; ss.
XX
XX   Oryza sativa.
OS

```

```

RESULT 3133
ABK70370
ID   ABK70370 standard; DNA; 21 BP.
XX
XX   ABK70370;
AC
XX
XX   15-JUL-2002 (first entry)
DT
XX
XX   Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #58.
DE
XX
XX   Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KM   insulin-like growth factor binding protein-2; hormone-regulated tumour;
KM   breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KM   hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;
KM   ODN; endocrine tumour therapy; ss.
XX
XX   Synthetic.
OS
XX
XX   WO200222642-A1.
PN
XX
XX   21-MAR-2002.
PD
XX
XX   13-SEP-2001; 2001WO-US028748.
PF
XX
XX   14-SEP-2000; 2000US-0232641P.
PR
XX
XX   (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX
XX   Gleave M, Satoshi K, Nelson C, Rennie PS;
PI
XX
XX   WPI; 2002-339861/37.
DR
XX
XX   Composition for treating hormone-regulated cancer, particularly of
PT   prostate or breast, comprises oligonucleotide antisense to insulin-like
PT   growth factor binding protein-2.
XX
XX   Example 1; Page 13; 36pp; English.
PS

```

XX The present invention relates to a new composition for treating hormone-
CC regulated cancer. The composition comprises an antihense oligonucleotide
CC that inhibits expression of IGFBP-2 (Insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antihense
CC IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy
XX

SO Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7415 GCACGACGACGACGACGCA 7432
DB 4 GCACTAGCAGCAGCAGCA 21

RESULT 3134
ID ABS52265 standard; DNA; 21 BP.
XX
AC ABS52265;
XX
DT 05-NOV-2002 (first entry)
XX
DE Plant vector PCR primer #29.
XX
XX Plant; PCR; primer; ss; plastome; plastid genome; antibiotic;
KM herbicide resistance gene.
XX
OS Synthetic.
XX
PN WO200257466-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-EP000481.
XX
PR 19-JAN-2001; 2001DE-01002389.
XX
PA (ICON-) ICON GENETICS AG.
XX
PI Ehl J C, Huang F, Klaus S, Muehlbauer S, Herz S, Koop H;
XX WPI; 2002-590747/63.
XX
DR Transforming multicellular plants, by altering the function of a plastid
XX gene, selecting plants expressing altered phenotype, transforming plants
XX with a vector capable of restoring function and separating transformed
XX plants.
XX
PS Example 6; Page 38; 56pp; English.
XX
XX The invention relates to producing multicellular plants, organs or
CC tissues transformed on their plastome, comprising altering/disrupting the
CC function of a gene in a plastid genome for producing a selectable
CC phenotype and selecting plants with plastids expressing the phenotype,
CC transforming the plastid genomes of selected plants with a transformation
CC vector with a restoring sequence for restoring function and separating
CC transformed plants. This method is useful for producing multicellular
CC plants, organs or tissues transformed on their plastome and for selection
CC of antibiotics and herbicide resistance genes. Sequences ABS52237-
CC ABS52269 represent PCR primers used to amplify plant vector genes of the
CC invention
XX
XX Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5072 AAAGAGGTGATGCTTAC 5089
DB 4 AAAGAGAGGATCTTAC 21

RESULT 3135
ID ABS51698 standard; DNA; 21 BP.
XX
AC ABS51698;
XX
DT 05-NOV-2002 (first entry)
XX
XX Human LDLB-like protein forward PCR primer #1.
XX
DE Human LDLB-like protein forward PCR primer #1.
XX
XX Human; NOVA; pathological condition; NOVA-associated disorder;
KM Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
KM pancreatitis; obesity; diabetes; autoimmune disease; infertility;
KM renal artery stenosis; interstitial nephritis; glomerulonephritis;
KM polycystic kidney disease; cataract; Alzheimer's disease; cancer;
KM acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
KM congenital heart defect; scleroderma; endometriosis; haemophilia;
KM dementia stroke; Parkinson's disease; Huntington's disease; epilepsy;
KM multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
KM acne; wound; asthma; human disease; calpain; epain; zinc finger;
KM low density lipoprotein B; LDLB; purinoceptor; CG841; synaptotagmin;
KM serine protease TSP; mitogen activated protein kinase kinase-2;
KM glypican-2 precursor; thymosin beta-10; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200255702-A2.
XX
PD 18-JUL-2002.
XX
XX 26-OCT-2001; 2001WO-US050925.
XX
PF 26-OCT-2000; 2000US-0243320P.
XX
PR 26-OCT-2000; 2000US-0243592P.
XX
PR 26-OCT-2000; 2000US-0243642P.
XX
PR 27-OCT-2000; 2000US-0243681P.
XX
PR 27-OCT-2000; 2000US-0243683P.
XX
PR 31-OCT-2000; 2000US-024443P.
XX
PR 01-NOV-2000; 2000US-0244959P.
XX
PR 01-NOV-2000; 2000US-0245029P.
XX
PR 02-NOV-2000; 2000US-0245293P.
XX
PR 02-NOV-2000; 2000US-0245315P.
XX
PR 02-NOV-2000; 2000US-0245316P.
XX
PR 19-JAN-2001; 2001US-0262994P.
XX
PR 15-FEB-2001; 2001US-0269056P.
XX
PR 02-MAR-2001; 2001US-0272923P.
XX
PR 15-MAR-2001; 2001US-0276565P.
XX
PR 07-SEP-2001; 2001US-0318119P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Gangoli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L,
XX Vannet CM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S,
XX Malyavkar U, Stone D, Miller I, Smithson G, Gunther E, Padigaru M,
XX Traupier RJ, Anderson D;
XX WPI; 2002-590673/63.
XX
XX Isolated NOVA polypeptides and nucleic acid molecules useful for
XX treating, preventing, diagnosing and researching pathological conditions
XX in humans with a NOVA-associated disorders, e.g. cancer, stroke or
XX Alzheimer's disease.
XX

PS Example 3; Page 170; 236pp; English.

XX The present invention relates to a new polypeptide that comprises any of
 CC 17 fully defined sequences of 43-990 amino acids given in the
 CC specification. The NOVX polypeptide, nucleic acid and antibody of the
 CC invention are useful for treating or preventing a pathological condition
 CC in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau
 CC syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,
 CC diabetes, autoimmune disease, renal artery stenosis, interstitial
 CC nephritis, glomerulonephritis, polycystic kidney disease, cataract,
 CC Alzheimer's disease, acoustic trauma, cancer, infertility,
 CC cardiomyopathies, atherosclerosis, hypertension, congenital heart
 CC defects, scleroderma, endometriosis, haemophilia, dementia, stroke,
 CC Parkinson's disease, Huntington's disease, epilepsy, multiple sclerosis,
 CC anxiety, pain, leukemias, hypothyroidism, psoriasis, acne, wounds and
 CC asthma. They are also useful for the manufacture of a medicament for
 CC treating a syndrome associated with a human disease, specifically a NOVX-
 CC associated disorder. They may also be useful in therapeutic applications
 CC including protein therapy, as small molecule drug targets, as antibody
 CC targets, as diagnostic and/or prognostic markers, in gene therapy, as
 CC research tools and in tissue regeneration. The present nucleic acid
 CC sequence represents a PCR primer that was used in the methods of the
 CC invention to amplify one of the 17 novel proteins of the invention

SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3683 GCCAGAAAGCCAGCTATT 3700
 DB 1 GCCAGAAAGCCACTATT 18

RESULT 3136
 ABL57072
 ID ABL57072 standard; DNA; 21 BP.

XX ABL57072;
 AC
 XX 05-NOV-2002 (first entry)
 DT
 XX Human proteolipid, PLP, protein RT-PCR primer #1.
 DE
 XX Human; ss; Ulp; CRMP; collagen response mediator protein; PCR;
 KW Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;
 KW paraneoplastic neurodegenerative disease; PND; myelination;
 KW demyelination; remyelination; myelin disorder; multiple sclerosis;
 KW autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;
 KW human T lymphocyte virus 1; reverse transcriptase PCR; primer;
 KW proteolipid protein; PLP.
 KM
 XX Homo sapiens.
 OS
 XX
 PN US2002119944-A1.
 XX
 XX 29-AUG-2002.
 PD
 XX 09-NOV-2001; 2001US-00986632.
 PF
 XX 09-NOV-2000; 2000US-0246751P.
 PR
 XX (AGUE//) AGUERA M.
 PA (BELI//) BELIN M.
 PA (CHAR//) CHARRIER B.
 PA (HONO//) HONORAT J.
 PA (RICA//) RICARD D.
 PA (ROGE//) ROGEMOND V.
 XX
 XX Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;
 PI WPI; 2002-627172/67.
 XX

XX Prevention or treatment of myelin disorders, such as multiple sclerosis,
 PT by administering an agent selected from a Ulp/CRMP protein, a nucleic
 PT acid coding for the protein, or an antibody directed against protein.
 FT
 PS Example; Page 8; 44pp; English.

XX The invention relates to a new method for prevention or treatment of
 CC myelin disorders, comprises administering to a patient an effective
 CC amount of an agent selected from a Ulp (Unc-33-like protein/CRMP
 CC (collapsin response mediator protein) protein, a nucleic acid coding for
 CC Ulp/CRMP, an antisense sequence capable of specifically hybridising with
 CC the nucleic acid, an antibody directed against Ulp/CRMP, or an aptamer
 CC capable of binding Ulp/CRMP, and a pharmacologically acceptable carrier.
 CC Also included are methods of diagnosing a myelin disorder in a subject,
 CC identifying agents useful for the prevention or treatment of myelin
 CC disorders, using the Ulp/CRMP proteins/nucleic acids, agents capable of
 CC modulating the function or expression of the proteins (increasing or
 CC decreasing), and a method for identifying an endogenous agent as a
 CC therapeutic target for the prevention or the treatment of myelin
 CC disorders. The agents are useful for preventing or creating a myelin
 CC disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus
 CC 1) associated myelopathy and neurodegenerative diseases, Alzheimer's
 CC disease, paraneoplastic neurodegenerative diseases (PND), autoimmune
 CC neurodegenerative disorder. Ulp/CRMP proteins are involved in
 CC the processes of myelination, demyelination and remyelination. Antibodies
 CC to a Ulp/CRMP protein are useful for diagnosing a myelin disorder. The
 CC present sequence is a reverse transcriptase (RT)-PCR primer for
 CC proteolipid protein (PLP), an oligodeoxynucleotide marker protein used as a
 CC control in an experiment to detect mRNA encoding Ulp proteins

SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 692 TGCATGCGCCATGAGGC 709
 DB 4 TGCATGTGACATGAGGC 21

RESULT 3137
 ABL57072/C
 ID ABL57072 standard; DNA; 21 BP.

XX ABL57072;
 AC
 XX 22-JUL-2002 (first entry)
 DT
 XX Molecular beacon target sequence (single mismatch).
 DE
 XX Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
 KW
 XX Synthetic.
 OS
 XX
 PN Key Location/Qualifiers
 FH misc_feature 9 /*tag= a
 FT misc /note= "mismatch site"
 FT
 XX W0200218951-A2.
 PN
 XX 07-MAR-2002.
 PD
 XX 29-AUG-2001; 2001WO-US041941.
 PF
 XX 29-AUG-2000; 2000US-0228728P.
 PR 30-MAR-2001; 2001US-0280350P.
 PA (VVRQ) UNIV ROCKEFELLER.
 PA
 XX Dubertret B, Calame M, Libhaber A;
 PI

```
XX WPI; 2002-404569/43.
DR
XX
XX Sensitive detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.
XX
XX Example 3; Page 62; 62pp; English.
XX
CC The present sequence is that of a single mismatch target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridized termin. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Experiments with the present
CC sequence and a perfectly-matched target (see ABL57071) showed that
CC hybridisation was very specific to the matched target. The invention
CC relates generally to the use of metal surface quenchers such as particles
CC or films for high sensitivity applications in, for example, detection and
CC diagnostic systems
XX
SQ Sequence 21 BP; 14 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4461 GACCTTTTCTTTTCTT 4478
DB 19 GAGCTTTTGTGTTTTT 2
XX
RESULT 3138
AAD22716/c
ID AAD22716 standard; DNA; 21 BP.
XX
AC AAD22716;
XX
DT 26-FEB-2002 (first entry)
XX
DE Fluorescent-oligonucleotide Flu. 4 used for hybridisation.
XX
KM Oligonucleotide array; hydrophobic attachment layer; diagnosis;
KM cholesterol; genetic analysis; DNA chip; hybridisation; ss.
XX
OS Undifferentiated.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Fluorescein labelled guanosine"
XX
XX WO200179544-A1.
XX
XX 25-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-KR000514.
XX
XX 14-APR-2000; 2000KR-00019557.
XX
XX (GENO-) GENOTECH CORP.
XX
XX Kim J, Cha S;
XX
XX WPI; 2002-026037/03.
XX
XX Attaching oligonucleotide on support by fluidizing hydrophobic attachment
PT
```

```
PT layer applied on support, spotting oligonucleotide solution having one of
PT its ends bonded to hydrophobic group on layer and solidifying layer.
XX
XX Example 1; Page 12; 32pp; English.
XX
XX The invention relates to a method for attaching oligonucleotide to a
XX solid support and an oligonucleotide array. The oligonucleotide array is
XX prepared by applying hydrophobic attachment layer onto a support which
XX can be solidified under certain conditions, spotting certain portions of
XX said attachment layer with aqueous oligonucleotide solution in which
XX hydrophobic groups are bonded to 3' or 5' terminals and solidifying said
XX attachment layer. The method is useful for attaching a oligonucleotide
XX (preferably a PCR amplified product from a PCR with its 5' terminal
XX bonded to a hydrophobic group) onto support. The method is useful in the
XX area of genetic diagnosis and analysis, and DNA chips which are based on
XX hybridisation. The present sequence is fluorescent oligonucleotide useful
XX in hybridisation
XX
SQ Sequence 21 BP; 11 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2904 TGCTTGTTCCTTCCTAT 2921
DB 20 TGACTTCCTTCCTTCAT 3
XX
RESULT 3139
ABS98296/c
ID ABS98296 standard; DNA; 21 BP.
XX
AC ABS98296;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human lactoferrin (LTF) gene polymorphic sequence #59.
XX
XX Human: db; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF;
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR117;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX multiting resistance associated protein 3; cancer; prostate;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200257410-A2.
XX
XX 25-JUL-2002.
XX
XX 28-NOV-2001; 2001WO-US044838.
XX
XX 28-NOV-2000; 2000US-00724389.
XX
XX (DNAS-) DNA SCI LAB INC.
XX
XX Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
```

PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.

XX Example 23; Page 149; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxidoreductase (SOD), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
 CC (MDR1), lactocortisterin (LRF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,
 CC ARNT, EPHX2, GST12, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KIK2 for altered serine
 CC protease activity in the prostate, in LRF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention

XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03; Mismatches 2; Indels 0; Gaps 0;

6049 GTTCTCTCATTCGCTTT 6066

20 GTATCTCATTCGCTTT 3

RESULT 3140

ID ABL51321 standard; DNA; 21 BP.

ABL51321;

27-JUN-2002 (first entry)

Bacteriophage lambda related LAMP primer SEQ ID NO:55.

Bacteriophage lambda: loop mediated isothermal amplification; LAMP;

polynucleotide synthesis; single nucleotide polymorphism; SNP;

Identification; primer; ss.

Bacteriophage lambda.
 Synthetic.

PN WO200224902-A1.

XX 28-MAR-2002.

19-SEP-2001; 2001WO-JP008142.

19-SEP-2000; 2000JP-00283862.

(BIKE) EIKEN KAGAKU KK.

WP1; 2002-315737/35.

PT Rapid isothermal polynucleotide synthesis using loop-mediated
 PT amplification for simple detection of single nucleotide polymorphisms.

XX Example 4; Page 68; 135pp; Japanese.

XX The present invention describes a method for polynucleotide synthesis by
 CC loop-mediated isothermal amplification (LAMP). The method comprises: (a)
 CC identifying a target sequence on the template and a set of primers (inner
 CC and outer primer) hybridised to it and annealed to form a single-stranded
 CC polynucleotide with a loop at each end, followed by self-primed strand
 CC displacement complementary chain synthesis to form a two-stranded
 CC polynucleotide having a loop at one end and containing two copies of the
 CC template; (b) using a second (loop) primer set to initiate complementary
 CC chain synthesis at a different position; (c) repeating the process; and
 CC (d) carrying out DNA polymerase catalysed complementary chain synthesis.
 CC The method is simple and efficient for polynucleotide amplification,
 CC allowing easy identification of the presence of single nucleotide
 CC polymorphisms (SNP). The method is isothermal, produces a high degree of
 CC amplification in a short time, and since it uses primers hybridising to
 CC several different sequences on the template it is highly accurate,
 CC without the amplification of irrelevant sequences which is a problem in
 CC conventional methods. The present sequence represents a primer which is
 CC used in an example from the present invention

XX Sequence 21 BP; 4 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03; Mismatches 2; Indels 0; Gaps 0;

4368 ACAAGCTGGGGAATTTTG 4385

2 ACAAGCTGGGCAATTTTG 19

RESULT 3141

ID ABQ94035 standard; DNA; 21 BP.

ABQ94035;

21-OCT-2002 (first entry)

NOV15 forward PCR primer #2.

Human; NOV; cytostatic; Cardiac; Antiinflammatory; Immunosuppressive;

Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;

Anticancer; Nephrotoxic; Hepatotoxic; Neuroprotective; Nootropic;

Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;

Gene Therapy; NOV; Cancer; heart disease; Inflammation;

autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity;

asthma; IGA nephropathy; cirrhosis; arthritis; Alzheimer's disease;

infection; stroke; muscular dystrophy; epilepsy; wasting disorder; PCR;
 primer; ss.
 Homo sapiens.
 WO200255704-A2.

PD 18-JUL-2002.
 XX
 PF 09-JAN-2002; 2002WO-US000554.
 XX
 PR 09-JAN-2001; 2001US-0260417P.
 PR 10-JAN-2001; 2001US-0260831P.
 PR 28-FEB-2001; 2001US-0272338P.
 PR 09-MAR-2001; 2001US-0274876P.
 PR 18-APR-2001; 2001US-0284704P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangoli EA, Burgess CE, Patturajan M, Vernet CM, Taylor S, Tcherny V, Miller CE, Guo X, Boldog FL, Grose WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K, MacDougall J, Malyanar U, Millet I, Peyman J, Smlthson G, Gunther E, Stone DJ;
 PI WPI; 2002-590674/63.
 XX
 DR NOVX polypeptides and encoding polynucleotides, useful for preventing or
 XX PT treating NOVX-associated disorders e.g. cancer, inflammation, or
 PT Alzheimer's disease, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Example 3; Page 316; 358pp; English.
 XX
 CC The present invention relates to coding sequences for NOV proteins
 CC (ABN85378-ABN85403 and ABN85401-ABN85424). The NOV proteins and coding
 CC sequences are useful for treating or preventing NOV-associated disorders
 CC or in the manufacture of a medicament for treating the disorders, such as
 CC cancer, heart disease, inflammation, autoimmune disorders, allergies,
 CC blood disorders, AIDS, diabetes, obesity, asthma, Iga nephropathy,
 CC cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial,
 CC viral, parasitic), stroke, muscular dystrophy, epilepsy, and other
 CC wasting disorders associated with chronic diseases. The present sequence
 CC is a PCR primer for a NOV coding sequence, which was used in an example
 CC from the invention
 CC
 XX
 SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3683 GCCAGAAAGCCAGCTATT 3700
 DB 1 GCCAGAAAGCCAGCTATT 18
 RESULT 3142
 ABX96561
 ID ABX96561 standard; DNA; 21 BP.
 XX
 AC ABX96561;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Human genomic DNA mthfr SNP primer #5.
 XX
 KW Human; allele-specific base detection; primer extension reaction;
 KW base-specific detection primer; allele-specific primer extension assay;
 KW AS; high throughput; single nucleotide polymorphism; SNP analysis;
 KW mutation detection; genetic variation; allele-specific extension; primer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200268684-A2.
 XX
 PD 06-SEP-2002.
 XX

PF 22-FEB-2002; 2002WO-GB000794.
 XX
 PR 23-FEB-2001; 2001GB-00004560.
 PR 23-FEB-2001; 2001US-00791190.
 PR 07-FEB-2002; 2002US-00071926.
 XX
 PA (PYRO-) PYROSEQUENCING AB.
 PA (DZIE/) DZIEGLEWSKA H.
 XX
 PI Lundberg J, Ahmadian A, Nyren P,
 PI WPI; 2002-707012/76.
 XX
 DR
 XX
 PT Detecting a base at a pre-determined position in a nucleic acid molecule,
 PT comprising performing primer extension reactions using base-specific
 PT detection primers in the presence of a nucleotide-degrading enzyme.
 XX
 PS Example 1; Page 26; 59pp; English.
 XX
 CC The present invention relates to a method for detecting a base at a pre-
 CC determined position in a nucleic acid molecule. The method comprises
 CC performing primer extension reactions using base-specific detection
 CC primers, each being specific for a particular base at the predetermined
 CC position. The allele-specific (AS) primer extension assay method of the
 CC invention is useful for detecting an allele-specific base at a pre-
 CC determined position in a nucleic acid molecule, for high throughput
 CC single nucleotide polymorphism (SNP) analysis, and for detecting
 CC mutations and genetic variations. The new method solves the deficiencies
 CC of previous methods by providing a method of allele-specific extension
 CC that allows accurate discrimination between matched and mismatched
 CC configurations, as well as reducing or eliminating false positive results
 CC observed in prior art. The use of two allele-specific primers increases
 CC the sensitivity by a factor of two because signals of two extensions are
 CC obtained. The present sequence represents a primer used in the examples
 CC of the present invention
 CC
 XX
 SQ Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5816 CTATGTGATGATGAATC 5833
 DB 2 CTGCGTGTGATGATGAATC 19
 RESULT 3143
 ABX96562
 ID ABX96562 standard; DNA; 21 BP.
 XX
 AC ABX96562;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Human genomic DNA mthfr SNP primer #6.
 XX
 KW Human; allele-specific base detection; primer extension reaction;
 KW base-specific detection primer; allele-specific primer extension assay;
 KW AS; high throughput; single nucleotide polymorphism; SNP analysis;
 KW mutation detection; genetic variation; allele-specific extension; primer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200268684-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-GB000794.
 XX
 PR 23-FEB-2001; 2001GB-00004560.
 PR 23-FEB-2001; 2001US-00791190.

PR 07-FEB-2002; 2002US-00071926.
XX (PYRO-) PYROSEQUENCING AB.
PA (DZIE//) DZIELEWSKA H.
XX
XX Lundeborg J, Ahmadian A, Nyren P;
XX WPI; 2002-707012/76.
DR
XX Detecting a base at a pre-determined position in a nucleic acid molecule,
PT comprises performing primer extension reactions using base-specific
PT detection primers in the presence of a nucleotide-degrading enzyme.
XX
XX Example 1; Page 26; 59pp; English.
XX
XX The present invention relates to a method for detecting a base at a pre-
CC determined position in a nucleic acid molecule. The method comprises
CC performing primer extension reactions using base-specific detection
CC primers, each being specific for a particular base at the predetermined
CC position. The allele-specific (AS) primer extension assay method of the
CC invention is useful for detecting an allele-specific base at a pre-
CC determined position in a nucleic acid molecule, for high throughput
CC single nucleotide polymorphism (SNP) analysis, and for detecting
CC mutations and genetic variations. The new method solves the deficiencies
CC of previous methods by providing a method of allele-specific extension
CC that allows accurate discrimination between matched and mismatched
CC configurations, as well as reducing or eliminating false positive results
CC observed in prior art. The use of two allele-specific primers increases
CC the sensitivity by a factor of two because signals of two extensions are
CC obtained. The present sequence represents a primer used in the examples
CC of the present invention
XX
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5816 CTATGTGATGATGAATC 5833
DB 2 CTGCGTGTGATGAATC 19
RESULT 3144
AADS0224
ID AADS0224 standard; DNA; 21 BP.
XX
AC AADS0224;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human GALT 8 specific PCR primer #2.
XX
XX Human; cystic fibrosis; Tay-sachs; familial hypercholesterolaemia; FH;
KM fragile X syndrome; haemophilia A; diabetes; cystinuria; tyrosinaemia;
KM urea cycle disorder; hereditary fructose intolerance; Baker's disease;
KM Wilson's disease; alcaptonuria; adult polycystic kidney disease; MCAD;
KM Huntington's disease; myotonic dystrophy; retinitis pigmentosa; cancer;
KM Gaucher's disease; Canavan's disease; galactosaemia; thrombocytopaenia;
KM thalassaemia; sickle cell disease; phenylketonuria; Marfan's syndrome;
KM haemoglobinopathy; Bloom syndrome; Neimann Pick's disease; PCR; primer;
KM galactose-1-phosphate uridylyl transferase; GALT; ss.
XX
OS Homo sapiens.
XX
PN WO200290374-A1.
XX
PD 14-NOV-2002.
XX
XX 06-MAY-2002; 2002WO-US014562.
XX
XX 08-MAY-2001; 2001US-00851501.
XX

PA (AMBR-) AMERY GENETICS CORP.
XX
XX Dunlop CLM, Weisel JM;
XX
XX WPI; 2003-103498/09.
DR
XX
XX Identifying the presence or absence of a mutation or polymorphism in a
PT subject, useful for diagnosing genetic diseases, comprises generating
PT extension products and analyzing the melting behavior of the mixed DNA
PT sample.
XX
XX Claim 56; Page 45; 49pp; English.
XX
XX The invention relates to a method for identifying the presence or absence
CC of a mutation or polymorphism in a plurality of genes. The method is used
CC for identifying the presence or absence of a mutation or polymorphism in
CC a subject, or the presence or absence of several genetic markers in a
CC subject for diagnosing genetic diseases, e.g. cystic fibrosis, Tay-sachs,
CC familial hypercholesterolaemia (FH), thalassaemia, sickle cell disease,
CC phenylketonuria, galactosaemia, fragile X syndrome, haemophilia A,
CC myotonic dystrophy, medium-chain acyl CoA dehydrogenase, maturity onset
CC diabetes, cystinuria, methylomonic acidemia, urea cycle disorders,
CC hereditary fructose intolerance, hereditary haemochromatosis, neonatal
CC thrombocytopaenia, Gaucher's disease, tyrosinaemia, Wilson's disease,
CC alcaptonuria, hypolactasia, Baker's disease, argininaemia adenomatous
CC polypsis coli (APC), adult polycystic kidney disease, Duchenne muscular
CC dystrophy, alpha-1-antitrypsin deficiency, hereditary non-polyposis
CC colorectal cancer, Huntington's disease, neurofibromatosis, Marfan's
CC syndrome, osteogenesis imperfecta, retinoblastoma, Friedreich's ataxia,
CC haemoglobinopathies, MCAD, Canavan's disease, Leber's hereditary optic
CC neuropathy, retinitis pigmentosa, Bloom syndrome, Fanconi's anaemia, or
CC Neimann Pick's disease. The present sequence is human galactose-1-
CC phosphate uridylyl transferase (GALT) specific PCR primer used to
CC illustrate the method of the invention
XX
SQ Sequence 21 BP; 5 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 597 CTCATCAGTGGCTAGC 614
DB 4 CTCATCAGTGGCTAGC 21
RESULT 3145
ACDS0312
ID ACDS0312 standard; RNA; 21 BP.
XX
AC ACDS0312;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV ribozyme substrate sequence #10.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KM RNA stability; RNA expression; RNA synthesis; antisense;
KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KM HBV reverse transcriptase; Enhancer I region; viral replication;
KM degenerative disease state; HBV infection; HCV infection; cirrhosis;
KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KM virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
XX
XX WO200281494-A1.
XX
PN 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX

XX The present invention provides the protein and coding sequences of four
 CC novel human G-protein coupled receptors (GPCR) which are amplified in
 CC breast cancers. The sequences are useful in the treatment of cancers,
 CC including breast and prostate cancers. The present sequence is a PCR
 CC primer used to isolate a coding sequence for a GPCR of the invention
 XX
 SQ Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3894 CTGAGTACTCTTCATAG 3911
 Db 18 CTGAGTACTCTTCATAG 1
 RESULT 3148
 ADA09668
 ID ADA09668 standard; DNA; 21 BP.
 AC ADA09668;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human G protein-coupled receptor HGPBRM26 Taqman PCR probe.
 XX
 KW 89; human; HGPBRM26; G protein-coupled receptor;
 KW male reproductive condition; amine disorder; testicular disorder;
 KW testicular cancer; choriocarcinoma; nonseminoma; seminoma;
 KW spermatogenesis; infertility; Klinefelter's syndrome; XX male;
 KW epididymitis; genital wart; germinal cell aplasia of the testis;
 KW cryptorchidism; varicocele; immature cilia syndrome; viral orchitis;
 KW premature puberty; incomplete puberty; Kallman syndrome;
 KW Cushing's syndrome; hyperprolactinaemia; haemochromatosis;
 KW congenital adrenal hyperplasia; follicle stimulating hormone deficiency;
 KW granulomatous disease; PCR; probe; reverse transcriptase PCR; RT-PCR.
 KW
 OS Homo sapiens.
 PN US2003064381-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 07-MAR-2002; 2002US-00092771.
 XX
 PR 07-MAR-2001; 2001US-0273963P.
 PR 27-MAR-2001; 2001US-0278927P.
 XX
 PA (FEDE/) FEDER J N.
 PA (RAMA/) RAMANATHAN C S.
 PA (MINT/) MINTIER G A.
 PA (CACA/) CACACE A.
 PA (BARB/) BARBER L E.
 XX
 PI Feder JN, Ramanathan CS, Mintier GA, Cacace A, Barber LE;
 XX
 DR WPI; 2003-555589/52.
 XX
 PT New human G-protein coupled receptor HGPBRM26 polypeptides and nucleic
 PT acids, useful for preventing, treating or ameliorating e.g. testicular
 PT disorder, choriocarcinoma, infertility, viral orchitis, or Cushing's
 PT syndrome.
 XX
 PS Example 4; Page 78; 149pp; English.
 CC The invention relates to an isolated nucleic acid molecule encoding a G
 CC protein-coupled receptor HGPBRM26. The nucleotide sequence comprises
 CC sequential nucleotide deletions from either the C-terminus or the N-
 CC terminus. Also included are an isolated polypeptide encoded by the
 CC nucleic acid, a recombinant vector comprising the nucleic acid, making a
 CC recombinant host cell comprising the nucleic acid, diagnosing a

CC pathological condition or a susceptibility to a pathological condition in
 CC testicular tissue of a subject, identifying a compound that modulates the
 CC biological activity of a human G-protein coupled receptor HGPBRM26 (and
 CC a member consisting of NFAT/CRE or NFAT G alpha 15, all undefined), and
 CC screening for candidate compounds capable of modulating activity of the
 CC HGPBRM26 polypeptide. The HGPBRM26 polypeptides, polynucleotides,
 CC compounds or pharmaceutical preparations comprising HGPBRM26 are useful
 CC for preventing, treating or ameliorating a male reproductive condition;
 CC an amine disorder or a condition where G-protein coupled receptors are
 CC (in)directly involved in disease progression, a testicular disorder,
 CC testicular cancer, choriocarcinoma, nonseminoma, seminoma,
 CC spermatogenesis, infertility, Klinefelter's syndrome, XX male,
 CC epididymitis, genital warts, germinal cell aplasia of the testis,
 CC cryptorchidism, varicocele, immature cilia syndrome, viral orchitis,
 CC premature puberty, incomplete puberty, Kallman syndrome, Cushing's
 CC syndrome, hyperprolactinaemia, haemochromatosis, congenital adrenal
 CC hyperplasia, follicle stimulating hormone (FSH) deficiency and
 CC granulomatous disease. The present sequence is a reverse transcriptase
 CC (RT)-PCR probe used to determine the tissue expression profile of
 CC HGPBRM26 mRNA.
 CC
 SQ Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 954 CCTCAGGACTCTCAGCG 971
 Db 1 CCCACGAGCTCCACGG 18
 RESULT 3149
 AD16552/C
 ID AD16552 standard; RNA; 21 BP.
 AC AD16552;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Short interfering double-stranded RNA oligonucleotide SEQ ID NO:277.
 XX
 KW expression interference; expression inhibition; target gene;
 KW short interfering double stranded RNA; cytosolic; gene therapy;
 KW proliferative disease; cancer; ds.
 XX
 OS Synthetic.
 PN WO2003012052-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 30-JUL-2002; 2002WO-US024226.
 XX
 PR 30-JUL-2001; 2001US-0308640P.
 PR 08-APR-2002; 2002US-0370970P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (CARN-) CARNEGIE INST WASHINGTON.
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Caplen NJ, Morgan RA, Fire A, Parrish S, Moussees S,
 PI Kallionemi O, Cornelison JR, Alton EW, Griesenbach U;
 XX
 DR WPI; 2003-248169/24.
 XX
 PT New RNA comprising double stranded RNA and a 3' or 5' overhang having a
 PT length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse
 PT genetic and/or therapeutic tools for interfering or inhibiting expression
 PT of a target gene.
 XX
 PS Claim 71; SEQ ID NO 277; 176pp; English.
 XX

CC The present invention describes an RNA (I) used for the interference or
 CC inhibition of expression of a target gene, where (I) comprises double
 CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang
 CC having a length of 0-nucleotide to 5-nucleotides on each strand, where
 CC the sequence of the double stranded RNA is substantially identical to a
 CC portion of a mRNA or transcript of the target gene. Also described: (1)
 CC interfering with or inhibiting the expression of a target gene in a cell
 CC by exposing the cell to an amount of (1); (2) a gene silencing array
 CC comprising a substantially flat substrate, and addressably arrayed
 CC different double-stranded RNAs; (3) an array-based method of assessing a
 CC phenotypic effect of a double-stranded RNA on a target gene; (4)
 CC validating a gene as a potential drug target for a disease or condition;
 CC (5) selecting an optimised sequence of a double-stranded RNA for
 CC interference with or inhibition of expression of a target gene in a cell;
 CC and (6) a short double-stranded RNA effective for interfering with or
 CC inhibiting expression of a target gene comprising any of 311 20-78
 CC nucleotide sequences (see ADCl6276 to ADCl6586). (I) has cytotoxic
 CC activity, and can be used in gene therapy. The RNAs are useful as reverse
 CC genetic and/or therapeutic tools for interfering or inhibiting expression
 CC of a target gene. They are useful for treating proliferative diseases,
 CC e.g. cancer.

XX
 XX Sequence 21 BP; 4 A; 6 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4926 GACTGTGAGTAAGTCTCT 4943
 |||||
 Db 20 GACTGCTGAGGAACTCTCT 3

RESULT 3150
 ADD14587
 ID ADD14587 standard; DNA; 21 BP.
 XX
 AC ADD14587;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human src biomarker reverse PCR primer SEQ ID NO:176.
 XX
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003062395-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US001981.
 XX
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX WPI; 2003-636735/60.
 XX
 DR New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 PT tyrosine kinase pathways.
 XX
 PS Example 2; SEQ ID NO 776; 139pp; English.
 XX
 CC The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of

CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cytostatic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the
 CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX
 XX Sequence 21 BP; 2 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4219 TCCTTCCTCTGTCAGAT 4236
 |||||
 Db 2 TCCTTCCTCTGTCAGAT 19

RESULT 3151
 ADD14405/C
 ID ADD14405 standard; DNA; 21 BP.
 XX
 AC ADD14405;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human src biomarker reverse PCR primer SEQ ID NO:594.
 XX
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003062395-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US001981.
 XX
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX WPI; 2003-636735/60.
 XX
 DR New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 PT tyrosine kinase pathways.
 XX

PS Example 2; SEQ ID NO 594; 139pp; English.

The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers, and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynucleotides and polypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polynucleotides or polypeptides, and selecting polynucleotides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides have cytoskeletal activities, and can be used in gene therapy. The polynucleotides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.

Sequence 21 BP; 6 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match	0.2%	Score 14.8;	DB 1;	Length 21;
Beet Local Similarity	88.9%;	Pred. No. 2.1e+03;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	6555 GCTGTGGACAGTTTG	6572		
b				
20 GCAGTGGGAAGTTTG	3			

RESULT 3152
ADE27642/c
ID ADE27642 standard; RNA; 21 BP.

AC ADE27642;

DT 29-JAN-2004 (first entry)

DE Stearoyl-CoA desaturase sRNA oligonucleotide SEQ ID NO:586.

KM short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
 KM stearyl-CoA deaturase; RNA interference; anorectic; antidiabetic;
 KM antiatherosclerotic; cytosolic; virucide; obesity; diabetes;
 KM atherosclerosis; cancer; viral infection; drug screening;
 KM genetic engineering; pharmacogenomic; gene mapping; ss.

Synthetic.

PN WO2003070885-A2.

PD 28-AUG-2003.

13-FEB-2003; 2003WO-US004317.

PR 20-FEB-2002; 2002US-0358580P
PR 11-MAR-2002; 2002US-0363124P
PR 06-JUN-2002; 2002US-0386782P
PR 29-UG-2002; 2002US-0466784P
PR 05-SEP-2002; 2002US-0408378P
PR 09-SEP-2002; 2002US-0409293P
PR 20-SEP-2002; 2002US-0412304P
PR 15-JAN-2003; 2003US-0440129P

XX
PA (RIBO-) RIBOZYME PHARM INC.

Mcswiggen J, Beigelman L, Thompson J;

DR WPI; 2003-721687/68.

PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

PS Example 3; SEQ ID NO 586; 139pp; English.

The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of the SCD (Stearyl-CoA desaturase) gene by RNA interference. Also described: (1) modulating expression of SCD genes in cells, tissue explants or organisms by introduction of siNA; (2) kits for *in vitro* or *in vivo* delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that express siNA. SCD inhibiting siNAs have anorectic, anti-diabetic, anti-atherosclerotic, cyrostatic and virucide activities. The siNAs can be used to modulate expression of SCD genes in cells, tissue explants or organisms, e.g. for treating obesity, diabetes (types I and II), atherosclerosis; cancer and viral infections. They can also be used for drug screening; diagnosis; "target" identification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents an SCD siNA, which is used in the exemplification of the present invention.

Sequence 21 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 0 Other;

Query Match	0.23	Score 14.8	DB 1	Length 21
Match Similarity	88.9%	Pred. No. 2.1e+03		
Best Local 16	Conservative	0	Mismatches 2	Indels 0
Gaps				0
Qy	7232	TCCCTCTCAAGTCGAGCA	7249	
db	18	TCCATCTCATGTCCAGCA	1	

RESULT 3153
ADE47931/c
ID ADE47931 standard; DNA; 21 BP.

AC ADE47931;

DT 29-JAN-2004 (first entry)

DE	Human NOVX reverse PCR primer SEQ ID NO:293.
AA	

AA human; cardiac; antiarteriosclerotic; hypotensive; immunosuppressive;
KW dematological; anorectic; cytostatic; antiadrenergic; haemostatic;
KW anti-IV; antisthmatic; antibacterial; virucide; neuroprotective;
KW nootropic; antiparkinsonian; antihypaemic; gene therapy; vaccine; PCR;
KW primer; ss.

Homo sapiens.

PN WO2003076642-A2

AA PD 18-SEP-2003.

AA
PF 02-AUG-2002; 2002WO-US024459.

PR	02-AUG-2001	2001US-0309501P
PR	03-AUG-2001	2001US-0310291P
PR	08-AUG-2001	2001US-0310951P
PR	09-AUG-2001	2001US-0311292P
PR	13-AUG-2001	2001US-0311979P
PR	14-AUG-2001	2001US-0312203P
PR	17-AUG-2001	2001US-0313156P
PR	17-AUG-2001	2001US-0313201P
PR	20-AUG-2001	2001US-0313702P

PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315853P.
 PR 31-AUG-2001; 2001US-0316508P.
 PR 21-SEP-2001; 2001US-0323936P.
 PR 03-DEC-2001; 2001US-0338078P.
 PR 05-FEB-2002; 2002US-0354655P.
 PR 05-MAR-2002; 2002US-0361764P.
 PR 19-APR-2002; 2002US-037825P.
 PR 15-MAY-2002; 2002US-0380971P.
 PR 15-MAY-2002; 2002US-0380980P.
 PR 16-MAY-2002; 2002US-0381039P.
 PR 28-MAY-2002; 2002US-0383761P.
 PR 29-MAY-2002; 2002US-0383887P.
 PR 01-AUG-2002; 2002US-00210130.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Zernusen BD, Paturajan M, Kekuda R, Miller CE, Rieger DK;
 PI Pena CEA, Shimeles RA, Li L, Berghs C, Zhong M, Caeman SU, Voss EZ;
 PI Boldog FL, Padigaru M, Smithson G, Shenoy SG, Ji W, German L;
 PI Verneer CM, Lette MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
 PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Raschelli L, Agee MT,
 PI Chaudhuri A, Chant JS, DiPippo VA, Edinger SR, Eisen A, Gangollia EA;
 PI Glot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalt T, Liu X;
 PI Taupier RJ, Caterton E;
 XX
 DR WPI; 2003-779062/73.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 PT
 PS Example 49; SEQ ID NO 293; 562pp; English.
 XX
 CC The invention relates to a novel (NOVX) human polypeptide. A polypeptide
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
 CC haemostatic, anti-HIV, antiaesthetic, antibacterial, virucide,
 CC neuroprotective, nictropic, antiparkinsonian, and antilipemic activity.
 CC A polynucleotide encoding a polypeptide of the invention may have a use
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, the disease selected from a pathology
 CC associated with the polypeptide. These may also be used in diagnosing,
 CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting
 CC disorders associated with chronic diseases. The nucleic acids are also
 CC used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine, and pharmacogenomics. The polypeptides are also
 CC useful as vaccines. The present sequence represents a PCR primer used in
 CC the invention.
 CC
 XX
 SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7384 TGTACAGTCTCTCTGAA 7401
 Db 19 TGTCCAGTCTCTCTGAA 2
 XX
 RESULT 3154
 AAT78996
 ID AAT78996 standard; DNA; 22 BP.

XX
 AC AAT78996;
 XX
 DT 13-JAN-1998 (first entry)
 XX
 DE Human Huntington's disease gene intron 1 3' acceptor site.
 XX
 KW Huntington's disease; animal model; transgenic animal; human; therapy;
 KW drug screening; Hdh gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN CA2178022-A.
 XX
 PD 02-DEC-1996.
 XX
 PF 03-JUN-1996; 96CA-02178022.
 XX
 PR 01-JUN-1995; 95US-00457273.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 PI Hayden M, Lin B, Nasir J;
 XX
 DR WPI; 1997-298677/28.
 XX
 PT Mouse Huntington's Disease gene - useful for generating transgenic mice
 PT as a model of Huntington's Disease.
 PT
 PS Disclosure; Page 60; 69pp; English.
 XX
 CC This oligonucleotide comprises the 5' acceptor site of intron 1 of the
 CC human Huntington's disease (HD) gene. The splice site sequences for the
 CC first 5 exons of the mouse HD gene (see AAT78997) and the human HD gene
 CC were compared (see AAT78985-T79002). Targeted disruption of the murine HD
 CC gene, e.g. at exon 5, can be used to examine the function of the HD gene
 CC and its role in development. Transgenic mice can be used as models of HD
 CC
 XX
 SQ Sequence 22 BP; 2 A; 3 C; 1 G; 16 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4463 CTTTCTTTTCTTTTCTTTT 4480
 Db 3 CTTCTTTTCTTTTCTTTT 20
 XX
 RESULT 3155
 AAT94992/C
 ID AAT94992 standard; DNA; 22 BP.
 XX
 AC AAT94992;
 XX
 DT 02-APR-1998 (first entry)
 XX
 DE Primer 6 for sequencing of human leukocyte antigen class I genes.
 XX
 KW Human leukocyte antigen-C class I gene; HLA-C; exon 1; exon 5;
 KW locus specific nucleic acid amplification; HLA typing; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9731126-A1.
 XX
 PD 28-AUG-1997.
 XX
 PF 20-FEB-1996; 96WO-US002408.
 XX
 PR 20-FEB-1996; 96WO-US002408.
 XX

PA (PEKE) PERKIN-ELMER CORP.
 XX Johnston-Dow L, Chadwick RB, Parham P;
 XX WPI; 1997-435175/40.
 DR
 XX Amplification and sequencing primers specific for HLA class I genes -
 PT useful for locus specific nucleic acid amplification for HLA typing.
 XX
 XX Claim 10; Page 57; 105pp; English.
 XX
 CC Sequencing primers AAT94987-92 were used to sequence PCR amplified human
 CC leukocyte antigen (HLA) class I genes. The primers are designed to
 CC hybridise to exon-intron borders of exons 2, 3 and 4 of the HLA genes.
 CC PCR primers were used for locus specific nucleic acid amplification for
 CC HLA typing. Typing HLA-A, -B or -C class I genes comprises providing a
 CC sample DNA containing a HLA-A, -B or -C class I gene having a 1st and 2nd
 CC exon and a target sequence, contacting the sample DNA with an
 CC amplification primer including sequence complementary to sequence located
 CC in exon 1 of the HLA-A, -B or -C gene, and a second amplification primer
 CC sequence complementary to sequence located in exon 5 of the HLA-A, -B or
 CC -C gene. The PCR product is sequenced using the above primers and the
 CC determined DNA sequence compared with the DNA sequences of known HLA
 CC types
 XX
 SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 942 GCAGCCCAAGCCCTCTCAG 959
 DB 21 GCTGCCAAGCCCTCTCAG 4
 RESULT 3156
 AAT95005/C
 ID AAT95005 standard; DNA; 22 BP.
 XX
 AC AAT95005;
 XX
 DT 02-APR-1998 (first entry)
 XX
 DE Primer for sequencing exon 4 sense strand of HLA class I genes.
 XX
 KW Human leukocyte antigen-C class I gene; HLA-C; exon 1; exon 5;
 KW locus specific nucleic acid amplification; HLA typing; exon 4; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09731126-A1.
 XX
 PD 28-AUG-1997.
 XX
 PE 20-FEB-1996; 96WO-US002408.
 XX
 PR 20-FEB-1996; 96WO-US002408.
 XX
 PA (PEKE) PERKIN-ELMER CORP.
 XX
 PI Johnston-Dow L, Chadwick RB, Parham P;
 DR WPI; 1997-435175/40.
 XX
 PT Amplification and sequencing primers specific for HLA class I genes -
 PT useful for locus specific nucleic acid amplification for HLA typing.
 XX
 PS Claim 29; Page 62; 105pp; English.
 XX
 CC The present sequencing primer was used to sequence PCR amplified human
 CC leukocyte antigen (HLA) class I genes. The primer is designed to sequence

CC the sense strand of exon 4, from the 5' exon-intron border. PCR primers
 CC were used for locus specific nucleic acid amplification for HLA typing.
 CC Typing HLA-A, -B or -C class I genes comprises providing a sample DNA
 CC containing a HLA-A, -B or -C class I gene having a 1st and 2nd exon and a
 CC target sequence, contacting the sample DNA with an amplification primer
 CC including sequence complementary to sequence located in exon 1 of the HLA
 CC -A, -B or -C gene, and a second amplification primer sequence
 CC complementary to sequence located in exon 5 of the HLA-A, -B or -C gene.
 CC The PCR product is sequenced using the above primers and the determined
 CC DNA sequence compared with the DNA sequences of known HLA types
 CC
 XX
 SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 942 GCAGCCCAAGCCCTCTCAG 959
 DB 21 GCTGCCAAGCCCTCTCAG 4
 RESULT 3157
 AAX59677/C
 ID AAX59677 standard; DNA; 22 BP.
 XX
 AC AAX59677;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE PCR primer p1 used to amplify termamyl-like alpha-amylase DNA.
 XX
 KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KW saccharification process; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 PN W09923211-A1.
 XX
 PD 14-MAY-1999.
 XX
 PE 30-OCT-1998; 98WO-DK000471.
 XX
 PR 30-OCT-1997; 97DK-00001240.
 PR 14-JUL-1998; 98DK-00000936.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
 PI Kjaerulf S;
 DR WPI; 1999-326987/27.
 XX
 PT New Termamyl-like alpha-amylase variants.
 XX
 PS Example 10; Page 58; 115pp; English.
 XX
 CC The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
 CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
 CC A186, W189, S193, N195, H107, G108, G109, D167, W167, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, G456, M457, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present PCR primer was used to construct the variants of
 CC the invention
 CC
 XX
 SQ Sequence 22 BP; 6 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1919 TTGGTGGCATTAAACACAA 1936
 |||||
 |||||

Db 19 TTGGCGGCATTAAATACAA 2

RESULT 3158
 AAA64619

ID AAA64619 standard; DNA; 22 BP.

XX AAA64619;

XX 02-JAN-2001 (first entry)

XX PCR primer used to assess frequency of expression of MAGE-A10 gene.

XX MAGE-A10; MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;
 KW human leukocyte antigen; HLA; T cell response; region q28; X chromosome;
 KM cancer; PCR primer; ss.

XX Homo sapiens.

XX W0200052163-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005346.

XX 02-MAR-1999; 99US-00260978.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;
 PI Boon-Falleur T;

XX WPI; 2000-579285/54.

XX Complementary polynucleotide of MAGE family, useful in the diagnosis of
 PT cancer in a patient.

XX Example 1; Page 4; 72pp; English.

XX PCR primers AAA64618-19 were used in reverse transcription PCR reactions
 CC to assess the frequency of expression of MAGE-A10 gene. The specification
 CC describes MAGE-A5, MAGE-A8, MAGE-A9, MAGE-A10 and MAGE-A11. The MAGE
 CC genes encode tumour rejection antigens which complex to human leukocyte
 CC antigens (HLAs), and provoke response by autologous, cytolytic T cells.
 CC The genes are located in region q28 of the X chromosome. The MAGE
 CC polynucleotides are useful for diagnosis of cancer in a patient

XX Sequence 22 BP; 4 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1738 ACCTACTCAGGGCTGCAG 1755
 |||||
 |||||

Db 3 ACCTCCTCAGGGCTGCAG 20

RESULT 3159

AAA90556/c

XX AAA90556 standard; DNA; 22 BP.

XX AAA90556;

XX 11-JAN-2001 (first entry)

DE HLA class I gene sequencing primer #6.

XX Human Leukocyte Antigen class I; HLA-A; antigen presentation; HLA typing;
 KW organ transplantation; autoimmune disease; sequencing primer;
 KM infectious disease susceptibility; chromosome 6p21.3; ss.

XX Homo sapiens.

XX US6103465-A.

XX 15-AUG-2000.

XX 03-OCT-1995; 95US-00538666.

XX 14-FEB-1995; 95US-00390251.

XX (PEKE) PERKIN-ELMER CORP.

XX Parham P, Johnston-Dow L, Chadwick RB;

XX WPI; 2000-542544/49.

XX Typing HLA class I genes for organ transplantation, involves contacting
 PT the sample DNA containing HLA class I gene comprising two exons and a
 PT target sequence, with amplification primers and detecting the amplicon.

XX Claim 40; Col 36; 60pp; English.

XX The present sequence is a sequencing primer for Human Leukocyte Antigen
 CC (HLA) class I gene. The HLA class I genes are found on chromosome 6p21.3.

CC HLA class I proteins are found on the surface of almost all nucleated
 CC cells and are involved in antigen presentation to immune system cells.

CC This primer can be used to type HLA class I genes: by carrying out PCR on
 CC a sample DNA, comprising HLA class I gene, and detecting the amplicon
 CC formed using a sequence-specific detection method e.g. DNA sequencing
 CC (using the present sequence). The present sequence is useful for
 CC discriminating among the HLA-A, HLA-B, and HLA-C genes and other related
 CC class I genes and pseudogenes. In addition, the present sequence is
 CC useful for organ transplantation studies, for the study of autoimmune
 CC disease and for the determination of susceptibility to infectious disease

XX Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

942 GCAGCCCAAGCCCTCAG 959
 |||||
 |||||

Db 21 GCTGCCGAAGCCCTCAC 4

RESULT 3160

AAA90562/c

ID AAA90562 standard; DNA; 22 BP.

XX AAA90562;

XX 11-JAN-2001 (first entry)

XX HLA class I gene sequencing primer #12.

XX Human Leukocyte Antigen class I; HLA-A; antigen presentation; HLA typing;
 KW organ transplantation; autoimmune disease; sequencing primer;
 KM infectious disease susceptibility; chromosome 6p21.3; ss.

XX Homo sapiens.

XX US6103465-A.

XX 15-AUG-2000.

XX 03-OCT-1995; 95US-00538666.


```
XX 14-FEB-1995; 95US-00390251.
XX
XX (PEXE ) PERKIN-ELMER CORP.
XX
XX Parham P, Johnston-Dow L, Chadwick RB;
XX
XX WPI; 2000-542544/49.
XX
XX Typing HLA class I genes for organ transplantation, involves contacting
XX the sample DNA containing HLA class I gene comprising two exons and a
XX target sequence, with amplification primers and detecting the amplicon.
XX
XX Claim 10; Col 35; 60pp; English.
XX
XX The present sequence is a sequencing primer for Human Leukocyte Antigen
XX (HLA) class I gene. The HLA class I genes are found on chromosome 6p21.3.
XX HLA class I proteins are found on the surface of almost all nucleated
XX cells and are involved in antigen presentation to immune system cells.
XX This primer can be used to type HLA class I genes: by carrying out PCR on
XX a sample DNA, comprising HLA class I gene, and detecting the amplicon
XX formed using a sequence-specific detection method e.g. DNA sequencing
XX (using the present sequence). The present sequence is useful for
XX discriminating among the HLA-A, HLA-B, and HLA-C genes and other related
XX class I genes and pseudogenes. In addition, the present sequence is
XX useful for organ transplantation studies, for the study of autoimmune
XX disease and for the determination of susceptibility to infectious disease
XX
XX Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 22;
XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 942 GCAGCCCAAGCCCTCTCAC 959
XX |||||
XX 21 GCTGCCGAGAGCCCTCTCAC 4
XX
XX RESULT 3161
XX AA291959
XX ID AA291959 standard; DNA; 22 BP.
XX
XX AA291959;
XX
XX 08-JUN-2000 (first entry)
XX
XX Mahogany protein gene exon 10 primer Celegel17.
XX
XX Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;
XX weight regulation; cell therapy; body weight disorder; cachexia;
XX anorexia; hyperpigmentation; increased metabolic rate disorder;
XX hyperphagia; Antiobesity; anti-anorexic; anticachectic; PCR primer; ss.
XX
XX Mammalia.
XX
XX WO200005373-A2.
XX
XX 03-FEB-2000.
XX
XX 21-JUL-1999; 99WO-US016484.
XX
XX 21-JUL-1998; 98US-0093630P.
XX 20-OCT-1998; 98US-0104978P.
XX 05-FEB-1999; 99US-00245041.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Moore K, Nagle DL;
XX
XX WPI; 2000-195103/17.
XX
XX New human and murine mahogany genes, useful, e.g. for diagnosis and
XX
```

```
PT treatment of body weight disorders.
XX
XX Example; Fig 5; 18pp; English.
XX
XX This sequence represents a PCR primer for a mahogany gene of the
XX invention. The mahogany genes are used: (i) to produce recombinant
XX mahogany (mg) proteins (ii); (iii) as a source of antisense, ribozyme or
XX triplex-forming therapeutics; (iii) as a source of diagnostic probes and
XX primers for detecting expression of mg genes or mutations, regulatory
XX defects, in this gene, or for isolation of related sequences; and (iv) in
XX (cell-based) gene therapy. (ii) are used to raise specific antibodies
XX (Ab); to identify other (extra)cellular products involved in weight
XX regulation, and to screen for agents that disrupt interaction between
XX (ii) and other macromolecules. The Ab are used to detect abnormal levels
XX (or function) of (ii) (for diagnosis, prognosis or monitoring of
XX treatment); to evaluate (ii)-expressing cells intended for cell therapy,
XX and as therapeutic mg inhibitors. Cells that express the mg gene (or
XX contain the mg polypeptide) are used to identify agents (A) that modulate
XX mg activity. (A) are potentially useful for the treatment of body weight
XX disorders, particularly obesity, cachexia or anorexia, or other
XX conditions associated with the mg gene such as hyperpigmentation,
XX hyperphagia and disorders that result in increased metabolic rate
XX
XX Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 22;
XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 7072 TGAATGACAGAGCCCT 7089
XX |||||
XX 1 TGAATGACAGAGCCCT 18
XX
XX RESULT 3162
XX AAC58261/C
XX ID AAC58261 standard; DNA; 22 BP.
XX
XX AAC58261;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO212 hybridisation probe SEQ ID NO:80.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumorigenesis; identification; cancer; PCR primer;
XX hybridisation; probe; cytostatic; neurotropic; neuroprotective;
XX antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic;
XX leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;
XX astrocytal disorder; hypothalamic disorder; glandular disorder;
XX macrophagal disorder; epithelial disorder; stromal disorder;
XX blastocoelec disorder; inflammatory disorder; angiogenic;
XX immunologic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US000376.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 26-JUL-1999; 99US-0145568P.
XX 30-NOV-1999; 99WO-US028313.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH ) GENENTECH INC.
XX
```


PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 DR WPI; 2000-572270/53.
 XX
 XX
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer.
 PS
 PS Example 23; Page 133; 286pp; English.
 XX
 CC The present invention describes an isolated antibody that binds to one of
 CC the human PRO proteins designated PRO2212, PRO290, PRO341, PRO353, PRO619,
 CC PRO717, PRO809, PRO830, PRO848, PRO341, PRO1005, PRO1009, PRO1025,
 CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO2094, PRO245 OR
 CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
 CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
 CC and prevention of cancer. The antibodies and other anti-tumour compounds
 CC maybe used to treat various conditions, including those characterised by
 CC overexpression and/or activation of the amplified PRO genes. Exemplary
 CC conditions or disorders to be treated with such antibodies and other
 CC compounds include benign or malignant tumours (e.g., renal, liver,
 CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
 CC pancreatic, lung, vulva, thyroid, hepatic carcinoma, sarcomas, and
 CC glioblastomas, and various head and neck tumours), leukemias and
 CC lymphoid malignancies, other disorders such as neuronal, glial,
 CC astrocytal, hypochalamic and other glandular, macrophagal, epithelial,
 CC stromal and blastococelial disorders, and inflammatory, angiogenic and
 CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
 CC hybridisation probes used in the isolation of the human PRO sequences.
 CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
 CC polynucleotide and protein sequences given in the exemplification of the
 CC present invention
 CC
 SQ Sequence 22 BP; 2 A; 10 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5210 GGCGTAGATCAGGGCAG 5227
 DB 22 GGCGCAGATCAGTGCAC 5
 XX
 RESULT 3163
 ABA82014/C
 ID ABA82014 standard; DNA; 22 BP.
 XX
 AC ABA82014;
 XX
 DT 25-JAN-2002 (first entry)
 XX
 DE Mouse wound healing related PCR primer SEQ ID NO 83.
 XX
 KM Human; mouse; vulnery; dermatological; skin disorder; wound healing;
 KM gene therapy; PCR primer; 88.
 XX
 OS Mus musculus.
 XX
 PN CA2325226-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 16-NOV-2000; 2000CA-02325226.
 XX
 PR 17-NOV-1999; 99DB-01055349.
 PR 17-DEC-1999; 99US-0172511P.
 PR 20-JUN-2000; 2000DE-01030149.
 XX
 PA (SWIT-) SWITCH BIOTECH AG.
 XX
 PI Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;

XX
 DR WPI; 2001-433142/47.
 XX
 PT Use of novel polypeptide or its variant or nucleic acid encoding the
 PT polypeptide for diagnosing and/or preventing and/or treating skin
 PT disorders and/or treatment in wound healing or for identifying active
 PT substances.
 XX
 PS
 PS Example 8; Page 64; 265pp; English.
 XX
 CC The invention relates to the use of a polypeptide (ABA44544-ABA44601,
 CC ABA44606-ABA44623) or its variant or encoding nucleic acid (ABA1990-
 CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological
 CC activity for the diagnosis, prevention and treatment of skin disorders
 CC and treatment in wound healing or for the identification of
 CC pharmacologically active substances. The nucleic acids are useful in gene
 CC therapy. The present sequence is that of a PCR primer, useful to the
 CC invention. Note: The printed sequence listing for this specification was
 CC incomplete, terminating part way through SEQ ID NO 106. The remaining
 CC data was obtained from EPO data for an equivalent patent (EP1114862)
 CC
 SQ Sequence 22 BP; 3 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5912 TTCCCGAAGCCGAGAT 5929
 DB 22 TTCCCGAAGCAGCAGAT 5
 XX
 RESULT 3164
 AAF84350
 ID AAF84350 standard; DNA; 22 BP.
 XX
 AC AAF84350;
 XX
 DT 20-JUN-2001 (first entry)
 XX
 DE Human CYP2C18i PCR primer #6.
 XX
 KM Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; 88.
 KM Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 PN JF2001017185-A.
 XX
 PD 23-JAN-2001.
 XX
 PF 10-DEC-1999; 99JP-00351610.
 XX
 PR 19-MAR-1999; 99JP-00076592.
 PR 06-MAY-1999; 99JP-00125918.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 DR WPI; 2001-285409/30.
 XX
 PT Detection of gene polymorphism of drug-metabolising enzymes useful for
 PT diagnosis and testing comprises carrying out polymerase chain reaction.
 XX
 PS
 PS Example 1; Page 13; 27pp; Japanese.
 XX
 CC The present invention relates to a kit and method for the detection of
 CC gene polymorphisms of drug-metabolising enzyme genes. The kit contains a
 CC polymerase chain reaction (PCR) buffer solution containing DNA polymerase
 CC and NTP, a normal forward primer, a mutated forward primer, a reverse
 CC primer and a fluorescence-labelling probe. The method involves carrying
 CC out PCR on sample DNA, containing a drug-metabolising enzyme gene,
 CC together with PCR buffer, the normal forward primer, the reverse primer
 CC and the fluorescence-labelling probe (step A); and carrying out PCR on
 CC the sample DNA together with PCR buffer, the mutated forward primer, the

CC reverse primer and the fluorescence-labelling probe (step B), and a step
CC of comparing the result of step a with that of step b. The present
CC sequence is a primer for human CYP2C18i, which was used to illustrate the
CC present invention

XX Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5289 GCCTTACTCCGACGAC 5306
DB 5 GCCTTATCCGACGAC 22

RESULT 3165
AA165435
ID AA165435 standard; DNA; 22 BP.

XX AA165435;

DT 10-DEC-2001 (first entry)

DE Reverse transcription primer for maize.

XX Plant androgenesis marker; maize; androgenesis; quantitative trait loci;
XX cereal; plant breeding; primer; ss.

XX Zea mays.

XX FR2806419-A1.

XX 21-SEP-2001.

XX 14-MAR-2000; 2000FR-00003245.

XX 14-MAR-2000; 2000FR-00003245.

XX (LIMA-) LIMAGRAIN GENETICS GRANDES CULTURES.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Dufour P, Murigneux A, Beckert M;

XX WPI; 2001-573132/65.

XX New markers for plant androgenesis, useful for evaluating androgenic
XX potential, cloning of androgenesis genes and genetic analysis.

XX Example; Page 13; 49pp; French.

XX The present sequence represents a primer used to produce maize cDNA. The
XX specification describes plant androgenesis markers, which are derived
XX from maize. Maize androgenesis markers are used to evaluate the
XX androgenic potential of plants and derived cultures of microspores. The
XX markers are also used to clone genes involved in androgenesis, and for
XX genetic analysis to identify quantitative trait loci involved in
XX androgenesis, particularly in cereals, specifically maize. Varieties
XX capable of androgenesis are useful in plant breeding programs

XX Sequence 22 BP; 3 A; 1 C; 2 G; 15 T; 0 U; 1 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4461 GACTTTTCTTTTCTTTT 4478
DB 4 GACTTTTCTTTTCTTTT 21

RESULT 3166
AAH37409/C

ID AAH37409 standard; DNA; 22 BP.

XX AAH37409;

DT 14-AUG-2001 (first entry)

DE SNP specific upper PCR primer SEQ ID 205.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.

XX WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000WO-US028436.

XX 15-OCT-1999; 99US-016096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polymorphic nucleotide polymorphism in a nucleic
XX acid sample.

XX Claim 1; Page 51; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a PCR primer specific
XX for a human SNP containing DNA sequence

XX Sequence 22 BP; 3 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2411 CAGTGAACCAACATCA 2428
DB 20 CAGTGTACCAACATCA 3

RESULT 3167

AAH40497
ID AAH40497 standard; DNA; 22 BP.
XX
AC AAH40497;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 3293.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WC200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 66; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPs) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 22 BP; 7 A; 10 C; 1 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3168
AAS14520
ID AAS14520 standard; DNA; 22 BP.
XX
AC AAS14520;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human GSTT1*0 3187bp fragment PCR primer GST-TR9n.
XX
XX Human; PCR primer; ss; GSTT1; Glutathione-S-transferase theta;
KM skin cancer; GSTT1*0 allele; oxidative stress; genotyping; GST-TR9n.
XX
OS Homo sapiens.
XX
PN EP110112-A1.
XX
XX
PD 05-SEP-2001.
XX
PF 24-FEB-2000; 2000EP-00103844.
XX
PR 24-FEB-2000; 2000EP-00103844.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Sprenger R, Schlagenhauer R, Brinkmann U, Kerb R;
XX
DR WPI; 2001-591524/67.
XX
PT PCR assay to detect presence of single allele e.g., glutathione S-
PT transferase thetasterisk0 allele, of deletion mutant involves performing
PT PCR with primers derived from sequences upstream and downstream of
PT deletion area.
XX
PS Disclosure; Page 17; 24pp; English.
XX
XX The invention relates to a PCR assay for detecting presence of at least a
CC single allele of deletion mutant GSTT1*0 (glutathione S-transferase theta
CC allele) involves performing PCR with two primers, of which one is from
CC the sequence upstream of the deletion area and the other is from the
CC sequence downstream of the deletion area, and checking the corresponding
CC DNA fragment produced in PCR. The method is useful for detecting presence
CC of at least GSTT1*0 allele, for diagnostic testing of individuals to
CC check whether they are susceptible to toxins or resistant to certain
CC therapeutic agents or belonging to risk groups (e.g. UV-mediated skin
CC damage, skin cancer and cancers associated with oxidative stress. The
CC method allows the characterisation and mechanism of the GSTT1 deletion
CC and identifies 18 kb homology regions flanking GSTT1 which are involved
CC in the deletion event that produced the *0 allele. The method permits the
CC unambiguous discrimination of all GSTT1 genotypes (*A/A, *0/0 (both
CC homozygous), */0 (heterozygous)). The technique allows the reproducible
CC simultaneous discrimination of all the genotypes. The three GSTT1
CC genotypes detected by these procedures correlated highly significant with
CC enzyme activity in erythrocytes. The trimodular distribution of
CC phenotypes at high-, intermediate- and null- activity in homo- and
CC heterozygotes for the *A allele and *0/0 homozygotes, respectively
CC indicate a gene dose effect. The present sequence is a PCR primer for
CC amplifying a 3187bp fragment from the human GSTT1*0 allele
XX
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3169
ABS59077/c
ID ABS59077 standard; DNA; 22 BP.

XX AC ABS59077;
 XX DT 05-NOV-2002 (first entry)
 XX DE Human G-protein coupled receptor, reverse primer #75.
 XX KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway modulation; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma; immune response; neurodegenerative disorder; inflammatory disorder; Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy; primer; PCR; ss.
 XX OS Homo sapiens.
 XX PN WO200259313-A2.
 XX PD 01-AUG-2002.
 XX PF 18-DEC-2001; 2001WO-US049394.
 XX PR 18-DEC-2000; 2000US-0256635P.
 XX PR 21-DEC-2000; 2000US-0257876P.
 XX PR 04-JAN-2001; 2001US-0259743P.
 XX PR 10-JAN-2001; 2001US-0260718P.
 XX PR 12-JAN-2001; 2001US-0261498P.
 XX PR 24-JAN-2001; 2001US-0263689P.
 XX PR 08-FEB-2001; 2001US-0267464P.
 XX PR 22-FEB-2001; 2001US-0271021P.
 XX PR 14-MAR-2001; 2001US-0275946P.
 XX PR 23-MAR-2001; 2001US-0278150P.
 XX PR 18-APR-2001; 2001US-0284591P.
 XX PR 23-APR-2001; 2001US-0285718P.
 XX PR 19-JUN-2001; 2001US-0293327P.
 XX PR 16-AUG-2001; 2001US-0312902P.
 XX PA (CIRRA-) CURAGEN CORP.
 XX PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA, Caeman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S; Gerlach V, Smithson G, Stone DJ, Sciore P, MacDougall JR, Gunther E; Peyman JA, Ellerman K, Gangolli EA, Millet I;
 XX DR WPI; 2002-599789/64.
 XX PT New G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer in humans.
 XX PS Claim 1; Page 455; 685pp; English.
 XX CC The invention relates to novel isolated G-protein coupled receptor (GPCR) polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid and antibody, are useful for treating, preventing or alleviating a GPCR-associated disorder or a pathological state in a subject, particularly a human. In particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing and metabolic pathway modulation. The GPCR polypeptide and nucleic acid are also useful for diagnosing the presence of or predisposition to a disease associated with altered levels of GPCR, particularly cancer. The GPCR nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant GPCR expression or activity. The DNA encoding the protein is useful in gene therapy for treating the above conditions. Furthermore, the nucleic acids and polypeptides are useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, neurodegenerative disorders, asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. ABS58747-ABS59231 represent human GPCR coding sequences, primers and probes of the invention

XX SQ Sequence 22 BP; 10 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
 XX Query Match 0.2%; Score 14.8; DB 1; Length 22;
 XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX QY 5705 TTGCTTTTCTCTCTCT 5722
 XX DB 21 TTGCTTTTCTCTCTCT 4
 XX RESULT 3170
 XX ABR33445/C
 XX ID ABR33445 standard; DNA; 22 BP.
 XX AC ABR33445;
 XX DT 23-APR-2002 (first entry)
 XX DE Human TNF-receptor I exon Pro12Pro (A/G) FAM probe (G allele).
 XX KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder; inflammatory disorder; chronic disease; receptor; probe; ss.
 XX OS Homo sapiens.
 XX PN EP1172444-A1.
 XX PD 16-JAN-2002.
 XX PF 10-JUL-2000; 2000EP-00114786.
 XX PR 10-JUL-2000; 2000EP-00114786.
 XX PA (CONA-) CONARIS RES INST GMBH.
 XX PI Schreiber S, Hampe J, Mascheretti S;
 XX DR WPI; 2002-156651/21.
 XX PT Detecting non-responders to anti-human necrosis factor therapy, comprises testing an individual for homozygosity for a single nucleotide polymorphism in the gene coding for the tumor necrosis factor receptor II.
 XX PS Disclosure; Page 6; 45pp; English.
 XX CC The present invention relates to a method for detecting non-responders to anti-tumour necrosis factor (TNF) therapy. The method involves testing an individual for homozygosity for at least one single nucleotide polymorphism (SNP) in the gene coding for TNF receptor II, which is located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168 A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and Met196Arg respectively, are also described. The method of the invention is useful for detecting non-responders to anti-TNF therapy such as infliximab therapy, or therapy of Crohn's disease. The genes containing the 2 novel polymorphisms are useful for diagnostic purposes in inflammatory, malignant or other chronic diseases. The present sequence represents a TaqMan probe used in the methods of the present invention
 XX SQ Sequence 22 BP; 2 A; 7 C; 8 G; 5 T; 0 U; 0 Other;
 XX Query Match 0.2%; Score 14.8; DB 1; Length 22;
 XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX QY 7412 TCAGCAGCAGCAGCAGCA 7429
 XX DB 18 TCACGACGCGCAGCAGCA 1

RESULT 3171
 ABK69044/c
 ID ABK69044 standard; DNA; 22 BP.
 XX
 AC ABK69044;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Rat ARP RT PCR probe.
 XX
 KM Alpha related protein; Beta related protein; ARP; BRP; hypothyroidism;
 KM glycoprotein hormone; reproductive disorder; cell proliferative disorder;
 KM ovulatory disease; fertility related disorder; metabolic disorder;
 KM pituitary disorder; spermatogenesis; lung fibrosis; liver fibrosis;
 KM reperfusion injury; systemic cytokine damage; inflammatory condition;
 KM septic shock; sepsis; systemic inflammatory response syndrome; SIRS;
 KM ischaemia; endotoxin lethality; arthritis; nephritis; Crohn's disease;
 KM complement-mediated hyperacute rejection; chemokine-induced lung injury;
 KM inflammatory bowel disease; anaphylaxis; hypersensitivity; ss; probe;
 KM reverse transcriptase; PCR.
 XX
 OS Rattus sp.
 XX
 PN WO200214348-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-US025240.
 XX
 PR 11-AUG-2000; 2000US-0225035P.
 PR 08-MAY-2001; 2001US-00851465.
 XX
 PA (ISTP) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX
 PI Campbell RK, El Tayar N, He C, Kelton CA,
 XX
 DR WPI; 2002-339445/37.
 XX
 PT Novel beta subunits of glycoprotein, termed as beta related protein, are
 PT useful for treating or preventing a reproductive disorder in a subject.
 XX
 PS Example 5; Page 91; 158pp; English.
 XX
 CC The invention relates to an isolated beta-related protein (BRP) a novel
 CC glycoprotein hormone, its fragment, derivative, analogue, homologue or
 CC naturally occurring allelic variant and the nucleic acid encoding it.
 CC Also disclosed are novel alpha related proteins (ARP) and their nucleic
 CC acids. Also included are a nucleic acid vector comprising BRP, a host
 CC cell comprising the vector, a protein multimer comprising BRP or ARP
 CC polypeptide, and a second polypeptide, an antibody that selectively binds
 CC to BRP or the multimer, screening for a modulator of activity, or of
 CC latency or predisposition to a reproductive disorder comprising
 CC administering a test compound to an animal at risk from a pathology
 CC associated with BRP, where the animal recombinantly expresses an ARP/BRP
 CC polypeptide, measuring the activity of the polypeptide and comparing it
 CC to a control level, determining the presence of, or predisposition to, a
 CC reproductive disorder in a subject by measuring the amount of an ARP/BRP
 CC nucleic acid in a sample and comparing it to a control and expressing an
 CC ARP/BRP polypeptide as a product of an endogenous gene in a cell. The
 CC BRP/ARP proteins, nucleic acids, antibodies and multimers are useful for
 CC treating, preventing or diagnosing reproductive and cell proliferative
 CC disorders including ovulatory diseases, fertility related disorders,
 CC hypothyroidism and metabolic disorders effecting pituitary function or
 CC pituitary target organs e.g. adrenal gland, thyroid, gonad and liver,
 CC they are also useful for stimulating spermatogenesis, increasing the
 CC function of the thyroid glandular cells, regulating gonadal function,
 CC regulating gonadal hormone production, and promoting or suppressing
 CC fertility, gut protection or regeneration and treatment of lung or liver
 CC fibrosis, reperfusion injury in various tissues and conditions resulting
 CC from systemic cytokine damage, for promoting or inhibiting
 CC differentiation of tissues from precursor tissues or cells, inhibiting
 CC the growth of tissues, for treating inflammatory conditions including
 CC chronic or acute conditions, e.g. inflammation associated with infection

CC (such as septic shock, sepsis or systemic inflammatory response syndrome
 CC (SIRS)) ischaemia-reperfusion injury, endotoxin lethality, arthritis,
 CC complement-mediated hyperacute rejection, nephritis, cytokine or
 CC chemokine-induced lung injury, inflammatory bowel disease, Crohn's
 CC disease, anaphylaxis and hypersensitivity, and disorders resulting from
 CC over production of cytokines. The present sequence is an ARP or BRP
 CC reverse transcriptase (RT)-PCR probe
 XX
 SO Sequence 22 BP; 3 A; 10 C; 4 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 5275 GGGAGCAGGTGGCAGCCT 5292
 DB 19 GGGTGCAGGTGGCAGCCT 2
 XX
 RESULT 3172
 ABK68344
 ID ABK68344 standard; DNA; 22 BP.
 XX
 AC ABK68344;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse HYPLIP1 locus specific primer 354X16S #1.
 XX
 KM Mouse; primer; antilipemic; cardiant; hypotensive; anorectic; HYPLIP1;
 KM FCHL1; lipid disorder; familial combined hyperlipidaemia;
 KM coronary artery disease; atherogenic lipoprotein phenotype; cancer;
 KM hyperapobetalipoproteinaemia; hypertriglyceridaemia; obesity; ss;
 KM familial dyslipidaemic hypertension; syndrome X; insulin resistance;
 KM hypercholesterolaemia; chromosome 3.
 XX
 OS Mus sp.
 XX
 PN WO200220847-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US028181.
 XX
 PR 08-SEP-2000; 2000US-0231322P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Bodnar JS, Caesteclani LM, Chatterjee A, De Jong P, Luis AJ;
 PI Ohmen J, Ross D, Tafari S, Wu C;
 XX
 DR WPI; 2002-339808/37.
 XX
 PT Novel HYPLIP1 and FCHL1 genes and their sequence variations associated
 PT with lipid disorder and cancer, useful for prognosis, diagnosis and
 PT treatment of lipid disorders.
 XX
 PS Claim 11; Page 77; 102pp; English.
 XX
 CC This invention relates to the cDNA and protein sequences of novel
 CC proteins HYPLIP1 or FCHL1 and to sequence variations within these genes
 CC that have been shown to be associated with lipid disorders.
 CC Oligonucleotide probes that hybridise to the cDNA sequence are useful for
 CC analysing the expression of FCHL1 by detecting the expression of the mRNA
 CC transcript in the sample. A host cell transformed with the cDNA of the
 CC invention is useful for producing the protein by recombinant means.
 CC Pharmaceutical compositions based on the sequences of the invention are
 CC useful for treating or preventing a lipid disorder associated with
 CC expression of FCHL1 such as familial combined hyperlipidaemia, coronary
 CC artery disease, atherogenic lipoprotein phenotype, familial
 CC hyperapobetalipoproteinaemia, hypertriglyceridaemia, familial
 CC dyslipidaemic hypertension, syndrome X, obesity, insulin resistance and
 CC hypercholesterolaemia. The cDNA sequence is useful in the diagnosis or

CC prognosis of predisposition to lipid disorders and cancers, and also to
CC identify a molecule which enhances or decreases the HPLP1 or FCHL1
CC activity. The present sequence represents an oligonucleotide primer
CC specific for the mouse HPLP1 locus of the invention. The mouse HPLP1
CC locus is situated on chromosome 3

XX Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 544 GTGCAGCTTGTGAGTGACA 561

Db 4 GTGCAGCTTGTGAGTGACA 21

RESULT 3173

ABQ88519

AC ABQ88519;

DT 23-SEP-2002 (first entry)

DE Human GPCR reverse PCR primer SEQ ID NO:231.

XX Human; G protein coupled receptor; GPCR; GPCR; neuroprotective;
KW nootropic; anti-HIV; antiallergic; antidiabetic; cytoskeletal;
KW immunomodulator; antidiabetic; anorectic; haemostatic;
KW antibacterial; fungicide; protozoal; virucide; nephrotoxic; osteopathic;
KW cardiant; antidiabetic; hepatotoxic; antiparkinsonian; HIV;
KW vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes;
KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;
KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;
KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;
KW systemic lupus erythematosus; PCR primer; ss.

XX Homo sapiens;
OS Synthetic.

XX WO200250276-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US049347.

XX 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278159P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0293327P.
PR 16-AUG-2001; 2001US-0312902P.

XX (CURA-) CURAGEN CORP.

XX Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Scioire P,
PI Smithson G, Peyman JA, Macdougall JR, Stone C, Verneet CAM, Shenoy S;
PI Gunther E, Millet I, Tchervet VT, Anderson D, Gusev V, Malyankar UM,
XX Zhong H, Ellerman KE, Wolenc A;

XX WPI; 2002-557660/59.

XX New isolated human G-protein coupled receptor X (GPCRX) polypeptide,
PT useful for treating or preventing GPCR-associated disorders e.g.

PT diabetes, atherosclerosis, cancer or obesity.

XX Example 3; Page 217; 354pp; English.

XX ABQ88519 to ABQ88417 represent human G protein coupled receptor (GPCR)
CC CDNA sequences, and ABP51624 represent human GPCR proteins
CC from the present invention. GPCR sequences can have neuroprotective,
CC nootropic, anti-HIV, antiallergic, antidiabetic, anorectic, haemostatic,
CC immunomodulator, antifungal, antiparkinsonian, antidiabetic, cytoskeletal,
CC antibacterial, fungicide, protozoal, virucide, nephrotoxic, osteopathic,
CC cardiant, antidiabetic, hepatotoxic, antiparkinsonian
CC activities, and can be used in vaccines and gene therapy. GPCR proteins,
CC nucleic acid molecules, and antibodies from the present invention can be
CC used for manufacturing a medicament for treating or preventing a GPCR-
CC associated disorder or syndrome related to cell signal processing and
CC metabolic pathway modulation, such as cardiomyopathy, atherosclerosis,
CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,
CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus
CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be
CC used diagnostically to monitor protein levels in tissues as part of a
CC clinical testing procedure such as in determining the efficacy of a given
CC treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes
CC for the human GPCR of the present invention

XX Sequence 22 BP; 6 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1750 CTGCAGCTCATTTATTC 1767

Db 5 CAGCAGCTCATTTATTC 22

RESULT 3174

ABX09454

AC ABX09454;

DT 22-JAN-2003 (first entry)

DE Arteriosclerosis-detecting probe from HCF2.

XX Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy;
KW mutation; probe; ss.

XX Homo sapiens.

XX WO200272882-A2.

XX 19-SEP-2002.

XX 13-MAR-2002; 2002WO-EP002780.

XX 13-MAR-2001; 2001DE-01011925.

XX (OGHA-) OGHAM GMBH.

XX Cullen P, Seedorf U;

XX WPI; 2002-723374/78.

XX Determining genetic risk of arteriosclerosis, for clinical diagnosis,
PT comprises hybridizing patient nucleic acid with an array of probes
PT derived from risk-associated reference genes and their mutations.

XX Example 1; Page 126; 146pp; German.

XX This invention describes a novel method for determining the genetic risk
CC of arteriosclerosis both for clinical diagnosis and for population

CC studies. The method comprises: (i) selecting risk-associated reference
 CC nucleic acid sequences, including their functionally characterizing
 CC mutations; (ii) applying probes from these sequences, or their
 CC complements, to a carrier; (iii) hybridising the probes with a nucleic
 CC acid from (or synthesised from) a patient sample; and (iv) detecting and
 CC evaluating the hybridisation pattern. The method provides a quick,
 CC inexpensive and informative diagnosis, and makes possible a
 CC multifactorial analysis for detecting e.g. synergism between different
 CC mutations or mutations that when present alone carry no risk but are risk
 CC -associated in presence of other mutations. The results may be combined
 CC with known risk-assessment methods to provide a more reliable diagnosis,
 CC especially important with new therapeutic methods (e.g. gene therapy)
 CC that are directed against specific genes. All relevant mutations in a
 CC reference sequence can be screened for in a single test and the method is
 CC well suited to automation. ABX09147-ABX09676 represent probes used to
 CC illustrate the method of the invention

XX
 SQ Sequence 22 BP, 2 A; 9 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5703 CCTTCCTTCTCTCTCTCT 5720
 |||||
 DB 4 CCTTCTTCTCTCATCT 21

RESULT 3175
 ABS97168/c
 ID ABS97168 standard; DNA, 22 BP.
 XX
 AC ABS97168;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human CYP4501A2 promoter 1B sequencing primer #2.
 XX
 KM Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTS;
 KM cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HNMT; kallikrein 2; KLR2; nicotinamide-N-methyl transferase; NMNT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KM multidrug resistance 1; lactoferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; sequencing.

XX
 OS Homo sapiens.
 XX
 XX MO200257410-A2.
 XX
 XX PD 25-JUL-2002.
 XX
 XX PF 28-NOV-2001; 2001WO-US044838.
 XX
 XX PR 28-NOV-2000; 2000US-00724389.
 XX
 XX PA (DNAS-) DNA SCI LAB INC.
 XX
 XX PI Guida M, Hall J;
 XX
 XX DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers

PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.

XX
 XX Example 2; Page 101; 714pp; English.

PS This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02B1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTS), cyclooxgenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLR2, nicotinamide-N-methyl
 CC transferase (NMNT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactoferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NMNT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLR2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC sequencing primer used to sequence the polymorphic genes of the invention

XX
 SQ Sequence 22 BP; 13 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TGGACCTTTTCTTTTCTTTT 4476
 |||||
 DB 18 TGAACATTTTCTTTTCTTTT 1

RESULT 3176
 ABK71248
 ID ABK71248 standard; DNA; 22 BP.
 XX
 XX AC ABK71248;
 XX
 XX DT 15-JUL-2002 (first entry)
 XX
 XX DE Mouse HYPLIP1 locus PCR primer #321.
 XX
 XX KM Human; mouse; HYPLIP1, FCHL1, familial combined hyperlipidaemia; cancer;
 KM lipid disorder; PCR; primer; ss.
 XX
 XX OS Mus sp.
 XX
 XX PN MO200220848-A2.
 XX
 XX PD 14-MAR-2002.
 XX


```
PF 07-SEP-2001; 2001WO-US028182.
XX
XX 08-SEP-2000; 2000US-0231322P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
PI Bodnar JF, Castellani LM, Chatterjee A, De Jong P, Lusis AV,
PI Ohnen J, Ross D, Tafuri S, Wu C,
XX WPI; 2002-329882/36.
XX
XX New mouse HYPLIP1 and human FCHL1 (familial combined hyperlipidemia)
PT genes and their sequence variations, useful for diagnosing, treating or
PT preventing lipid disorders and cancers.
XX
XX Claim 11; Page 77; 102pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC variation of a mouse HYPLIP1 cDNA or a human FCHL1 (familial combined
CC hyperlipidaemia) gene. The FCHL1 polynucleotide, the FCHL1 polypeptide or
CC antibody immunoreactive to the FCHL1 polypeptide are useful for treating
CC or preventing cancer associated with expression of FCHL1, as well as for
CC treating lipid disorder. The mouse HYPLIP1 cDNA or human FCHL1 gene are
CC also useful for diagnosing or prognosis a predisposition to lipid
CC disorder and cancer. ABK70902-ABK71303 represent mouse HYPLIP1, human
CC FCHL1 coding sequences and PCR primers of the invention
XX
SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 544 GTCGACCTTGAGTGACA 561
DB 4 GTCGACATTTAGTGACA 21
XX
RESULT 3177
ABK15346
ID ABK15346 standard; DNA; 22 BP.
XX
AC ABK15346;
XX
DT 08-MAY-2002 (first entry)
XX
DE Cyclooxygenase-2 (COX-2) sense PCR primer DNA sequence.
XX
XX Mouse; cyclooxygenase-2; COX-2; PCR; primer; sepsis; pancreatitis; burn;
KM trauma; blood loss; penetrating injury; septic shock; pneumonia;
KM septicemia; bacteraemia; urinary tract infection; wound infection;
KM drug reaction; systemic inflammatory response syndrome; PGE_2;
KM prostaglandin E_2; receptor; ss.
XX
OS Mus sp.
XX
XX US2002006915-A1.
XX
PD 17-JAN-2002.
XX
PF 14-FEB-2001; 2001US-00782936.
XX
PR 15-FEB-2000; 2000US-0182524P.
XX
XX (STRO/) MACK STRONG V B.
PA (STAP/) STAPLETON P P.
PA (DALY/) DALY J M.
XX
XX Mack Strong VE, Stapleton PP, Daly JM,
XX WPI; 2002-179019/23.
XX
PT Treating a patient at risk for systemic inflammatory response syndrome
```

```
PT e.g. trauma involves administering cyclooxygenase-2 inhibitor or a drug.
XX
XX Example 1; Page 5; 39pp; English.
XX
XX The present invention relates to a new method of treating a patient at
CC risk for systemic inflammatory response syndrome. The method involves
CC administering a selective cyclooxygenase-2 inhibitor or a drug which
CC stimulates at least one prostaglandin E 2 (PGE 2) receptor or a drug
CC which interferes with binding of PGE 2 to at least one of PGE 2
CC receptors. The invention can be used for treating a patient at risk for
CC systemic inflammatory response syndrome e.g. sepsis, pancreatitis, burns,
CC trauma, life threatening blood loss from penetrating injury, or a patient
CC who has undergone surgery, septic shock, infections such as pneumonia,
CC septicemia, bacteraemia, urinary tract infection, wound infection or
CC drug reaction and can also be used for beneficial immune modulation. The
CC inhibitor or the drugs selectively modulate the immune response after
CC trauma, reduce the incidence of infectious complications and improve
CC survival after traumatic injury. The present nucleic acid sequence
CC represents the mouse cyclooxygenase-2 (COX-2) sense PCR primer that was
CC used in the invention with the COX-2 antisense PCR primer (ABK15347) for
CC the isolation and determination of COX-2 mRNA
XX
SQ Sequence 22 BP; 7 A; 11 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1575 CGCACCCCAAAACAGTG 1592
DB 2 CCACACCCCAACACAGTG 19
XX
RESULT 3178
ACA54762
ID ACA54762 standard; DNA; 22 BP.
XX
AC ACA54762;
XX
XX 05-JUN-2003 (first entry)
XX
DE Human NF-kappaB associated polynucleotide PCR primer #19.
XX
XX Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
KM inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
KM haematopoietic tumour; hyper-IGM syndrome; viral infection; asthma;
KM hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
KM X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
KM influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB;
KM experimental allergic encephalomyelitis; autoimmune disorder; wound;
KM hyper immune activity; acute phase response; hypercongenital condition;
KM birth defect; necrotic lesion; organ transplant rejection; pancreas;
KM signal transduction; hyperproliferative disorder; diabetes mellitus;
KM vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
KM Turner's syndrome; bacterial infection; cardiovascular disorder;
KM infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;
KM cytosarctic; hepatotropic; virucide; antineumatic; antiarteritic;
KM antiaesthetic; immunomodulator; antidiabetic; antiallergic;
KM neuroprotective; immunosuppressive; vulnery; antibacterial;
KM antifertility; antinaemic; antiporiatic; cerebroprotective; cardiac;
KM antiatherosclerotic; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200286076-A2.
XX
XX 31-OCT-2002.
XX
XX 19-APR-2002; 2002WO-US012636.
XX
XX 19-APR-2001; 2001US-0284962P.
XX
XX 26-APR-2001; 2001US-0286645P.
```


PR 09-JAN-2002; 2002US-0346986P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Carman J, Feder J, Nadler S;
 XX WPI, 2003-093119/08.
 DR
 PT Novel NF-kappab-associated polypeptides and polynucleotides useful for
 PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant
 PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.
 XX
 PS Example 3; Page 341; 608pp; English.
 XX
 CC The present invention relates to the isolation of human nuclear factor-
 CC kappab (NF-kappab) associated polypeptides and polynucleotides. The NF-
 CC kappab associated polypeptide and polynucleotide sequences are useful for
 CC preventing, treating or ameliorating various disorders including immune
 CC disorders, inflammatory disorders, cancers, disorders relating to
 CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
 CC haematopoietic tumours, hyper-igm syndromes, hypohidrotic ectodermal
 CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
 CC inconitinentia pigmenti, viral infections (e.g. those caused by human
 CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
 CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),
 CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
 CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental
 CC allergic encephalomyelitis (EAE), autoimmune disorders, disorders related
 CC to hyper immune activity, disorders related to aberrant acute phase
 CC responses, hypercongenital conditions, birth defects, necrotic lesions,
 CC wounds, organ transplant rejection, disorders related to aberrant signal
 CC transduction, hyperproliferative disorders, diseases of the pancreas
 CC (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological
 CC disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial
 CC infections, cardiovascular disorders, infertility, psoriasis and
 CC haemolytic anaemia. The present sequence represents a PCR primer used in
 CC the examples of the present invention
 XX
 SQ Sequence 22 BP; 3 A; 2 C; 7 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 683 TGCAGCCTTGATGCG 700
 Db 2 TGCAGCTTGGATGCG 19
 RESULT 3179
 ADA05936
 ID ADA05936 standard; DNA; 22 BP.
 XX
 AC ADA05936;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOVX reverse PCR primer SEQ ID NO:296.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX

PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-037360P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PA
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X,
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyanekar UW,
 PI Ort-T, Gorman L, Zethoven BD, Anderson DW, Zhong M, Carterton B,
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEJ, Shenoy SG,
 PI Shimkete RA, Rothensberg ME, Leach MD, Agree MU, Bergins C, DiPippo VA,
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI, 2003-381626/36.
 DR
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Example C; Page 384; 586pp; English.
 XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,

CC immunomodulator, cytosolic, neuroprotective, antiparkinsonian
CC and antilipase activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a PCR primer for a
CC human NOV sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 22 BP; 3 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5654 GCCTCATCTCTTACTTG 5671
Db 3 GCCTCATCTCTTACTG 20
RESULT 3180
ACD02547
ID ACD02547 standard; DNA; 22 BP.
XX
AC ACD02547;
XX
DT 31-JUL-2003 (first entry)
XX
DE PCR primer #2 for perennial ryegrass construct p2P221lp/TT16Baase.
XX
KM Perennial ryegrass; salt-inducible; salt responsive; ES13; CSA; LTI16;
KM glutathione peroxidase homologue; low-temperature-inducible protein;
KM salt-stress induced protein; SALT; WSR5; ALDP; plant tolerance;
KM early salt-responsive glucose 6 phosphate 1 dehydrogenase; salt shock;
KM plastidic fructose 1,6-bisphosphate aldolase homologue; osmotic stress;
KM environmental stress; sodium compartmentalisation; salt stress; PCR;
KM sodium ion influx; sodium ion efflux; plant metabolism; primer; ss.
XX
OS Lolium perenne.
XX
PN W02003031631-A1.
XX
PD 17-APR-2003.
XX
PF 04-OCT-2002; 2002WO-AU001346.
XX
PR 05-OCT-2001; 2001AU-00008112.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRERESEARCH LTD.
XX
PI Spengenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2003-381721/36.
XX
PT New substantially purified or isolated nucleic acid or nucleic acid
PT fragment encoding a salt-inducible or salt responsive protein, useful as
PT genetic markers for modifying plant tolerance to environmental and/or
PT osmotic stress.
XX
PS Example 6; Page 38; 297pp; English.
XX
CC The present invention relates to the isolation of perennial ryegrass
CC (Lolium perenne) nucleic acids and nucleic acid fragments encoding salt-
CC inducible or salt responsive proteins. The salt-inducible or salt
CC responsive proteins include salt-inducible proteins (ES13), glutathione
CC peroxidase homologues (CSA), low-temperature-inducible proteins (LTI16),
CC salt-stress induced proteins (SALT), early salt-responsive glucose 6

CC phosphate 1 dehydrogenase (WSR5), and plastidic fructose 1,6-bisphosphate
CC aldolase homologues (ALDP). The nucleic acids and nucleic acid fragments
CC are useful as genetic markers. The nucleic acids, nucleic acid fragments,
CC constructs, and vectors containing them are useful for modifying plant
CC tolerance to environmental stress and/or osmotic stress, plant capacity
CC to survive salt shock, compartmentalisation of sodium in a plant, sodium
CC ion influx and/or efflux in a plant, plant recovery after exposure to
CC salt stress, or plant metabolism under salt stress. The present sequence
CC represents a PCR primer used in the examples of the present invention
XX
SQ Sequence 22 BP; 8 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5500 ACTTGAAATACCCCGA 5517
Db 4 ACTTGAAATACCCCGA 21
RESULT 3181
ADA15387
ID ADA15387 standard; DNA; 22 BP.
XX
AC ADA15387;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mouse HYPLIP1 locus PCR primer #327.
XX
KM Mouse; PCR; primer; ss; HYPLIP1; FCHL1 variation; lipid disorder;
KM allele; anti-lipid disorder; anti-cancer therapy; gene therapy;
KM familial combined hyperlipidaemia; coronary artery disease;
KM atherogenic lipoprotein phenotype; hyperobesity; hypercholesterolaemia;
KM hypertriglyceridaemia; low density lipoprotein subclass B; LDL;
KM familial dyslipidaemia; hypertension; syndrome X; hypercholesterolaemia;
KM obesity; insulin resistance; cancer; cytostatic; antilipase;
KM hypotensive; anorectic.
XX
OS Mus sp.
XX
PN US2003064372-A1.
XX
PD 03-APR-2003.
XX
PF 07-SEP-2001; 2001US-00949428.
XX
PR 22-JUN-2000; 2000US-0213322P.
XX
PA (BODN/) BODNAR J S.
PA (CAST/) CASTELLANI L W.
PA (CHAT/) CHATTERJEE A.
PA (JONG/) JONG P D.
PA (LUST/) LUSTS A J.
PA (OHME/) OHMEN J.
PA (ROSS/) ROSS D.
PA (TAFU/) TAFURI S.
PA (WUCC/) WU C.
XX
PI Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusts AJ;
PI Ohmen J, Ross D, Tafuri S, Wu C;
XX
DR WPI; 2003-540780/51.
XX
PT Novel isolated polynucleotide comprising a mouse or human familial
PT combined hyperlipidaemia 1 gene having a variation that is associated with
PT a lipid disorder, useful for identifying susceptibility to the lipid
PT disorder.
XX
PS Claim 11; Page 40; 63pp; English.
XX
CC The invention discloses isolated polynucleotides comprising mouse HYPLIP1

CC cDNA sequence, mouse HYPLIP1 genomic DNA, or the homologous human
 CC familial combined hyperlipidaemia 1 (FCHL1) gene, where a variation in
 CC the sequence is associated with a lipid disorder. Also claimed is an
 CC isolated polypeptide comprising a variant form of the mouse HYPLIP1 amino
 CC acid sequence, or a variant form of a fully defined human FCHL1 amino
 CC acid sequence, where the variant is associated with the lipid disorder,
 CC an isolated polynucleotide having at least 12 contiguous nucleotides of
 CC the isolated polynucleotide, where the 12 contiguous nucleotides span
 CC the variation position, an isolated polypeptide comprising 4 contiguous
 CC amino acids of the encode polypeptides, where the 4 contiguous amino
 CC acids span the variation position, a kit for the detection of the FCHL1
 CC locus comprising, an isolated antibody, identifying susceptibility to a
 CC lipid disorder which comprises comparing the nucleotide sequence of the
 CC suspected FCHL1 allele with a wild-type FCHL1 nucleotide sequence, where
 CC the difference between the suspected allele and the wild-type sequence
 CC identifies a sequence variation of FCHL1 nucleotide sequence and a
 CC pharmaceutical composition. Also disclosed is a transgenic animal which
 CC carries an altered HYPLIP1 or FCHL1 allele and a method for screening
 CC drugs for inhibition or restoration of FCHL1 gene function as an anti-
 CC lipid disorder or anti-cancer therapy. The polynucleotides, polypeptides
 CC and antibodies are useful for treating or preventing (e.g. gene therapy)
 CC a lipid disorder associated with expression of FCHL1, for diagnosis or
 CC prognosis of predisposition to lipid disorder, and cancer and for
 CC treating a lipid disorder such as familial combined hyperlipidaemia,
 CC coronary artery disease, atherogenic lipoprotein phenotype,
 CC hyperapoproteinemia, hypertriglyceridaemia, low density
 CC lipoprotein (LDL) subclass B, familial dyslipidemic hypertension,
 CC syndrome X, hypercholesterolemia, obesity, insulin resistance and
 CC cancer. The sequence presented is a PCR primer which was used to amplify
 CC part of the mouse HYPLIP1 locus.

XX SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGACCTTGAGTGACA 561
 |||||
 DB 4 GTGCACATTGAGTGACA 21

RESULT 3182

AD85949 standard; DNA; 22 BP.

XX AC ADB95949;

XX DT 04-DEC-2003 (first entry)

XX DE Mouse HYPLIP1 PCR primer #327.

XX KM cytostatic; antilipemic; gene therapy; peptide therapy; HYPLIP1; FCHL1;
 KW cancer; metabolic pathway; cellular mechanism; lipid disorder;
 KM familial combined hyperlipidaemia; mouse; PCR; primer; ss.

XX OS Mus sp.

XX PN US2003054418-A1.

XX PD 20-MAR-2003.

XX PF 07-SEP-2001; 2001US-00949427.

XX PR 08-SEP-2000; 2000US-0231322P.

XX PA (BODNAR J S.
 PA (CAST/) CASTELLANI L W.
 PA (CHAT/) CHATTERJEE A.
 PA (JONG/) JONG P D.
 PA (LUSI/) LUSIS A J.
 PA (OHME/) OHMEN J.
 PA (ROSS/) ROSS D.

PA (TAFU/) TAFURI S.
 PA (WUCC/) WU C.
 XX PI Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusis AJ;
 PI Ohmen J, Ross D, Tafuri S, Wu C;
 XX DR WPI; 2003-695901/66.
 XX PT Novel human FCHL1 or mouse HYPLIP1 polypeptide, useful for drug
 PT screening, peptide therapy of lipid disorder or cancer.
 XX XX Claim 11; Page 39; 56pp; English.
 CC The invention describes an isolated polypeptide (I) comprising a variant
 CC form of a mouse HYPLIP1 polypeptide sequence (S1) or a human FCHL1
 CC polypeptide sequence (S2), not given in the specification, where the
 CC variant form is associated with cancer, or an amino acid sequence having
 CC at least 65 % sequence identity to (S1) or (S2). A composition comprising
 CC DNA encoding (I) is useful for treating or preventing cancer associated
 CC with expression of FCHL1. FCHL1 gene or HYPLIP1 gene and its product are
 CC useful for the study of metabolic pathway and cellular mechanism to
 CC identify other genes, receptors and relationships that contribute to
 CC lipid disorder and cancer. FCHL1 gene or its fragments are useful in gene
 CC therapy to increase the amount of the expression products of the gene for
 CC the treatment of lipid disorder or cancerous cells. The sequence
 CC variation of FCHL1 gene or HYPLIP1 gene is also useful in the diagnosis
 CC and prognosis of predisposition to lipid disorder and cancer. Antisense
 CC polynucleotide sequences are useful in preventing or diminishing the
 CC expression of HYPLIP1 or FCHL1 locus. This sequence represents a primer
 CC used in the analysis of the mouse HYPLIP1 gene.

XX SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGACCTTGAGTGACA 561
 |||||
 DB 4 GTGCACATTGAGTGACA 21

RESULT 3183

AD64386/c standard; DNA; 22 BP.

XX AC AD64386;

XX DT 01-JAN-2004 (first entry)

XX DE Human papillomavirus type 18 detection oligonucleotide #9.

XX KM probe; human papilloma virus; HPV; detection; identification; ss.

XX OS Human papillomavirus.

XX PN EP1302550-A1.

XX PD 16-APR-2003.

XX PF 10-OCT-2001; 2001EP-00123379.

XX PR 10-OCT-2001; 2001EP-00123379.

XX PA (KING-) KING CAR FOOD IND CO LTD.

XX PI Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Fan C;
 PI Hau H, Shin C, Yeh C, Kao Y, Pan C, Chan P;

XX DR WPI; 2003-432398/41.

XX PT Detector for identifying human papilloma virus subtypes, comprises
 PT carrier having two parts carrying first and second oligonucleotides that

PT respectively hybridize with DNA contained in first and second subtypes of
 PT the virus.
 XX
 PS Claim 4; SEQ ID NO 616; 221pp; English.
 CC The invention comprises oligonucleotides for detecting and identifying
 CC subtypes of human papilloma virus (HPV) contained in a sample. The
 CC oligonucleotides of the invention are useful for simultaneously detecting
 CC and identifying subtypes of HPVs. The present DNA sequence represents an
 CC HPV detection oligonucleotide of the invention.
 XX
 SQ Sequence 22 BP; 2 A; 10 C; 9 G; 1 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 40 AGGCTCCGCGCGCGCGC 57
 DB 22 AGGCTTGGCGCGCGCGC 5
 RESULT 3184
 ADC98229
 ID ADC98229 standard; DNA; 22 BP.
 AC
 AC ADC98229;
 DT 15-JAN-2004 (first entry)
 XX
 DE Mouse type I hair keratin Ha3 PCR primer mHa3 247R.
 XX
 KW Mouse; murine; hard keratin; type I hair keratin; Ha3; Bg8;
 KW hard keratin expression; hair loss; hair shaft injury; hair growth;
 KW skin disease; tongue disease; nail disease; hair disease;
 KW dot keratoderm; dermatological; trichological; Tagman analysis;
 KW expression analysis; PCR; primer; ss.
 XX
 OS Mus musculus.
 OS
 PN WO2003087362-A1.
 PN
 PD 23-OCT-2003.
 PD
 XX 02-APR-2003; 2003WO-JP004236.
 PF
 XX 03-APR-2002; 2002JP-00100843.
 PR
 PR 20-DEC-2002; 2002JP-00369385.
 XX
 PA (BANY) BANYU PHARM CO LTD.
 XX
 PI Inoue S, Nambu T, Shimomura T, Itadani H, Tanaka K;
 PI
 DR WPI, 2003-833733/77.
 XX
 PT Protein for treatment and prevention of diseases associated with the
 PT function of hard keratin producing cells, such as hair loss, hair shaft
 PT injury, abnormal or insufficient hair growth, diseases of the skin,
 PT tongue, nails and hair.
 XX
 PS Example 5; SEQ ID NO 11; 67pp; Japanese.
 PS
 XX The invention relates to a human G protein coupled receptor (GPCR), Bg8
 CC (ADC98222), and nucleic acids encoding it (ADC98221). The human Bg8 gene
 CC is located on chromosome 19p12. Bg8 is involved in controlling the
 CC expression of hard keratin such as the type I hair keratins Ha3 and Ha4.
 CC The invention also relates to antibodies against Bg8, a drug screening
 CC method using the antibodies, the compounds identified, and a method for
 CC detecting and controlling functional abnormalities in cells producing
 CC hard keratin. The invention provides for the treatment and prevention of
 CC diseases associated with the function of hard keratin-producing cells,
 CC such as hair loss, hair shaft injury, abnormal or insufficient hair
 CC growth, diseases of the skin, tongue, nails and hair, and abnormal

CC formation of hard keratin such as dot keratoderm. Sequences ADC98228-
 CC ADC98229 represent mouse type I hair keratin Ha3 PCR primers used with
 CC probe ADC98227) in Tagman expression analysis of Bg8-mediated expression
 CC of type I hair keratin Ha3 in mouse hair follicle tissue.
 XX
 SQ Sequence 22 BP; 5 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1892 ACCTGCGCTCAAGATCA 1909
 DB 1 ACCTGTGCTTCAGATCA 18
 RESULT 3185
 ADE47875
 ID ADE47875 standard; DNA; 22 BP.
 XX
 AC ADE47875;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human NOVA forward PCR primer SEQ ID NO:237.
 XX
 KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;
 KW dermatological; anorectic; cyostatic; antidiabetic; haemostatic;
 KW anti-HIV; antiaesthetic; antibacterial; antiviral; neuroprotective;
 KW nootropic; antiparkinsonian; antilipemic; gene therapy; vaccine; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO2003076642-A2.
 PN
 PD 18-SEP-2003.
 PD
 XX 02-AUG-2002; 2002WO-US024459.
 PF
 XX 02-AUG-2001; 2001US-0309501P.
 PR
 PR 03-AUG-2001; 2001US-0310291P.
 PR
 PR 08-AUG-2001; 2001US-0310951P.
 PR
 PR 09-AUG-2001; 2001US-0311232P.
 PR
 PR 13-AUG-2001; 2001US-0311979P.
 PR
 PR 14-AUG-2001; 2001US-0312203P.
 PR
 PR 17-AUG-2001; 2001US-0313156P.
 PR
 PR 17-AUG-2001; 2001US-0313201P.
 PR
 PR 20-AUG-2001; 2001US-0313702P.
 PR
 PR 21-AUG-2001; 2001US-0314031P.
 PR
 PR 23-AUG-2001; 2001US-0314466P.
 PR
 PR 28-AUG-2001; 2001US-0315403P.
 PR
 PR 29-AUG-2001; 2001US-0315853P.
 PR
 PR 31-AUG-2001; 2001US-0316508P.
 PR
 PR 21-SEP-2001; 2001US-0323936P.
 PR
 PR 03-DEC-2001; 2001US-0338078P.
 PR
 PR 05-FEB-2002; 2002US-0354655P.
 PR
 PR 05-MAR-2002; 2002US-0361764P.
 PR
 PR 19-APR-2002; 2002US-0373825P.
 PR
 PR 15-MAY-2002; 2002US-0380971P.
 PR
 PR 15-MAY-2002; 2002US-0380980P.
 PR
 PR 16-MAY-2002; 2002US-0381039P.
 PR
 PR 28-MAY-2002; 2002US-0383761P.
 PR
 PR 29-MAY-2002; 2002US-0383887P.
 PR
 PR 01-AUG-2002; 2002US-00210130.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Zexhuen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK, Vose EZ;
 PI Pena CE, Shimkets RA, Li L, Berghs C, Zhong M, Casman ST, Gorman L;
 PI Boldog FU, Padigar M, Smithson G, Shenoy SG, Ji W, Gorman L;
 PI Verne CM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
 PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee WL;

PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA,
 PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;
 PI Taupier RJ, Caterton E;
 XX WPI; 2003-779062/73.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 PS
 XX Example 49; SEQ ID NO 237; 562bp; English.
 CC The invention relates to a novel (NOVX) human polypeptide. A polypeptide
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
 CC haemostatic, anti-HIV, antiaesthetic, antibacterial, virucide,
 CC neuroprotective, nootropic, antiparkinsonian, and antilipase activity.
 CC A polynucleotide encoding a polypeptide of the invention may have a use
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, the disease selected from a pathology
 CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting
 CC disorders associated with chronic diseases. The nucleic acids are also
 CC used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine, and pharmacogenomics. The polypeptides are also
 CC useful as vaccines. The present sequence represents a PCR primer used in
 CC the invention.
 CC
 XX
 SQ Sequence 22 BP; 1 A; 11 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5318 CTCCTCTTCTCTCTCTT 5335
 Db 3 CTCCTCTTCTCTCTCT 20
 RESULT 3186
 ADE47878
 ID ADE47878 standard; DNA; 22 BP.
 XX
 AC ADE47878;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human NOVX forward PCR primer SEQ ID NO:240.
 XX
 KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;
 KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;
 KW anti-HIV; antiaesthetic; antibacterial; virucide; neuroprotective;
 KW nootropic; antiparkinsonian; antilipase; gene therapy; vaccine; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003076642-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024459.
 XX
 PR 02-AUG-2001; 2001US-0309501P.
 PR 03-AUG-2001; 2001US-0310291P.
 PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 14-AUG-2001; 2001US-0312203P.
 PR 17-AUG-2001; 2001US-0313156P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315853P.
 PR 31-AUG-2001; 2001US-0316508P.
 PR 21-SEP-2001; 2001US-0323936P.
 PR 03-DEC-2001; 2001US-0338078P.
 PR 05-FEB-2002; 2002US-0354655P.
 PR 05-MAR-2002; 2002US-0361764P.
 PR 19-APR-2002; 2002US-0373825P.
 PR 15-MAY-2002; 2002US-0380971P.
 PR 15-MAY-2002; 2002US-0380980P.
 PR 16-MAY-2002; 2002US-0381039P.
 PR 28-MAY-2002; 2002US-0383761P.
 PR 29-MAY-2002; 2002US-0383887P.
 PR 01-AUG-2002; 2002US-00210130.
 XX
 XX (CURAGEN CORP.)
 XX
 PI Zernhusen BD, Paturajan M, Kekuda R, Miller CE, Rieger DK;
 PI Pena CE, Shinkels RA, Li L, Berghe C, Zhong M, Casman SD, Voas EZ;
 PI Boldog FI, Patigara M, Smithson G, Shenoy SG, Ji W, Gorman L;
 PI Verne CM, Lettice MW, Guo X, Anderson DW, Szytek KA, Gerlach VJ;
 PI Burgess CE, Kaitumbosov NV, Ort T, Ellerman K, Raetelli L, Agee ML;
 PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;
 PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;
 PI Taupier RJ, Caterton E;
 XX
 DR WPI; 2003-779062/73.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 PS
 XX Example 49; SEQ ID NO 240; 562bp; English.
 CC The invention relates to a novel (NOVX) human polypeptide. A polypeptide
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
 CC haemostatic, anti-HIV, antiaesthetic, antibacterial, virucide,
 CC neuroprotective, nootropic, antiparkinsonian, and antilipase activity.
 CC A polynucleotide encoding a polypeptide of the invention may have a use
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, the disease selected from a pathology
 CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting
 CC disorders associated with chronic diseases. The nucleic acids are also
 CC used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine, and pharmacogenomics. The polypeptides are also
 CC useful as vaccines. The present sequence represents a PCR primer used in
 CC the invention.
 CC
 XX
 SQ Sequence 22 BP; 1 A; 11 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5318 CTCCTCTTCTCTCTCTT 5335
 Db 3 CTCCTCTTCTCTCTCT 20

```

Db          3  CTTCTCCTTTTACACTCTCT 20

RESULT 3187
AAAN70276/c
ID  AAAN70276 standard; DNA; 26 BP.
XX
XX
AC  AAAN70276;
XX
DT  03-OCT-2002 (revised)
DT  26-MAY-1991 (first entry)
XX
DE  Sequence of scissile link probe MRC060 (HL).
XX
XX  Hybridisation; probe; ss.
XX
OS  Synthetic.
XX
PN  EP227976-A.
XX
PD  08-JUL-1987.
XX
PF  04-DEC-1986; 86EP-00116906.
XX
PR  05-DEC-1985; 85US-00805279.
XX
PA  (MEIO-) MEIOGENICS INC.
XX
PI  Duck P, Bender R, Crosby W, Robertson JG;
XX
XX  WPI: 1987-186567/27.
DR
XX
XX  Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT  linked by a scissile linkage.
XX
XX  Example; p29; 46pp; English.
PS
XX
XX  The patent claims a new molecule of formula (NA1---S---NA2)n. NA1 and
CC  NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC  linkage; n 1 or 1,000, which is used for the detection of specific DNA
CC  or RNA sequences in a test soln. The scissile link probes may be PL
CC  (Permanent Linkage to Solid Support) or HL (Hydrolyzable Linkage to Solid
CC  Support). The differential liability of DNA and RNA may be exploited in a
CC  heterogeneous system when the scissile linkage is an RNA molecule. In the
CC  examples, counter probe molecules 9 through 16 were used to determine
CC  suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC  OS field.)
SQ
SQ  Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match          0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0.

QY          4012 AAATGAGAAAAAGAGAAACAA 4037
Db          26 AAAAAAAAAAAAAAAAAAAAAA 1
      ||| | | | | | | | | | | | | | | |
      ||| | | | | | | | | | | | | | | |

RESULT 3188
AAAN70275/c
ID  AAAN70275 standard; DNA; 26 BP.
XX
XX
AC  AAAN70275;
XX
DT  03-OCT-2002 (revised)
DT  26-MAY-1991 (first entry)
XX
DE  Sequence of scissile link probe MRC059 (HL).
XX
XX  Hybridisation; probe; ss.
XX
OS  Synthetic.

```

XX	PN	EP27976-A.
XX	PD	08-JUL-1987.
XX	PX	
XX	PF	04-DEC-1986; 86EP-00116906.
XX	PR	05-DEC-1985; 85US-00805279.
XX	PA	(MEIO-) MEIOGENICS INC.
XX	PI	Duck P, Bender R, Crosby W, Robertson JG;
XX	DR	WPI; 1987-186567/27.
XX	PT	Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX	PS	linked by a scissile linkage.
XX	PP	Example; p29; 46pp; English.
XX	CC	The patent claims a new molecule of formula (NA1----S-----NA2)n. NA1 and
XX	CC	NA2 are noncomplementary nucleic acid sequences; --S-- = a scissile
XX	CC	linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX	CC	or RNA sequences in a test soln. The scissile link probes may be PL
XX	CC	(Permanent Linkage to Solid Support) or HL (Hydrolyzable Linkage to Solid
XX	CC	Support). The differential liability of DNA and RNA may be exploited in a
XX	CC	heterogeneous system when the scissile linkage is an RNA molecule. In the
XX	CC	examples, counter probe molecules 9 through 16 were used to determine
XX	CC	suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
XX	CC	OS field.)
XX	SQ	Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
XX	QM	
XX	Query Match	0.2%; Score 14.8; DB 1; Length 26;
XX	Best Local Similarity	73.1%; Pred. No. 2.6e+03;
XX	Matches 19; Conservative	0; Mismatches 7; Indels 0; Gaps 0.
XX	OY	4012 AAAATGAGAAAAAAGAGAAACAA 4037 26 AAAAAAAAAAAAAAAAAAAAAA 1
XX	ID	AA992241/C
XX	AC	AA992241 standard; DNA; 26 BP.
XX	DT	25-MAR-2003 (revised)
XX	DT	31-OCT-2002 (revised)
XX	DT	25-APR-1990 (first entry)
XX	SS	probe MRCO59.
XX	KM	Probe MRCO59; solid support; ribonuclease.
XX	OS	Synthetic.
XX	FT	Key Location/Qualifiers
XX	FT	misc_feature 1..10
XX	FT	/*tag= a
XX	FT	/note= "deoxyribonucleotides."
XX	FT	11..14
XX	FT	/*tag= b
XX	FT	/note= "ribonucleotides."
XX	FT	15..26
XX	FT	/*tag= c
XX	FT	/note= "deoxyribonucleotides."
XX	PN	WO910415-A.
XX	PX	
XX	PD	02-NOV-1989.
XX	XX	

```

PF 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX (MEIO-) MEIOGENICS INC.
XX
XX Duck P, Bender R;
XX WPI, 1989-339977/46.
XX
XX Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX
XX Probe MRC059 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3190
AAN92242/c
ID AAN92242 standard; DNA; 26 BP.
XX
XX AAN92242;
AC
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
XX SS probe MRC060.
DE
XX
XX Probe MRC060; solid support; ribonuclease.
KM
XX
XX Synthetic.
OS
XX
XX Key
FH Location/Qualifiers
XX 1..12
FT /*tag= a
FT /*note= "deoxyribonucleotides."
FT 13..16
FT /*tag= b
FT /*note= "ribonucleotides."
FT 17..26
FT /*tag= C
FT /*note= "deoxyribonucleotides."
XX
XX WO8910415-A.
XX
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX

```

```

PA (MEIO-) MEIOGENICS INC.
XX
XX Duck P, Bender R;
XX WPI, 1989-339977/46.
XX
XX Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX
XX Probe MRC060 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3191
AAF77536/c
ID AAF77536 standard; DNA; 26 BP.
XX
XX AAF77536;
AC
XX 23-MAY-2001 (first entry)
DT
XX
XX CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
XX CDNA library production; SCLA; gene chip technology;
KM differential screening; pathological diagnosis; genetic identification;
KM single-cell CDNA library amplification; db.
XX
XX Synthetic.
OS
XX
XX US6197554-B1.
PN
XX
XX 06-MAR-2001.
PD
XX
XX 20-NOV-1998; 98US-00197951.
PF
XX 20-NOV-1998; 98US-00197951.
PR
XX
XX (LINS/) LIN S.
XX (CHUO/) CHUDONG C.
XX (YING/) YING S.
XX
XX Lin S, Chuong C, Yang S;
PI
XX
XX WPI, 2001-243448/25.
DR
XX
XX Generating a complete full-length CDNA library from single cells for use
PT in gene chip technology, involves reverse transcribing intracellular
PT mRNA, adding polynucleotide tail and amplifying formed cDNAs.
XX
XX Disclosure; Col 11-12; 11pp; English.
XX
XX The present invention describes a method of producing full-length CDNA
CC

```


CC libraries from single cells, designated single-cell cDNA library
CC amplification (SGLA). The method is useful in gene chip technology,
CC differential screening, pathological diagnosis, physiological prognosis
CC and genetic identification. No further information about this sequence is
CC given in the specification
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 3192
AAD03682/C
ID AAD03682 standard; DNA; 26 BP.
AC AAD03682;
XX
XX
DT 19-JUN-2001 (first entry)
XX
XX
DE Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.
XX
XX
KW Human; phosphodiesterase; PDE; zcytor13; antiaesthetic; antiarthritic;
KW antipsoriatic; cytoskeletal; antiatherosclerotic; antiinfectivity;
KW cardiant; antiinflammatory; dermatological; wound healing; antiviral;
KW antibacterial; therapy; inflammatory bowel disease; diverticulitis;
KW spermatogenesis; sperm capacitation; immunosuppressive; vaccine;
KW cancer; reperfusion ischemia; psoriasis; melanoma; myocarditis; PID;
KW pelvic inflammatory disease; eczema; scleroderma; vasorestriction;
KW heart arrhythmia; congestive heart disease; muscle spasms; fatigue;
KW chromosomal abnormality; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX
PN WO200125444-A2.
XX
PD 12-APR-2001.
XX
XX
PE 06-OCT-2000; 2000WO-US027734.
XX
XX
PR 07-OCT-1999; 99US-00414025.
XX
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Preenell SR, Novak JE, Gao Z;
XX
XX
DR WPI; 2001-266312/27.
XX
XX
PT Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide
PT encoding it, for detecting human chromosomal abnormalities, identifying
PT modulators and treating inflammatory and cardiovascular diseases.
XX
XX
PS Example 1C; Page 118; 122pp; English.
XX
XX
CC The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA
CC and its corresponding protein. Zcytor13 protein is used to promote wound
CC healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC to identify modulators (e.g. agonists or antagonists). Zcytor13, its
CC agonists or antagonists are useful in the treatment of inflammatory heart
CC or cardiovascular conditions, muscle inflammation, inflammation during
CC and after surgery, arthritis, asthma, inflammatory bowel disease or
CC diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC immunosuppressive or anti-fertility vaccine and for treating male
CC infertility. Zcytor13 protein and its antibodies are used to diagnose
CC cancer, reperfusion ischemia, asthma, psoriasis and melanoma. Zcytor13
CC proteins are used to enhance fertilisation. Zcytor13 antagonists are used
CC to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),
CC psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13

CC sequences and/or its antibodies are useful for treatment of disorders
CC associated with vasoconstriction, heart arrhythmia, congestive heart
CC disease, muscle spasms and fatigue. They are used for detecting human
CC chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.
CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins
CC are useful for enhancing in vivo killing of target tissue. The present
CC sequence is a polyA PCR primer, ZC7764b which is used to isolate full
CC length zcytor13 cDNA by screening human placental cDNA library
XX
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4011 TAAATGAGAAAAAGAGAAACAA 4036
Db 26 TAAAAAAAAAAAAAAAAAAAAA 1
RESULT 3193
AAF23526/C
ID AAF23526 standard; DNA; 26 BP.
AC AAF23526;
XX
XX
DT 22-MAR-2001 (first entry)
XX
XX
DE Primer #4.
XX
XX
KW Primer; mRNA; amplification; ss.
XX
OS Unidentified.
XX
XX
PN WO200075356-A1.
XX
PD 14-DEC-2000.
XX
XX
PE 04-JUN-1999; 99WO-US012461.
XX
XX
PR 04-JUN-1999; 99WO-US012461.
XX
XX
PA (LINS//) LIN S.
PA (YING//) YING S.
PA (CHUO//) CHUONG C.
PA (WIDE//) WIDELITZ R B.
XX
XX
PI Lin S, Ying S, Chuong C, Widelitz RB;
XX
XX
DR WPI; 2001-061734/07.
XX
XX
PT Generating amplified messenger RNA sequences from single cells, involves
PT cycling steps of reverse transcription, denaturation, double-stranded DNA
PT sequences and in vitro transcription.
XX
XX
PS Disclosure; Page 17; 31pp; English.
XX
XX
CC The present invention relates to generating amplified messenger RNAs with
CC polymerase reaction activity, comprising cycling steps of reverse
CC transcription, denaturation, double-stranded cDNA synthesis and in vitro
CC transcription. The invention is used for generating amplified mRNAs from
CC limited mRNAs from single cells
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1


```

RESULT 3194
AAS20596/c
ID AAS20596 standard; DNA; 26 BP.
XX
XX AAS20596;
AC
XX 23-APR-2002 (first entry)
DT
XX
XX Human zsig63 cDNA sequencing primer ZC7764a.
DE
XX
XX Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KM microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KM gastrointestinal disease; urinary tract infection; vaginal infection;
KM skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KM acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KM chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX
XX Homo sapiens.
OS
XX
XX US6331413-B1.
PN
XX
XX 18-DEC-2001.
PD
XX
XX 17-MAR-2000; 2000US-00527345.
PF
XX
XX 17-MAR-1999; 99US-0124820P.
PR
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX
XX Adler DA, Sheppard PO;
PI
XX
XX WPI; 2002-096707/13.
DR
XX
XX Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
PT
XX
XX Example 1; Col 53; 29pp; English.
PS
XX
XX The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
CC
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 4011 TAAATGAGAAAAAGAGAAACA 4036
DB 26 TAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 3195
AAS2638/c
ID AAS2638 standard; DNA; 26 BP.
XX
XX AAS2638;
AC
XX
XX 15-NOV-2002 (first entry)
DT
XX
XX Human secreted salivary protein zsig63 PCR primer ZC7764a.
DE
XX
XX Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KM

```

```

KM antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KM fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KM tooth decay; periodontal disease; thrush; gastrointestinal disease;
KM urinary tract infection; vaginal infection; skin infection; microflora;
KM epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KM chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KM incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KM chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KM digestion; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US2002081701-A1.
PN
XX
XX 27-JUN-2002.
PD
XX
XX 03-AUG-2001; 2001US-00922480.
PF
XX
XX 17-MAR-1999; 99US-0124820P.
PR
XX
XX 17-MAR-2000; 2000US-00527345.
PA
XX
XX (ADLER) ADLER D A.
PA (SHEP) SHEPPARD P O.
PI
XX
XX Adler DA, Sheppard PO;
PI
XX
XX WPI; 2002-635468/68.
DR
XX
XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
PT
XX
XX Example 1; Page 29; 33pp; English.
PS
XX
XX The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
CC
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 4011 TAAATGAGAAAAAGAGAAACA 4036
DB 26 TAAAAAAAAAAAAAAAAAAAAA 1

```

XX	RESULT 3196
ID	AAD45055/c
XX	AAD45055 standard; DNA; 26 BP.
AC	
XX	
XX	AAD45055;
DT	27-DEC-2002 (first entry)
DE	ZC7764a primer used in the identification of human zsig63 DNA.
KM	Human; secreted salivary protein; zsig63 protein; host defense protein;
KM	immune modulating factor; antipathogenic; cell-cell signalling molecule;
KM	growth factor; cytokine; growth factor hormone activity; dental carries;
KM	infection; tooth decay; periodontal disease; gastrointestinal disease;
KM	thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KM	anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KM	gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KM	forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
OS	
XX	Homo sapiens.
PN	US2002090677-A1.
PD	11-JUL-2002.
PF	03-AUG-2001; 2001US-00923236.
PR	17-MAR-1999; 99US-0124820P.
PR	17-MAR-2000; 2000US-00527345.
PA	(ADLER/) ADLER D A.
PA	(SHEP/) SHEPPARD P O.
PI	Adler DA, Sheppard PO;
XX	
DR	WPI; 2002-642378/69.
PT	Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT	agent for treating microbial infection, dental carries, periodontal
PT	disease, thrush gastrointestinal disease, and for aiding digestion.
PS	
XX	Example 1; Page 30; 33pp; English.
CC	The invention relates to human secreted salivary polypeptide designated
CC	as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC	can be used in detecting agonists and antagonists of its activity, and it
CC	also useful as a host defense polypeptide, immune modulating factor,
CC	antipathogenic polypeptide, cell-cell signalling molecule, growth factor
CC	cytokine, or as secreted extracellular matrix associated proteins with
CC	growth factor hormone activity. It is useful for treating conditions
CC	associated with pathological microbes, including bacterial, fungal and
CC	viral infections, for treating dental carries (tooth decay), periodontal
CC	disease, thrush and gastrointestinal disease, for treating urinary tract
CC	infection, vaginal infection and for preventing infection in skin and
CC	other epithelial wounds. zsig63 is useful for establishing normal
CC	microflora and protect against pathogenic colonisation and invasion,
CC	treating chronic tissue damage e.g. damage in extremities associated with
CC	diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC	of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC	prostate gland. It is also therapeutically useful for aiding digestion.
CC	Polynucleotides of the invention are used in gene therapy for increasing
CC	or inhibiting zsig63 activity, for detecting abnormalities on human
CC	chromosome 4 associated with disease or other human traits and as
CC	diagnostics in forensic DNA profiling. Sequences of the invention are
CC	useful for stimulating proliferation or differentiation of cardiac
CC	myocytes, for proliferation or differentiation of adipocytes and for
CC	inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC	presenting sequence is a primer used in the identification of human zsig63
CC	DNA
XX	
XQ	Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match	0.2%	Score 14.8	DB 1	Length 26
Best Local Similarity	73.1%	Pred. No. 2.6e+03		
Matches 19	Conservative 0	Mismatches 7	Indels 0	Gaps 0
Qy	4011 TAAATGAGAAAAAGAGCAAAACA	4036		
Db	26 TAAATGAGAAAAAGAGCAAAACA	1		
RESULT 3197				
AAS20671/C				
ID	AAS20671 standard; DNA; 26 BP.			
XX				
AC	AAS20671;			
XX				
DT	09-APR-2002 (first entry)			
DE	Human zalphall ligand sequencing primer ZC7764a.			
XX				
KW	Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;			
KM	natural killer cell proliferation; T-cell proliferation;			
KW	B-cell proliferation; anti-tumour response; immune system;			
KM	immunostimulant; cyclostatic; human; sequencing primer; ss.			
XX				
OS	Homo sapiens.			
XX				
PN	US6307024-B1.			
XX				
PD	23-OCT-2001.			
XX				
PF	09-MAR-2000; 2000US-00522217.			
XX				
PR	09-MAR-1999; 99US-0123547P.			
XX				
PR	11-MAR-1999; 99US-0123904P.			
XX				
PR	01-JUL-1999; 99US-0142013P.			
XX				
PA	(Zymo) ZYMOGENETICS INC.			
XX				
PI	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;			
XX				
PI	Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;			
XX				
XX	WPI; 2002-040208/05.			
XX				
PT	New zalphall ligand polypeptides and polynucleotides, useful for			
XX				
PT	stimulating proliferation, activation, differentiation and/or induction			
XX				
PT	of inhibition of specialized cell function, or for stimulating an			
XX				
PT	antigenic response.			
XX				
PS	Example 7; Col 139; 105BP; English.			
XX				
CC	The present invention relates to the isolation of a novel cytokine,			
XX				
CC	zalphall ligand and the polynucleotide encoding it. The invention also			
XX				
CC	gives the sequence for the zalphall receptor and the polynucleotide			
XX				
CC	encoding it. The zalphall ligand polypeptide stimulates proliferation of			
XX				
CC	natural killer (NK) cells or NK cell progenitors, the activation of NK			
XX				
CC	cells, proliferation of T-cells, proliferation of B-cells stimulated with			
XX				
CC	anti-CD40 antibodies, stimulates an antigenic response in a mammal, and			
XX				
CC	reduces proliferation of B-cells stimulated with anti-IgM antibodies. The			
XX				
CC	zalphall ligand polypeptide is also useful in preparing antibodies that			
XX				
CC	bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can			
XX				
CC	be used as probes or primers to clone regions of a zalphall ligand gene,			
XX				
CC	and in gene therapy. Zalphall ligand may also be used to identify			
XX				
CC	inhibitors of its activity, to enhance the generation of anti-tumour			
XX				
CC	responses with or without the infusion of donor lymphocytes, and to			
XX				
CC	activate or stimulate the immune system. The present sequence represents			
XX				
CC	a sequencing primer used to sequence cDNA clones in the isolation of			
XX	human zalphall ligand			
XX				
SO	Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;			
XX				
Query Match	0.2%	Score 14.8	DB 1	Length 26
Best Local Similarity	73.1%	Pred. No. 2.6e+03		
Matches 19	Conservative 0	Mismatches 7	Indels 0	Gaps 0

QY 4011 TAAATGAGAAAAAGAGAAAAACA 4036
 |||||
 DB 26 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3198
 AAD43853/C
 ID AAD43853 standard; DNA; 26 BP.
 XX
 AC AAD43853;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Primer #2 used to illustrate the method of the invention.
 XX
 KM Single stranded polynucleotide tag; cleavage agent; gene expression;
 KM primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200259357-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-DK000052.
 XX
 PR 24-JAN-2001; 2001DK-00000126.
 PR 12-FEB-2001; 2001US-0267704P.
 XX
 PA (GENO-) GENOMIC EXPRESSION APS.
 XX
 PI Pedersen ML;
 PT
 DR WPI; 2002-636542/68.
 XX
 PT Obtaining single stranded polynucleotide tags from a biological sample,
 PT for analyzing gene expression or diagnosing clinical conditions,
 PT comprises employing nicking endonucleases that cleave complementary
 PT strands.
 XX
 PS Example; Page 294; 302pp; English.
 XX
 CC The invention relates to a method for obtaining a single stranded
 CC polynucleotide tag from a biological sample by cleaving one of the
 CC complementary strands of a double stranded polynucleotide with a cleavage
 CC agent capable of recognising a double stranded polynucleotide comprising
 CC complementary strands and cleaving only one of the strands of the
 CC polynucleotide in the process of generating a single stranded
 CC polynucleotide tag. The method is useful for separating, analysing,
 CC quantifying or obtaining single stranded polynucleotides comprising tags
 CC originating partly, and preferably wholly from a source of DNA and/or RNA
 CC in a sample comprising biological cells. The method is particularly for
 CC analysing gene expression (expression profiling or differential gene
 CC expression), or in diagnosing clinical conditions. The present sequence
 CC is a primer used in the exemplification of the invention
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2.6e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4012 AAAATGAGAAAAAGAGAAAAACA 4037
 |||||
 DB 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3199
 AB224784/C
 ID AB224784 standard; DNA; 26 BP.
 XX
 AC AB224784;
 XX

XX
 DT 07-APR-2003 (first entry)
 XX
 DE Oligodeoxynucleic acid molecule ODN 24.
 XX
 KM Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
 KM ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..26
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note="thiophosphate backbone"
 XX
 PN WO200295027-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 17-MAY-2002; 2002WO-EP005448.
 XX
 PR 21-MAY-2001; 2001AT-0000805.
 XX
 PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Lingnau K, Schellack C, Schmidt W;
 XX
 DR WPI; 2003-183880/18.
 XX
 PT New oligodeoxynucleic acid molecules useful for the preparation of
 PT vaccine.
 XX
 PS Example 8; Page 32; 57pp; English.
 XX
 CC The present sequence is that of a thiosubstituted oligodeoxynucleic acid
 CC (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
 CC invention is based on the discovery that ODNs containing deoxyuridine
 CC residues (U-ODNs) have an immunostimulatory effect comparable to, or in
 CC many instances greater than, ODNs containing Cpg motifs, producing higher
 CC numbers of specific T cells to a given antigen. The U-ODNs do not induce
 CC the systemic production of pro-inflammatory cytokines and, in contrast to
 CC Cpg ODNs, are not dependent on a specific motif or a palindromic
 CC sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
 CC Combining the U-ODN with an antigen strongly increases the potential of
 CC the antigen to raise the protection/immune response of a vaccinated
 CC individual. An example of the invention demonstrated the generation of a
 CC specific immune response against a melanoma-derived peptide (see
 CC APP58360) by injection of mice with the peptide in combination with ODN
 CC 24
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
 QY
 Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2.6e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4012 AAAATGAGAAAAAGAGAAAAACA 4037
 |||||
 DB 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3200
 ABX93599/C
 ID ABX93599 standard; DNA; 26 BP.
 XX
 AC ABX93599;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Human zsig63 PCR/sequencing primer ZC7764a.
 XX

KM ss; PCR; zsig63; adhesin; salivary gland; dental carries;
 KM periodontal disease; thrush; gastrointestinal disease; epithelial wound;
 KM urinary tract infection; vaginal infection; skin infection; primer; AIDS;
 KM pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
 KM lung infection; cystic fibrosis; lung dysfunction; digestive;
 KM salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
 KM chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
 KM cell culture media; gene therapy; human chromosome 4q12-4q13;
 KM dentinogenesis imperfecta; dentin dysplasia type II.
 OS Synthetic.
 PN US2002173027-A1.
 PD 21-NOV-2002.
 PF 03-AUG-2001; 2001US-00922469.
 PR 17-MAR-1999; 99US-0124820P.
 PR 17-MAR-2000; 2000US-00527345.
 PA (ADLER/) ADLER D A.
 PA (SHEP/) SHEPPARD P O.
 PI Adler DA, Sheppard PO;
 DR WPI; 2003-328428/31.
 XX Novel isolated zsig63 polypeptide, member of the adhesin family, useful
 PT for treating dental carries, periodontal disease, thrush,
 PT gastrointestinal disease, urinary tract infections, vaginal infections,
 PT skin infections.
 PS Example 1; Page 29; 32pp; English.
 XX The invention relates to an isolated zsig63 polypeptide comprising at
 CC least 90% identity to an amino acid sequence which comprises domain 1 of
 CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
 CC included are the polynucleotide encoding zsig63, a zsig63 expression
 CC vector, a cultured cell comprising the vector and expressing the protein,
 CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
 CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
 CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
 CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is
 CC useful for detecting in a test sample, the presence of antagonist of
 CC zsig63 protein activity. Zsig63 has antimicrobial activity and since
 CC exhibits high expression in salivary gland, can be used for treating
 CC dental carries, periodontal disease, thrush, and gastrointestinal
 CC disease, urinary tract infections, vaginal infections, skin infections
 CC and other epithelial wounds. The polypeptides can be used to establish
 CC normal microflora and protect against pathogenic colonization and
 CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
 CC for treating chronic, tissue damage particularly in areas having limited
 CC or damaged vascular system, e.g. in diabetes, and for treating
 CC immunocompromised AIDS patients or in individuals that have undergone
 CC chemotherapy, radiation treatment, for treating lung infections e.g. in
 CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
 CC levels in the trachea may indicate that such polypeptides may serve as a
 CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
 CC conditions associated with salivary gland or lung dysfunction including
 CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
 CC chronic bronchitis, prostate dysfunctions such as prostate
 CC adenocarcinoma, aiding digestion, and as components of defined cell
 CC culture media and may be used to replace serum that is commonly used in
 CC culture. The DNA is useful in gene therapy applications to increase or
 CC inhibit zsig63 activity, and for detecting abnormalities on human
 CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
 CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
 CC present sequence is a primer used to isolate and sequence nucleic acids
 CC encoding human zsig63
 XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2.6e+03;
 Matches, 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 4011 TAAATGAGAAAAAGAGAAACA 4036
 Db 26 TAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 3201
 ACA62282/c
 ID ACA62282 standard; DNA; 26 BP.
 XX
 AC ACA62282;
 XX
 DT 12-AUG-2003 (first entry)
 XX
 DE Oligo (dt) primer #1.
 XX
 KM ss; PCR; primer; antisense therapy; mRNA expression profile;
 KM promoter containing primer.
 OS Synthetic.
 PN US2003022318-A1.
 PD 30-JAN-2003.
 PF 07-SEP-2001; 2001US-00949305.
 PR 25-JAN-2000; 2000US-00494212.
 PA (EPIC-) EPICLONE INC.
 PI Lin S, Ying S;
 DR WPI; 2003-479488/45.
 XX Improved polymerase thermocycling reaction for nucleic acid
 PT amplification, by thermal cycling of promoter-linked nucleic acid
 PT template synthesis and in vitro transcriptional amplification of nucleic
 PT acid sequences.
 PS Example 4; Page 14; 28pp; English.
 XX The invention relates to an improved polymerase thermocycling reaction
 CC (M1) for linear amplification of nucleic acid sequences, involves
 CC denaturing a number of nucleic acid templates (I1), combining the
 CC denatured (I1) with a promoter-containing primer (P1), a primer (P2), a
 CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
 CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
 CC polymerase, contacting P1 with (I1) to generate a number of promoter-
 CC containing templates, denaturing the promoter-containing templates,
 CC contacting P2 with the denatured promoter-containing templates to
 CC generate a number of promoter-containing double-stranded DNA templates,
 CC where the double-stranded nucleic acid templates are flanked by P1 in one
 CC end and P2 in the other end of the other orientation, transcribing the
 CC promoter-containing double-stranded DNA templates to form a number of
 CC amplified RNA sequences, including the primer region of the promoter-
 CC containing double-stranded DNA templates, contacting the amplified RNA
 CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA
 CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
 CC is useful for improved polymerase thermocycling reaction for linear
 CC amplification of nucleic acid sequences, and thus for producing mRNA
 CC expression profile of a cell by M1 to generate multiple copies of the
 CC mRNA. M1 is also useful for determining aberrant protein production of
 CC cells in a diseased state, by generating an expression profile by the
 CC above method, of cells in both normal and diseased states, comparing the
 CC expression profile of the cells in the normal and diseased states,
 CC determining the differences in mRNA composition of the cell(s) in the
 CC diseased state, isolating the mRNA sequences of cell(s) in the diseased
 CC state that differ from mRNA in cell(s) in non-diseased state, amplifying
 CC the isolated mRNA by M1, and determining aberrant protein function of the

protein coded for by the isolated mRNA. M1 is also useful for treating a cell in a diseased state caused by aberrant protein production, by determining protein expression of a cell in a diseased state, determining the mRNA sequence for the aberrant proteins, synthesizing an antisense sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and delivering a pharmaceutically effective dosage of a composition comprising the anti-sense mRNA and a compatible lipid based biological carrier. M1 is also useful for predicting the efficacy of a proposed drug targeted against an aberrant protein, by determining aberrant protein production of cell in a diseased state by the above method, amplifying the aberrant protein by M1 and using recombinant techniques to determine the effect of proposed drug on the aberrant protein. M1 is also useful for differential screening of tissue-specific gene expression at a cellular level, for preparing labeled RNA/DNA probes for a gene chip technology, and for determining the efficacy of a drug regimen against a gene or its cDNAs. The present sequence is an Oligo (dt) primer used to produce second strand cDNA in the method of the invention

SO Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAACAA 4037
DB 26 AAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3202
AAV71935/c
ID AAV71935 standard; DNA; 27 BP.
AC AAV71935;
XX 18-FEB-1999 (first entry)
XX Anchored poly T RT-PCR primer.
DE Normalised; cDNA library; mRNA cloning; reverse transcription;
XX Immobilise; screening; hybridisation; nucleic acid amplification;
KM expression pattern; drug development; PCR primer; RT-PCR; ss.
XX Synthetic.
OS
XX WO9851789-A2.
PN 19-NOV-1998.
PD 13-MAY-1998; 98MO-DK000186.
PE 13-MAY-1997; 97DK-00000547.
PR 19-MAY-1997; 97US-00871030.
PR 27-MAR-1998; 98DU-00000432.
XX
PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
XX Marchoe PR;
PT WPI; 1999-009772/01.
XX
XX Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT reverse transcription and amplification, used to screen for new genes and
PT intersecting proteins, potential drugs, and for diagnosis.
XX
XX Example 1; Page 29; 71pp; English.
XX
XX The invention relates to preparation of a normalised, subdivided library
CC of amplified cDNA from the coding regions of mRNA in a sample. The method
CC involves reverse transcription, with at least one cDNA primer of formula
CC 5'-Con1-dn2-Vn3-Nn4 to form first strand cDNA where Con1 = any sequence
CC of 1-100 nucleotides; dn2 = deoxythymidyl; n2 is at least 1; n3 and n4
CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand

cDNA synthesis using the first strand as template and a second cDNA primer of a similar formula, in the presence of DNA polymerase I (or its Klenow fragment) and amplification of double-stranded cDNA with a set of amplification primers. Comparison of cDNA in the prepared library with a database (a computer-generated list of molecular weights of restricted cDNA fragments of known sequence) is used to determine presence of an expressed protein in a cell, also to detect changes in such expression (particularly for diagnosis of disease). Surfaces (chip) having amplified cDNA stably immobilised on it, obtained by a similar method, are used to screen for genes of a particular family, by hybridisation with nucleic acid from the family (to identify new genes) and to detect differences in expression patterns between cells. The polypeptides expressed by the cDNA libraries can be used for drug development. Sequences AAV71935 to CCAAV71946 represent primers used to exemplify the method of the invention

SO Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4011 TAAATGAGAAAAAGAGAAACAA 4036
DB 26 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3203
AAA40358/c
ID AAA40358 standard; DNA; 28 BP.
XX AAA40358;
XX 10-NOV-2000 (first entry)
XX pBluescriptSK+ phagemid primer SEQ ID NO: 8.
DE Primer; cloning; ligation; ss.
XX
XX Synthetic.
OS
XX WO200036088-A1.
PN 22-JUN-2000.
PD 17-DEC-1999; 99MO-US030277.
PF 17-DEC-1998; 98US-00213834.
PR 17-DEC-1998; 98US-00213834.
XX
XX (ROMA/) ROMANTCHIKOV Y.
XX
XX Romantchikov Y;
PI
XX WPI; 2000-442381/38.
DR
XX Inserting a nucleic acid into a circular vector comprising joining their
PT ends, melting, and reannealing ends at two different concentrations,
PT useful for cloning small amounts of nucleic acids and forming genomic
PT libraries.
XX
XX Example 3; Page 67; 71pp; English.
XX
XX This invention describes a novel method (M1) for inserting a nucleic acid
CC (M1) into a circular vector (V1) comprising joining ends of M1 and V1
CC under a first nucleic acid concentration, melting hybridized cohesive
CC circularization ends, and reannealing the ends at a second concentration.
CC The methods are useful for the cloning small amounts of nucleic acids and
CC forming genomic libraries of complex populations of DNA or cDNA. The
CC methods allow the cloning of minute amounts of nucleic acids efficiently
CC and avoids the size selection problems of prior art systems. Larger
CC nucleic acid fragments are just as easily cloned, allowing highly
CC representative libraries to be made. Vector to vector ligation is avoided
CC using the methods. AAA40351-A40366 represents primers used to illustrate
CC the method of the invention

```
XX SQ Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 4012 AAATGAGAAAAAGAGAAAAACA 4037
Db 27 AAAAAAAAAAAAAAAAAAAAACTA 2

RESULT 3204
AA57856/C
ID AA57856 standard; DNA; 28 BP.
XX AA57856;
AC
XX 11-OCT-2000 (first entry)
DT
XX Deoxy-T22-tagged substrate oligonucleotide.
DE
XX Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW nucleic acid substrate; in vitro selection; ribozyme ligase;
KM conformation dependent activity; allosteric activation; ss.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH misc_RNA 23..28
FT /*tag= a
FT misc_binding 24..28
FT /*tag= b
FT /bound_molecy= "Bases 13-17 of N90 RNA pool (AA57851)"
FT
XX WO200024931-A2.
XX
XX 04-MAY-2000.
XX
XX 22-OCT-1999; 99WO-IL000557.
XX
XX 23-OCT-1998; 98IL-00126731.
XX
XX (INTE-) INTELIGENE LTD.
XX
XX Nachan A, Ellington A;
XX
XX WPI; 2000-350763/30.
XX
XX Detecting an analyte in a sample comprises providing nucleic acid
PT sequence which is catalytically active in presence of analyte, contacting
FT catalytic nucleic acid with substrate and amplifying catalytic product.
XX
XX Disclosure; Page; 36pp; English.
XX
XX The invention relates to a method of detecting an analyte in a sample.
CC The method comprises providing a nucleic acid sequence which is initially
CC catalytically inactive, but which becomes catalytically active in the
CC presence of an analyte (the effector); providing a nucleic acid substrate
CC for the catalytic activity of the nucleic acid sequence; and contacting
CC the nucleic acid sequence and the substrate with the sample under
CC conditions allowing catalytic activity of nucleic acid sequences. The
CC catalytic nucleic acid sequence will be able to convert the nucleic acid
CC substrate into a nucleic acid product only if the analyte of interest is
CC present. The nucleic acid catalytic product is then amplified, and a
CC significant increase in the amount of product indicates the presence of
CC the analyte in the sample. The method is useful for the qualitative or
CC quantitative determination of an analyte in a sample in diagnostic
CC assays. The invention describes the in vitro selection of a ribozyme
CC ligase (L1; AA57859, AA57860) which is catalytically active only in the
CC presence of an oligonucleotide effector (AA57854). The L1 ribozyme
CC ligase was selected from a pool of RNA molecules comprising a central
CC randomised region 90 nucleotides in length flanked on both sides by
```

```
CC constant sequence regions (the N90 RNA pool; AA57851). In the presence
CC of the effector, selection was performed using one of the tagged
CC substrate molecules AA57855-A57857. RNAs with ligase activity (i.e.,
CC those which have become ligated to the substrate molecule) were reverse
CC transcribed using the effector oligo, and then PCR amplified using the
CC effector and a DNA primer identical in sequence to the substrate used for
CC the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC can only adopt its active conformation (AA57859) in the presence of the
CC effector oligo (analyte). In the absence of the effector, L1 adopts an
CC inactive conformation (AA57860). The present sequence represents the
CC deoxy-T22-tagged substrate oligonucleotide. The dt22 tag enables
CC successfully ligated products to be isolated using oligo (dt) cellulose
CC Type 7. Note: The present sequence is not given in the specification, but
CC is created from the information given on page 11
XX
XX SQ Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 4014 AATGAGAAAAAGAGAAAAACA 4039
Db 28 AGTCAGAAAAAAGAAAAA 3

RESULT 3205
AA57856/C
ID AA57856 standard; DNA; 28 BP.
XX AA57856;
AC
XX 27-APR-2001 (first entry)
DT
XX RNA oligonucleotide #7.
DE
XX Protein-RNA fusion; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "C6-psoralen-2-Ome-U"
FT modified_base 28
FT /*tag= b
FT /mod_base= OTHER
FT /note= "A-TBG2"
FT
XX WO200107657-A1.
XX
XX 01-FEB-2001.
XX
XX 19-JUL-2000; 2000WO-US019653.
XX
XX 27-JUL-1999; 99US-0145834P.
XX
XX (PHYL-) PHYLLOS INC.
XX
XX Kurz M, Lohse P, Wagner R;
XX
XX WPI; 2001-182803/18.
XX
XX Affixing a peptide acceptor to an RNA molecule useful for producing
PT fusion proteins for isolating proteins or nucleic acids with desired
PT properties through attachment of a peptide acceptor to the 3' end of an
PT RNA molecule.
XX
XX Example 6; Page 29; 56pp; English.
XX
XX The present invention relates to a method for affixing a peptide acceptor
CC to an RNA molecule through the formation of a covalent bond, noncovalent
```

CC bond, or by chemical ligation. The method is useful for producing RNA-
CC protein fusions which can be used for the isolation of proteins or
CC nucleic acids with desired properties from large pools of partially or
CC completely random amino acid or nucleic acid sequences. The present
CC sequence is an RNA oligonucleotide used in the present invention

XX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 65.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6159 TAGGGATGACATTAAGAAAAGA 6184
:|||||:|||||:|||||:
Db 1 UAGCGGAGUGCAAAAAAAAAAAAAA 26

RESULT 3206

AA45359
ID AAL45359 standard; RNA; 28 BP.

XX AAL45359;

DT 06-JUN-2002 (first entry)

DE Puromycin linker DNA sequence.

XX Peptide cleavage; chemical active ingredient targeted release; diagnosis;
XX antidiabetic; osteoporotic; cytostatic; asthma; osteoporosis; cancer;
XX stroke; neuronal disease; arthritis; pancreatitis; hypertension;
XX thrombosis; infection; schistosomiasis; herbicide; insecticide;
XX fungicide; cerebroprotective; neurological; antirheumatic; pancreatic;
XX hypotensive; antihypertensive; virucide; protozoacide; ds.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1

FT /*tag= a
/mod_base= OTHER
/note= "modified by psoralen and 2'-O-methyl"

FT modified_base 28

FT /*tag= b
/mod_base= OTHER
/note= "modified by (PBG) 2 CC (Puromycin linker)"

FT WO200216574-A2.

XX 28-FEB-2002.

XX 07-AUG-2001; 2001WO-EP009102.

XX 22-AUG-2000; 2000DE-01041238.

XX (XZIL-) XZILION GMBH & CO KG.

XX Reimholz R, Ploeger F;

XX WPI; 2002-269356/31.

XX Identifying specifically cleavable peptide, useful for targeted drug
PT delivery and developing protease inhibitors, by incubating test compound
PT with peptide-nucleic acid fusion.

XX Example 1; Page 19; 38pp; German.

XX The present invention relates to the identification of specific
CC proteolytically cleavable peptides by incubating a library of fusion
CC molecules, comprising a peptide and nucleic acid encoding said peptide,
CC with a proteolytically active sample, then isolating the cleavage
CC fragments and determining the coding sequences in the separated fusion
CC molecules. The coding sequences identified by the method are used for
CC production of specifically proteolytically cleavable substances, which

CC are useful in the treatment of asthma, osteoporosis, cancer, stroke,
CC neuronal diseases, arthritis, pancreatitis, hypertension, thrombosis,
CC viral infections and schistosomiasis. Also contemplated are similar
CC compounds designed to release herbicides, insecticides and fungicides,
CC when cleaved. The present sequence is a puromycin linker described in the
CC exemplification of the invention

XX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 65.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6159 TAGGGATGACATTAAGAAAAGA 6184
:|||||:|||||:|||||:
Db 1 UAGCGGAGUGCAAAAAAAAAAAAAA 26

RESULT 3207

AAF26222/C
ID AAF26222 standard; DNA; 30 BP.

XX AAF26222;

DT 26-APR-2001 (first entry)

DE APC binding protein associated primer ON-AT- SEQ ID 7.

XX ABC binding protein; cell proliferation; adenomatous polyposis coli;
XX tumor cell detection; primer; ss.

XX Unidentified.

XX DE19933237-A1.

XX 18-JAN-2001.

XX 15-JUL-1999; 99DE-01033237.

XX 15-JUL-1999; 99DE-01033237.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Mueller O;

XX WPI; 2001-148321/16.

XX Determining proliferative capacity of cells, useful e.g. for detecting
PT tumor cells, by measuring concentration and subcellular localization of
PT adenomatous polyposis coli protein.

XX Claim 10; Page 13; 26pp; German.

XX This invention describes a novel method for determining the proliferative
CC activity of cells, comprising detecting, in a sample, the concentration
CC and/or subcellular localization of APC (adenomatous polyposis coli)
CC protein (I). The invention also describes (I) determining function of (I)
CC in a sample by detecting presence of the C-terminal, DNA-binding domain
CC of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC (II) that contains the sequence GCGCGA 2 3G (S1) and/or GATCCT 2 3GC
CC (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC one of which is Ab and the other directed against the N-terminal region
CC (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC its fragments in a sample consisting of (II), Ab or the set of (7). The
CC method is used to detect proliferative, especially tumor (precursor),
CC cells, to detect function of (I) and mutations in (I), and to purify
CC and/or enrich (I), or its fragments, from a sample. The method allows
CC simple, rapid and reliable detection of proliferation, without the need
CC for polymerase chain reaction or sequencing

XX Sequence 30 BP; 1 A; 3 C; 2 G; 24 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4018 AGAAAAAGAGGAAACAAATGTT 4043
Db 27 AAAAAAAAAAAAAAAAAAGCAT 2

RESULT 3208

ADCl6682/c
ID ADCl6682 standard; DNA; 30 BP.

XX ADCl6682;

XX 18-DEC-2003 (first entry)

XX Aminoacylation RNA molecule related DNA oligo, P3-2.

XX ribozyme; aminoacylate; tRNA; non-cognate; catalytic RNA molecule; cis;
XX aminoacylation; trans; proteomic; ds.

XX OS Unidentified.

XX FN WO2003070740-A1.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-US0005007.

XX 15-FEB-2002; 2002US-0357424P.

XX (UYNY) UNIV NEW YORK STATE RES FOUND.

XX Suga H, Murakami H, Saito H;

XX WPI; 2003-748198/70.

XX New polynucleotide, useful for preparing peptides containing non-cognate
PT amino acids, encodes ribozyme that can aminoacylate tRNA with such amino
PT acids.

XX Example 3; SEQ ID NO 42; 85bp; English.

XX The invention relates to a novel polynucleotide comprising a sequence
CC encoding a ribozyme that can aminoacylate tRNA with a non-cognate amino
CC acid. Ribozymes encoded by the polynucleotide of the invention are used
CC to prepare polypeptides that contain non-cognate, including non-natural,
CC amino acids. The invention more specifically provides catalytic RNA
CC molecules having cis aminoacylation activity with a catalytic and
CC aminoacylation domain, or an RNA molecule with trans aminoacylation
CC activity with only a catalytic domain. The products of the invention are
CC potentially useful for biomedical and therapeutic use, e.g. for probing
CC the structure and function of proteins; preparation of peptide libraries
CC and in proteomics. This polynucleotide sequence represents a DNA oligo
CC relating to the RNA molecule with aminoacylation activity of the
CC invention.

XX SQ Sequence 30 BP; 3 A; 5 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4004 TTAGTCTAAATGAGAAAAAGACA 4029
Db 26 TTAGGTAAAAAAGAAAAAAGAAAA 1

RESULT 3209

AAL44170/c
ID AAL44170 standard; DNA; 33 BP.

XX AAL44170;

XX 03-OCT-2002 (first entry)

XX Porphyrin yezensis cytochrome C - related PCR primer, SEQ ID NO 4.

XX Cytochrome C; ss; maturation protein; nitrogen oxide trapping;

XX polluted atmosphere purification; PCR; primer.

XX Porphyrin yezensis.

XX WO200259339-A1.

XX 01-AUG-2002.

XX 23-JAN-2002; 2002WO-JP000467.

XX 23-JAN-2001; 2001JP-00014510.

XX (UYNI-) UNIV NIPPON.

XX Oku T, Nishio T, Satoh T;

XX WPI; 2002-557951/59.

XX Production of cytochrome c by culturing prokaryote transformed with
PT vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome
PT c maturation protein for use in reagents and drugs for trapping nitrogen
PT oxide.

XX Example 1; Page 7-8; 27pp; Japanese.

XX The invention comprises a method for the production of cytochrome C. The
CC method involves culturing a prokaryote that has been transformed with a
CC vector encoding a signal peptide and a cytochrome C maturation protein.
CC The method of the invention is useful for producing cytochrome C.
CC Cytochrome C produced by the method of the invention is used in reagents
CC and drugs for trapping nitrogen oxide (e.g. in purifying polluted
CC atmosphere by trapping nitrogen oxide). The present DNA sequence
CC represents a Porphyrin yezensis cytochrome C - related PCR primer

XX SQ Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 33;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4018 AGAAAAAGAGGAAACAAATGTT 4043
Db 30 AAAAAAAAAAAAAAAAAAGCAT 5

RESULT 3210

ABK32799/c
ID ABK32799 standard; DNA; 15 BP.

XX ABK32799;

XX 23-APR-2002 (first entry)

XX Human APPBP1 gene, allele-specific oligonucleotide #29.

XX Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;

XX Alzheimer's disease; transgenic animal; platelet aggregation;

XX single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200202820-A1.

PD 10-JAN-2002.
 XX 02-JUL-2001; 2001WO-US020951.
 PF 30-JUN-2000; 2000US-0215511P.
 PR (GENA-) GENAISSANCE PHARM INC.
 PA Anaestasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Saueker EA,
 PI Stephens CJ;
 PT WPI; 2002-164539/21.
 XX
 PT Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
 PT polymorphic variants, useful e.g. in studying the expression and function
 PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.
 XX
 PS Claim 17; Page 13; 104pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a sequence
 CC which is a polymorphic variant of a reference sequence for the amyloid
 CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
 CC fragment. The polymorphic variants are useful in studying the expression
 CC and function of APPBP1, in expressing APPBP1 protein for use in screening
 CC for candidate drugs to treat diseases related to APPBP1 activity, in
 CC studying the effect of the variation on the biological activity of
 CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
 CC the treatment of disorders such as Alzheimer's disease. The haplotyping
 CC methods are useful in validating APPBP1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC APPBP1 activity, or in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease associated with APPBP1
 CC activity. The transgenic animals are useful for studying expression of
 CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against APPBP1 protein, and for testing the efficacy of
 CC therapeutic agents and compounds for disorders related to platelet
 CC aggregation in a biological system. ABK32771-ABK32327 represent human
 CC APPBP1 gene allele-specific oligonucleotides used in the method of the
 CC invention
 CC
 SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;
 XX
 QY Query Match 0.2%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.5e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4470 TTTT TTTT TTTT TTTG 4484
 Db 15 TTTT TTTT TTTT TTTG 1
 XX
 RESULT 3211
 AAT6167/C
 ID AAT6167 standard; DNA; 20 BP.
 XX
 AC AAT6167;
 XX
 DT 15-JUL-1997 (first entry)
 XX
 DE UDP-glucose:thiohydroximate S-glucosyltransferase primer g13.
 XX
 KW Glucosinolate: UDP-glucose:thiohydroximate S-glucosyltransferase; S-GT;
 KW transgenic plant; rapeseed oil; oilseed rape; canola; Brassica napus;
 KW polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 PS
 PN EP771878-A1.
 XX
 PD 07-MAY-1997.
 XX
 PF 31-OCT-1995; 95EP-00402425.
 XX

PR 31-OCT-1995; 95EP-00402425.
 XX
 XX (PIBZ) PLANT GENETIC SYSTEMS NV.
 PA (CANA) NAT RES COUNCIL CANADA.
 PI Van Audenhove K, Peferoen M, Grootsaersink JWD, Underhill EW;
 PI Hemmingen SM, Reed DW, Kolenovsky AD;
 XX
 DR WPI; 1997-247418/23.
 XX
 PT Plants genetically transformed to interfere with UDP-
 PT glucose:thiohydroximate S-glucosyltransferase gene expression - useful
 PT for production or rapeseed oil with reduced glucosinolate content.
 XX
 PS Example 2; Page 17; 35pp; English.
 XX
 CC Degenerate primers based on 7 peptide sequences (AAW09826-32) of Brassica
 CC oleracea UDP-glucose:thiohydroximate S-glucosyltransferase (S-GT) were
 CC used in the PCR-RACE amplification of Brassica napus S-GT cDNA (see also
 CC AAT6166). Primer g13 (AAT6167) was combined with the Anchor Primer of
 CC the Clontech 3'RACE kit (AAT6170), and the product was used as template
 CC in a second semi-nested PCR to yield S-GT partial clone pGL2-7 (AAT6173)
 CC
 SQ Sequence 20 BP; 6 A; 1 C; 1 G; 4 T; 0 U; 8 Other;
 XX
 QY Query Match 0.2%; Score 14.6; DB 1; Length 20;
 Best Local Similarity 55.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 7110 AAAATGAATTAATCTCTCTG 7129
 Db 20 AATTTAAATTTMSWTCYTG 1
 XX
 RESULT 3212
 AEN83985
 ID AEN83985 standard; DNA; 20 BP.
 XX
 AC AEN83985;
 XX
 DT 02-OCT-2002 (first entry)
 XX
 DE Leishmania kinetoplast mini circle DNA PCR primer #1.
 XX
 KW Leishmania parasite; pharmaceutical; kinetoplast; PCR; primer; ss.
 KM
 OS Leishmania sp.
 XX
 PN BR200004507-A.
 XX
 PD 30-APR-2002.
 XX
 PF 28-SEP-2000; 2000BR-00004507.
 XX
 PR 28-SEP-2000; 2000BR-00004507.
 XX
 PA (FIOC-) FIOCRUZ FUNDAÇÃO CRUZ OSWALDO.
 PA (UFTM-) UNIV FEDERAL MINAS GERAIS.
 XX
 PI Romanha AJ, Volpini AC, De Azeredo Passos VM, Correa Oliveira G;
 PI
 DR WPI; 2002-417703/45.
 XX
 PT Molecular differentiation of Leishmaniosis parasites consists of
 PT detection by PCR RFLP technique via initiators and nucleotides.
 XX
 PS Claim 2; Page 11; 38pp; Portuguese.
 XX
 CC The invention relates to the molecular differentiation of Leishmaniasis
 CC parasites. The method of the invention comprises detection of parasites
 CC of the Leishmania (Viana) braziliensis, Leishmania (Viana) guyanensis
 CC and Leishmania amazonensis species. The method employs initiators
 CC nucleotides and buffer solution in a polymerase chain reaction-

```

CC restriction length polymorphism (PCR-RFLP) technique. Methods of the
CC invention are useful in pharmaceuticals. The current sequence represents
CC a PCR primer for amplification of conserved regions of Kinetoplast mini
CC circle DNA
XX
SQ Sequence 20 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 2 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5150 GGGAGGAGGAGTTCCTCC 5156
    ||||| ||||| |||||
Db 1 GGGAGGAGGAGCTTCTSC 17

RESULT 3213
AAQ90391
ID AAQ90391 standard; DNA; 21 BP.
XX
AC AAQ90391;
XX
DT 08-JAN-1996 (first entry)
XX
DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
KW CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
KW SAED; hybridisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 21
FT /*tag= a
FT /note= "3' ribonucleoside terminal"
XX
PN WO9512808-A1.
XX
PD 11-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012270.
XX
PR 01-NOV-1993; 93US-00146504.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E;
XX
DR WPI; 1995-185870/24.
XX
FT New self-addressable electronic devices - used for multi-step and
FT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
FT and bio:polymer synthesis.
XX
PS Example 1; Page 40; 86pp; English.
XX
CC The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
CC are synthetic DNA probes with 5' amino termini. These sequences were
CC specific for the polymorphisms of HLA gene dQa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAED) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy 4020 AAAAAGAGAGAAACAAAT 4040
    ||||| ||||| |||||
Db 1 AAAAAGAGAGAGAGAAAU 21

RESULT 3214
AA110743
ID AA110743 standard; RNA; 21 BP.
XX
AC AA110743;
XX
DT 09-SEP-1996 (first entry)
XX
DE Oligonucleotide probe, CP-1.
XX
KW Electronically self-addressable device; ED; electrode; current source;
KW attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 21
FT /*tag= a
FT /note= "3'-ribonucleoside terminus"
XX
PN WO9601836-A1.
XX
PD 25-JAN-1996.
XX
PF 05-JUL-1995; 95WO-US008570.
XX
PR 07-JUL-1994; 94US-00271882.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
DR WPI; 1996-097582/10.
XX
FT Electronically self-addressable device - used for electronic control of,
FT e.g. nucleic acid hybridisation.
XX
PS Example 1; Page 60; 155pp; English.
XX
CC The sequences given in AA110742-67 are synthetic oligonucleotides which
CC are used in the construction of the electronically self-addressable
CC device (ED) of the invention. The ED comprises a substrate, an electrode
CC or opt. a number of electrodes supported by the substrate, a current
CC source operatively connected to the electrode and an attachment layer
CC adjacent to the electrode which is permeable to a counterion but not
CC permeable to the molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 4020 AAAAAGAGAGAAACAAAT 4040
    ||||| ||||| |||||
Db 1 AAAAAGAGAGAGAGAAAU 21

RESULT 3215
AAK81302
ID AAK81302 standard; DNA; 21 BP.
XX

```

AC AAX81302;
 XX
 DT 20-AUG-1999 (first entry)
 XX
 DE 3' ribonucleoside oligonucleotide probe CP-1.
 XX
 KM Microelectronic device; multi-step reaction; microscopic format;
 XX ion-permeable permeation layer; electrode; electrical control; transport;
 KM attachment; binding; DNA/RNA hybrid; probe; ss.
 XX
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT mibc_RNA 21 /*tag= a
 XX
 PN MO9929711-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025475.
 XX
 PR 05-DEC-1997; 97US-00986065.
 XX
 PA (NANO-) NANOGEN INC.
 XX
 PI Sosnowski RG, Butler WF, Tu E, Nerenberg MT, Heller MJ, Edman CF;
 XX WPI; 1999-305567/32.
 DR
 XX
 PT New microelectronic device designed to carry out and control multi-step
 PT and multiplex molecular biological reactions in microscopic format.
 XX
 PS Example 1; Page 89; 179pp; English.
 XX
 XX The specification describes a self-addressable, self-assembling
 CC microelectronic device which is designed to actively carry out and
 CC control multi-step and multiplex molecular biological reactions in
 CC microscopic formats. A key aspect of this invention is played by the ion
 CC -permeable permeation layer which overrules the electrode. This permeation
 CC layer allows attachment of nucleic acids to permit immobilization but
 CC also separates the attached oligonucleotides and hybridized target DNA
 CC sequences from the highly reactive electrochemical environment generated
 CC immediately at the electrode surface. The microelectronic device is
 CC designed and fabricated to actively carry out and control reactions such
 CC as nucleic acid hybridizations, antibody/antigen reactions, sample
 CC preparation, diagnostics and biopolymer synthesis. The device can
 CC electronically control the transport and attachment of specific micro-
 CC entities, such as nucleic acids and polypeptides, to specific micro-
 CC locations. The device can subsequently control the transport and reaction
 CC of analyses or reactants at the addressed specific micro-locations. The
 CC device is able to concentrate analyses and reactants, remove non-
 CC specifically bound molecules, provide stringency control for DNA
 CC hybridization reactions and improve the detection of analyses. The
 CC present sequence represents a probe used to exemplify the invention
 XX
 SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 76.2%; Pred. No. 2.3e+03;
 Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4020 AAAAAAGAGAGAAAAAAT 4040
 DB 1 AAAAAAAAAAAAAAAAAAAU 21
 RESULT 3216
 AAQ75780/c
 ID AAQ75780 standard; DNA; 21 BP.
 XX
 AC AAQ75780;
 XX

DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 PI WPI; 1995-018287/03.
 DR
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ7547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4016 TGAGAAAAAGAGAAAAACA 4036
 DB 21 TGAGAAAAAAAAAAAAAAAA 1
 RESULT 3217
 AAQ75761/c
 ID AAQ75761 standard; DNA; 21 BP.
 XX
 AC AAQ75761;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 PI WPI; 1995-018287/03.
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PS Disclosure: Page 8, 11pp; Japanese.
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4014 AATGAGAAAAAGAGAGAAA 4034
 DB 21 AATGAGAAAAAGAGAGAAA 1
 RESULT 3218
 AA226485/C
 ID AA226485 standard; DNA; 21 BP.
 XX
 AC AA226485;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human polymorphic region 674.
 XX
 KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASi;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9841648-A2.
 XX
 PD 24-SEP-1998.
 XX
 PF 19-MAR-1998; 98WO-US005419.
 XX
 PR 20-MAR-1997; 97US-0041057P.
 XX
 PA (VARI-) VARIAGENICS INC.
 XX
 PI Housman D, ledley FD, Stanton VP;
 XX
 DR WPI; 1998-521232/44.
 XX
 PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 XX
 PS Disclosure; Fig 7, 605pp; English.
 XX
 CC This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASi) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor

CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.,
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA225812-226825 represent
 CC human polymorphic sites described in the method of the invention
 XX
 SQ Sequence 21 BP; 16 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4468 TTTTCTCTCTCTCTCTTT 4488
 DB 21 TTTTCTCTCTCTCTCTTT 1
 RESULT 3219
 AAQ13763/C
 ID AAQ13763 standard; DNA; 21 BP.
 XX
 AC AAQ13763;
 XX
 DT 18-DEC-1991 (first entry)
 XX
 DE Oligonucleotide for detection of Agrobacterium rhizogenes derived plasmid
 DE DNA in transformed plant.
 XX
 KW Agrobacterium rhizogenes A4 strain; ss.
 XX
 OS Synthetic.
 XX
 PN JP03198780-A.
 XX
 PD 29-AUG-1991.
 XX
 PF 27-DEC-1989; 89JP-00341678.
 XX
 PR 27-DEC-1989; 89JP-00341678.
 XX
 PA (SHMA) SHIMADZU CORP.
 XX
 DR WPI; 1991-299436/41.
 XX
 PT Oligo:nucleotide for detection of transformant of plant - uses polymerase
 PT chain reaction process to enable detection of specific extraneous gene
 PT with high sensitivity and selectivity.
 XX
 PS Claim 1, Page 1, 6pp; Japanese.
 XX
 CC The oligonucleotide sequence is used as a probe to selectively detect
 CC Agrobacterium rhizogenes-derived plasmid DNA, as inserted into a plant
 CC genome. It is chemically synthesised and is complementary to T-DNA coding
 CC for the Ri plasmid of A. rhizogenes. It can also be used as a PCR primer
 CC and can easily detect a particular extraneous gene from a transformant
 CC plant with high sensitivity and selectivity
 XX
 SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3007 CTCACCCCATCTTGTACATC 3027
 DB 21 CTCATCCCTGCTGTGTACATC 1
 RESULT 3220

AAQ14885	standard; DNA; 21 BP.
AAQ14885	
20-FEB-1992	(first entry)
Oligo #10	hybridisable to synovial fluid phospholipase A2 cDS.
arachidonic acid; antisense oligonucleotide; rheumatoid arthritis; osteoarthritis; lupus; anaphylaxis; urticaria; asthma; psoriasis; hepatitis; cerebral oedema; contact dermatitis; ulcerative colitis; phosphorothioate linkage; SF-PLA2; ss.	
Synthetic.	
WO9116901-A.	
14-NOV-1991.	
30-APR-1990;	90US-00516969.
30-APR-1990;	90US-00516969.
(ISIS-) ISIS PHARM INC.	
Bennett CF, Ecker DJ, Crooke ST, Mirabelli CK;	
WPI; 1991-353508/48.	
Oligo-nucleotide analogues which modulate arachidonic acid metabolism - for treatment and diagnosis of conditions caused by lipoygenase, phospholipase, leukotriene(s) etc.	
Claim 18; Page 54; 87gp; English.	
This oligonucleotide can hybridise to nucleic acids encoding phospholipase A2 typical of the synovial fluid of patients with rheumatoid arthritis. (SF-PLA2 is more closely related to group II PLA2 enzymes such as those in rattlesnake venom than to pancreatic PLA2). The oligonucleotide (especially its phosphorothioate analogue) would be useful in inhibiting SF-PLA2 expression. SF-PLA2 secretion has been detected from a human epidermal carcinoma cell line and primary human epidermal keratinocytes. This suggests that the inhibitory oligonucleotide would be useful in the treatment of inflammatory disorders of the skin. See AAQ14859-Q14895	
Sequence 21 BP; 6 A; 2 C; 10 G; 3 T; 0 U; 0 Other;	
Query Match	0.2%; Score 14.6; DR 1; Length 21;
Best Local Similarity	81.0%; Pred.No.2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
1631 GGAAGATTCCAGATGCCG 1651	
1 GGAAGCTTCCAGGAGAGG 21	
RESULT 3221	
AAQ42900/C	
ID AAQ42900	standard; DNA; 21 BP.
AAQ42900;	
07-OCT-1993	(first entry)
HLA type analysis method DR1 & DR4 primer RRGb.	
Human leukocyte antigen; HLA classII gene; DNA polymerase method; ss.	
Synthetic.	
JP05111490-A.	

```

XX 07-MAY-1993.
XD
XX 02-MAR-1992; 92JP-00044935.
XF
XX 29-AUG-1991; 91JP-00244530.
XR
XX (SUMO ) SUMITOMO METAL IND LTD.
XA
XX WPI; 1993-184838/23.
XD
XX HLA type analysis method and its reagents - includes e.g. amplification
XX of HLA class II gene, digestion by restriction enzyme, electrophoresis
XX and detection.
XX
XX Example; Page 16; 21pp; Japanese.
XX
XX The sequence is that of DR1 & DR4 primer RRGb which was used as part of a
XX method of HLA type analysis involving amplification of a HLA class II
XX gene, or fragments of it, using 2 or more kinds of primers by the DNA
XX polymerase method and subsequent restriction enzyme digestion and
XX analysis. The method enables easier analysis of HLA type
XX
XX Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred.No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1610 AGAAGCTTCACAGACGCTGC 1630
DB 21 AGAGCTTCACAGTGCAGCGGC 1
RESULT 3222
AAQ42902/C
ID AAQ42902 standard; DNA; 21 BP.
XX
XX AC AAQ42902;
XX
XX DT 07-OCT-1993 (first entry)
XX
XX HLA type analysis method DR3, 5, 6, 8 primer RRGb.
XX
XX Human leukocyte antigen; HLA classII gene; DNA polymerase method; ss.
XX
XX OS Synthetic.
XX
XX JP05111490-A.
XX
XX PD 07-MAY-1993.
XX
XX PF 02-MAR-1992; 92JP-00044935.
XX
XX PR 29-AUG-1991; 91JP-00244530.
XX
XX (SUMO ) SUMITOMO METAL IND LTD.
XX
XX WPI; 1993-184838/23.
XX
XX HLA type analysis method and its reagents - includes e.g. amplification
XX of HLA class II gene, digestion by restriction enzyme, electrophoresis
XX and detection.
XX
XX Example; Page 16; 21pp; Japanese.
XX
XX The sequence is that of DR3, 5, 6, 8 primer RRGb which was used as part
XX of a method of HLA type analysis involving amplification of a HLA class
XX II gene, or fragments of it, using 2 or more kinds of primers by the DNA
XX polymerase method and subsequent restriction enzyme digestion and
XX analysis. The method enables easier analysis of HLA type
XX
XX Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ

```

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1610 AGAAGCTTCACAGACCGCTGC 1630
DB 21 AGAGCTTCACAGTGCAGCGGC 1

RESULT 3223
AAQ35258/C
ID AAQ35258 standard; DNA; 21 BP.

XX AAQ35258;
AC
XX 24-MAY-1993 (first entry)
DT
XX
XX Agrobacterium rhizogenes dwarfism gene PCR primer.
DE
XX
XX Polymerase chain reaction; detection; ss.
KW
XX

OS Synthetic.
XX
XX JP04356189-A.
PN
XX
XX 09-DEC-1992.
PD
XX
XX 31-MAY-1991; 91JP-00128924.
PF
XX
XX 31-MAY-1991; 91JP-00128924.
PR
XX
XX (SHMA) SHIMADZU CORP.
PA

XX WPI; 1993-030366/04.
DR
XX
XX Oligo:nucleotide for detecting plant transforming principle - is gene
PT coded to DNA of agrobacterium rhizogenes.
PT
XX
XX Claim 2; Page 2; 10pp; Japanese.

XX
XX The sequence is that of a PCR primer which is used as part of a method
CC for the detection of a gene relating to dwarfism of Agrobacterium
CC rhizogenes. The method provides highly sensitive, easy and highly
CC selective detection
CC
XX

Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3007 CTCACCCCATCTGTGCATC 3027
DB 21 CTCATCGCTGCTGTGCATC 1

RESULT 3224
AAQ35262/C
ID AAQ35262 standard; DNA; 21 BP.

XX AAQ35262;
AC
XX 24-MAY-1993 (first entry)
DT
XX
XX Agrobacterium rhizogenes dwarfism gene PCR primer.
DE
XX
XX Polymerase chain reaction; detection; ss.
KW
XX

OS Synthetic.
XX
XX JP04356189-A.
PN
XX

PD 09-DEC-1992.

XX 31-MAY-1991; 91JP-00128924.
PP

XX 31-MAY-1991; 91JP-00128924.
PR

XX (SHMA) SHIMADZU CORP.
PA

XX WPI; 1993-030366/04.
DR

XX Oligo:nucleotide for detecting plant transforming principle - is gene
PT coded to DNA of agrobacterium rhizogenes.
PT

XX Claim 2; Page 2; 10pp; Japanese.
PS

XX The sequence is that of a PCR primer which is used as part of a method
CC for the detection of a gene relating to dwarfism of Agrobacterium
CC rhizogenes. The method provides highly sensitive, easy and highly
CC selective detection
CC
XX

Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3007 CTCACCCCATCTGTGCATC 3027
DB 21 CTCATCGCTGCTGTGCATC 1

RESULT 3225
AAQ35268/C
ID AAQ35268 standard; DNA; 21 BP.

XX AAQ35268;
AC
XX 24-MAY-1993 (first entry)
DT
XX
XX Agrobacterium rhizogenes dwarfism gene PCR primer.
DE
XX
XX Polymerase chain reaction; detection; ss.
KW
XX

OS Synthetic.
XX

XX JP04356189-A.
PN

XX 09-DEC-1992.
PD

XX 31-MAY-1991; 91JP-00128924.
PF

XX 31-MAY-1991; 91JP-00128924.
PR

XX (SHMA) SHIMADZU CORP.
PA

XX WPI; 1993-030366/04.
DR

XX Oligo:nucleotide for detecting plant transforming principle - is gene
PT coded to DNA of agrobacterium rhizogenes.
PT

XX Claim 2; Page 2; 10pp; Japanese.
PS

XX The sequence is that of a PCR primer which is used as part of a method
CC for the detection of a gene relating to dwarfism of Agrobacterium
CC rhizogenes. The method provides highly sensitive, easy and highly
CC selective detection
CC
XX

Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;


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FT      /*tag= a
FT      /note= "Labeled with 32P"
XX      WO9408053-A1.
XX      14-APR-1994.
XX      29-SEP-1993; 93WO-US009297.
XX      29-SEP-1992; 92US-00954185.
XX      (ISIS-) ISIS PHARM INC.
XX      Hanecek RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL,
PI      Ecker DJ, Vickers TA, Wyatt JR, Imbach JL,
XX      WPI; 1994-135613/16.
XX      New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT      of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT      of chromosomes.
XX      Example 21; Page 60; 144pp; English.
XX      This sequence may be used for inhibiting replication of human immuno-
CC      deficiency virus (HIV). Oligonucleotides such as this may also be used
CC      for inhibiting activity of HSV, human cytomegalovirus or influenza virus,
CC      or for treating inflammatory and neurological disorders caused by
CC      phospholipase A2 activity in cases of hyper-proliferation, malignancy,
CC      cardiovascular disease and snake bite. They may also be used for
CC      inhibiting division of malignant cells by modulating telomere length,
CC      which may also retard aging. (Updated on 25-MAR-2003 to correct PN
CC      field.)
XX      Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4468 TTTTGTGCTT 4488
DB 1 TTTTGTGCTT 21
RESULT 3229.
AAT11995/C
ID AAT11995 standard; DNA; 21 BP.
XX
AC AAT11995;
XX
DT 25-MAR-2003 (revised)
DT 13-MAR-1996 (first entry)
XX
DE CMV antisense oligonucleotide (ISIS 4847).
XX
KM antisense; cytomegalovirus; CMV; human; therapy; prophylaxis; diagnosis;
KM intermediate early complex; IE1; IE2; DNA polymerase gene; ss.
XX
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 1..21 a
FT /*tag= a
FT /note= "phosphorothioate backbone"
XX
XX US542049-A.
XX
XX 15-AUG-1995.
XX
XX 25-JAN-1993; 93US-00009263.
XX
XX 19-NOV-1992; 92US-00927506.

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XX      (ISIS-) ISIS PHARM INC.
XX      Baker B, Draper K, Anderson K;
XX      WPI; 1995-292538/38.
XX      New oligo-nucleotide inhibits cytomegalovirus replication - by binding to
PT      a portion of cytomegalovirus RNA, for the diagnosis, prophylaxis and
PT      treatment of CMV diseases.
XX      Example 12; Col 17-18; 66pp; English.
XX      A series of 21 phosphorothioate antisense oligonucleotides (ONS)
CC      (AAT11987-2007) were examined for anti-cytomegalovirus (CMV) activity.
CC      ISIS 4847 targets the DNA polymerase gene 5' untranslated region. It has
CC      an IC50 value of 0.9 microm. (ONS which inhibit CMV at one-third the
CC      dosage (or below) at which the negative control shows activity in this
CC      experiment (IC50 = 1 microm. or less) are preferred). Antisense ONS
CC      targeting CMV DNA or RNA coding for the IE1, IE2 or DNA polymerase
CC      protease have been shown to be effective in therapy, prophylaxis and
CC      diagnosis of CMV infection. The ONS may be modified to reduce nuclease
CC      resistance and to increase their efficacy. Modifications include
CC      phosphorothioate backbone, alkyl and halogen-substituted sugar moieties
CC      at the 2' position. (Updated on 25-MAR-2003 to correct PF field.)
XX      Sequence 21 BP; 6 A; 6 C; 9 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3024 CACTGCGCTGACCCCACTG 3044
DB 21 CTTCTGCGCCTGCGCCGCTG 1
RESULT 3230
AAT01661/C
ID AAT01661 standard; DNA; 21 BP.
XX
AC AAT01661;
XX
DT 17-DEC-1995 (first entry)
XX
DE Peptide nucleic acid targeting CMV DNA pol 5'-UTR.
XX
KM peptide nucleic acid; PNA; cytomegalovirus; CMV; papillomavirus;
KM antiviral; diagnostic; ss.
XX
OS Synthetic.
XX
FT Key Location/Qualifiers
FT misc_feature 1..21 a
FT /*tag= a
FT /note= "at least one (and preferably all) of the backbone
FT subunits are composed of amide units, so that the
FT oligomer consists of the nucleobases attached covalently
FT to a polyamide backbone"
XX
XX NO9504748-A1.
XX
XX 16-FEB-1995.
XX
XX 09-AUG-1994; 94WO-US009039.
XX
XX 09-AUG-1993; 93US-00104438.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP, Crooke ST, Mirabelli CK, Ecker DJ, Cowsett LM,
XX WPI; 1995-090841/12.

```


CC AAT34988-PT35001 represent HIV inhibitors. Sequences containing only G and
CC T residues (such as these sequences) are triplex forming
CC oligonucleotides, and form purine rich promoter elements used to inhibit
CC transcription. These sequences bind to the HIV gp120 protein at the V3
CC loop via the internal guanine quartet. This binding prevents cell-to-
CC cell and virus-to-cell infection. The sequences may also be used for
CC inhibiting viral growth, and other viral genes, for inhibiting the enzyme
CC p1A2, and to modulate telomere length. In some cases these sequences need
CC to be chemically modified. The chemically modified oligonucleotides
CC preferably include at least one phosphorothioate linkage. Other modified
CC intersugar links, or 2'-modified sugar residues can also be used. These
CC oligonucleotides can be used for coating gloves, condoms, etc, or for
CC topical application. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4468 TTTTCTTTTCTTTTCTT 4468
DB 1 TTTTCTTTTCTTTTCTT 21
RESULT 3233
AAT31784/c
ID AAT31784 standard; DNA; 21 BP.
XX
AC AAT31784;
XX
DT 27-JAN-1997 (first entry)
XX
DE Cytokeratin 19 mRNA specific antisense PCR primer.
XX
KM Determination; tumour; metastasis; cytokeratin 19; CK19; detection;
KM epithelial cell; colorectal; stomach; mucinous ovarian; gall bladder;
KM adenocarcinoma; bladder; transitional cell; carcinoma; primer; PCR;
KM polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN W09617080-A1.
XX
PD 06-JUN-1996.
XX
PF 24-NOV-1995; 95WO-GB002734.
XX
PR 26-NOV-1994; 94GB-00023912.
XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Selby PJ, Burchill SA;
XX
DR WPI; 1996-277793/28.
XX
PT Detection of human tumours or metastasis - by detecting a cyto-keratin 20
PT gene prod. in a tissue sample which does not normally contain CK20.
XX
PS Example 1; Page 17; 36pp; English.
XX
CC Determining whether a human patient has a tumour or a metastasised
CC tumour, comprises determining whether a cytokeratin 20 (CK20) gene prod.
CC is present in a tissue sample that does not normally contain CK20. This
CC method is partic. useful for the detection of epithelial cell tumours,
CC e.g. colorectal, stomach, mucinous ovarian or gall bladder adenocarcinoma
CC or bladder or transitional cell carcinoma. In an example RNA was
CC extracted from normal human blood samples and samples spiked with
CC adenocarcinoma HT29 cells, transitional cell carcinoma RT12 cells or
CC breast adenocarcinoma MCF-7 cells and subjected to PCR amplification
CC using the CK20, CK8 or CK19 mRNA specific primers AAT31769/70,
CC AAT31781/82 and AAT31783/84, respectively. CK20, CK8 and CK19 mRNA was
CC not detected in normal blood, but a respective 370, 244 or 214 bp prod.

CC was detected in the HT29, RT112 and MCF-7 spiked blood
XX
SQ Sequence 21 BP; 3 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 985 AAGGAGTCAGGCGCTGAAG 1005
DB 21 ATGCAGATCGAAGGCTGAAG 1
RESULT 3234
AAX33889/c
ID AAX33889 standard; DNA; 21 BP.
XX
AC AAX33889;
XX
DT 30-JUN-1999 (first entry)
XX
DE Initialising oligonucleotide for pUC19 fragment amplification.
XX
KM Primer; sequence determination; genomic analysis; genetic identification;
KM forensic analysis; genetic counselling; medical diagnostics;
KM Initialising oligonucleotide; amplification; ss.
XX
OS Synthetic.
XX
PN W09633205-A1.
XX
PD 24-OCT-1996.
XX
PF 16-APR-1996; 96WO-US005245.
XX
PR 17-APR-1995; 95US-00424663.
XX
PA (SPEC-) SPECTRAGEN INC.
XX
PI Macevicz SC;
XX
DR WPI; 1996-485723/48.
XX
PT Sequencing DNA by parallel oligo:nucleotide extension - involving
PT extending initialising oligonucleotide by ligating probe to form duplex,
PT avoiding electrophoretic segms.
XX
PS Example 1; Page 20; 40pp; English.
XX
CC This sequence represents an initialising oligonucleotide for a fragment
CC of pUC19. The invention relates to a method for the identification of a
CC sequence of nucleotides in a polynucleotide (PNT), which involves: (a)
CC extending an initialising oligonucleotide (ONT) along the PNT by ligating
CC an ONT probe to form a duplex; (b) identifying one or more nucleotides of
CC the PNT; and (c) repeating steps (a) and (b) until the nucleotide
CC sequence is determined. The method is useful e.g. in gene function and
CC control investigations, genomic analysis, genetic identification,
CC forensic analysis, genetic counselling or medical diagnostics. The method
CC avoids the need for electrophoretic separation of similarly sized DNA
CC fragments, eliminates the difficulties associated with detection and
CC analysis of spatially overlapping bands of DNA fragments in a gel or
CC similar medium and avoids the need to generate DNA fragments from long
CC single-stranded template with a DNA polymerase
SQ Sequence 21 BP; 7 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3441 CCCACCTTACTCTCTCTCC 3461
DB 21 CCTCTCTTCTCTCTCTCTCC 1

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RESULT 3235
ID AAX3890/c
XX AAX3890 standard; DNA; 21 BP.
AC AAX3890;
XX
DT 30-JUN-1999 (first entry)
XX
DE Initialising oligonucleotide for pUC19 fragment amplification.
XX
KM Primer: sequence determination; genomic analysis; genetic identification;
KM forensic analysis; genetic counselling; medical diagnosis;
KM initialising oligonucleotide; amplification; ss.
XX
OS Synthetic.
XX
PN WO9633205-A1.
XX
PD 24-OCT-1996.
XX
PF 16-APR-1996; 96WO-US005245.
XX
PR 17-APR-1995; 95US-00424663.
XX
PA (SPEC-) SPECTRAGEN INC.
XX
PI Macev1cz SC;
XX
DR WPI; 1996-465723/46.
XX
PT Sequencing DNA by parallel oligonucleotide extension - involving
PT extending initialising oligonucleotide by ligating probe to form duplex,
PT avoiding electrophoretic seps.
XX
PS Example 1; Page 20; 40pp; English.
XX
CC This sequence represents an initialising oligonucleotide for a fragment
CC of pUC19. The invention relates to a method for the identification of a
CC sequence of nucleotides in a polynucleotide (PNT), which involves: (a)
CC extending an initialising oligonucleotide (ONT) along the PNT by ligating
CC an ONT probe to form a duplex; (b) identifying one or more nucleotides of
CC the PNT; and (c) repeating steps (a) and (b) until the nucleotide
CC sequence is determined. The method is useful e.g. in gene function and
CC control investigations, genomic analysis, genetic identification,
CC forensic analysis, genetic counselling or medical diagnostics. The method
CC avoids the need for electrophoretic separation of similarly sized DNA
CC fragments, eliminates the difficulties associated with detection and
CC analysis of spatially overlapping bands of DNA fragments in a gel or
CC single-stranded template with a DNA polymerase
CC
XX Sequence 21 BP; 8 A; 0 C; 13 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3442 CCACCTTACTTCTCTCCCT 3462
DB 21 CTCCTCTTCCCTCTCCCTCT 1

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XX
KM Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
KM thioester; DNA synthesis; antisense oligonucleotide; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..21
FT /tag= a
FT /note= "Phosphorothioate linkages between alternate
FT nucleotides (1 and 2, 3 and 4 etc.)."
XX
PN WO9729116-A1.
XX
PD 14-AUG-1997.
XX
PF 06-FEB-1997; 97WO-GB000327.
XX
PR 06-FEB-1996; 96GB-00002326.
XX
PA (CRUA-) CRUACHEM LTD.
XX
PI Reese CB, Rao MV;
XX
DR WPI; 1997-415290/38.
XX
PT Solid phase synthesis of phosphorothioate oligonucleotide(s) using new
PT dimeric synthon(s) - useful as anti-sense molecules for inhibiting gene
PT expression.
XX
PS Example 3; Page 20; 38pp; English.
XX
CC The present sequence represents a phosphorothioate oligonucleotide which
CC was prepared by solid phase synthesis. The method comprises adding at
CC least one dimeric phosphoramidite synthon, optionally having a protected
CC thioester group in its internucleotide link, during the synthesis cycle.
CC These novel dimeric phosphoramidite synthons are used as anti-sense
CC molecules for inhibition of gene expression. The method gives increased
CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
CC needed) and facilitates separation of impurities (greater difference in
CC size compared with use of monomeric synthons)
CC
XX Sequence 21 BP; 0 A; 10 C; 0 G; 11 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5327 TCTCTCTTGCCTCACTCTCT 5347
DB 1 TCTCTCTCTCTCTCTCTCT 21

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RESULT 3236
ID AAT86582
XX AAT86582 standard; DNA; 21 BP.
AC AAT86582;
XX
DT 25-MAR-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide #1.
XX

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RESULT 3237
ID AAT77232
XX AAT77232 standard; DNA; 21 BP.
AC AAT77232;
XX
DT 12-FEB-1998 (first entry)
XX
DE Rat fibroblast growth factor FGF-10 RACE primer B.
XX
KM Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KM wound healing; cartilage; RACE primer; ss.
XX
OS Synthetic.
XX
PN WO9720929-A1.
XX
PD 12-JUN-1997.
XX

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PF 06-DEC-1996; 96MO-JP003579.
XX
XX 07-DEC-1995; 96JP-00345689.
PR 28-MAR-1996; 96JP-00103240.
PR 24-JUL-1996; 96JP-00214378.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI Itoh N, Negoro T, Katsunuma T, Tagashira S;
DR WPI; 1997-319776/29.
XX
PT Recombinant fibroblast growth factor FGF-10 and related DNA - useful for
PT the treatment of bone disease and for wound healing.
XX
PS Example 1; Page 35; 51pp; Japanese.
XX
CC The present sequence represents a RACE primer involved in the
CC amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,
CC vector, containing the DNA, and host cells, containing the vectors, are
CC useful for the recombinant production of FGF-10. The recombinant FGF-10
CC is useful for the treatment of diseases and injury of bone or cartilage,
CC and as a wound healing promoter
XX
SQ Sequence 21 BP; 2 A; 9 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5740 TCCCTTCTCTATCTCACTC 5760
DB 1 TCCATTTCTCTATCTCTCTC 21
RESULT 3238
AAV30731
ID AAV30731 standard; DNA; 21 BP.
XX
AC AAV30731;
XX
DT 13-AUG-1998 (first entry)
XX
DE Telomerase reverse transcriptase primer 260-280.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; phosphorothioate;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key modified_base 1..21
FT /tag= a
FT /note= "phosphorothioate linkages"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00911312.
XX 14-AUG-1997; 97US-00912951.
XX 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.

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PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1996-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Disclosure; Page 44; 387pp; English.
XX
CC The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
SQ Sequence 21 BP; 5 A; 4 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4735 GGCCAGCTGGAGGAAGGG 4755
DB 1 GGACACCTGGCGGAGGAGGG 21
RESULT 3239
AAV08273/c
ID AAV08273 standard; DNA; 21 BP.
XX
AC AAV08273;
XX
XX 27-JAN-1999 (first entry)
XX
DE PCR primer ABCR-EXON43:F for ABCR coding sequence.
XX
KW ATP binding cassette; ABC transporter; ABCR; Stargardt Disease; therapy;
KW Fundus Flavimaculatus; age-related macular degeneration; diagnosis;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9837764-A1.
XX
XX 03-SEP-1998.
XX
XX 27-FEB-1998; 98MO-US003895.
XX
XX 27-FEB-1997; 97US-0039388P.
XX
XX 27-FEB-1997; 97US-0039388P.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
PA (UYTO ) UNIV JOHNS HOPKINS.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UTAH ) UNIV UTAH.

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XX Allikmets R, Anderson KL, Dean M, Leppart M, Lewis RA, Li Y;
PI Lupski JR, Nathans J, Rattner A, Shroyer NF, Singh N, Smallwood PM;
PI Sun H;
XX WPI; 1998-495375/42.
XX
PT Retina-specific ATP-binding cassette transporter and DNA - useful for,
PT e.g. diagnosis and treatment of macular degeneration, such as in
PT Stargardt Disease, Fundus Flavimaculatus and age-related degeneration.
XX
PS Claim 41; Page 31; 79pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the human retina
CC specific ATP binding cassette transporter (ABCR) of the invention. ABCR
CC may be used in compositions for screening agents that alters ABCR. The
CC agent can inhibit Stargardt Disease, Fundus Flavimaculatus and age-
CC related macular degeneration (MD). Primers (such as this sequence) and
CC probes for the ABCR DNA can be used in a diagnostic kit for detecting MD
XX
SQ Sequence 21 BP; 4 A; 9 C; 1 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3228 GAGGAGAGATTTTTCGAG 3248
DB 21 GAGCAAGAGATGTTTGGAG 1
XX
RESULT 3240
AAV08280
ID AAV08280 standard; DNA; 21 BP.
XX
AC AAV08280;
XX
DT 27-JAN-1999 (first entry)
XX
DE PCR primer ABCR.EXON46.R for ABCR coding sequence.
XX
XX ATP binding cassette; ABC transporter; ABCR; Stargardt Disease; therapy;
XX Fundus Flavimaculatus; age-related macular degeneration; diagnosis;
XX PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9837764-A1.
XX
XX 03-SEP-1998.
XX
XX 27-FEB-1998; 98WO-US003895.
XX
XX 27-FEB-1997; 97US-0039388P.
XX
XX 27-FEB-1997; 97US-0039388P.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (UTXO ) UNIV JOHNS HOPKINS.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UTAH ) UNIV UTAH.
XX
XX Allikmets R, Anderson KL, Dean M, Leppart M, Lewis RA, Li Y;
PI Lupski JR, Nathans J, Rattner A, Shroyer NF, Singh N, Smallwood PM;
PI Sun H;
XX WPI; 1998-495375/42.
XX
PT Retina-specific ATP-binding cassette transporter and DNA - useful for,
PT e.g. diagnosis and treatment of macular degeneration, such as in
PT Stargardt Disease, Fundus Flavimaculatus and age-related degeneration.
XX
PS Claim 41; Page 32; 79pp; English.
XX

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CC This sequence represents a PCR primer for DNA encoding the human retina
CC specific ATP binding cassette transporter (ABCR) of the invention. ABCR
CC may be used in compositions for screening agents that alters ABCR. The
CC agent can inhibit Stargardt Disease, Fundus Flavimaculatus and age-
CC related macular degeneration (MD). Primers (such as this sequence) and
CC probes for the ABCR DNA can be used in a diagnostic kit for detecting MD
XX
SQ Sequence 21 BP; 5 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 5907 ACCTGTTCCCAAGCCAGAG 5927
DB 1 ACCTCTTCCCAACCCAGAG 21
XX
RESULT 3241
AAV37790/c
ID AAV37790 standard; DNA; 21 BP.
XX
AC AAV37790;
XX
DT 09-SEP-1998 (first entry)
XX
DE Interleukin-15 gene inhibitor oligonucleotide 1.
XX
XX Interleukin gene; IL-15; inhibitor; oligomer; expression;
XX transcription-inhibiting complex; polypurine-pyrimidine region;
XX inflammatory poly-arthritis; rheumatoid arthritis; asthma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9818812-A1.
XX
XX 07-MAY-1998.
XX
XX 29-AUG-1997; 97WO-US015397.
XX
XX 25-OCT-1996; 96US-00740215.
XX
XX (HISM ) HISAMITSU PHARM CO LTD.
XX
XX Veerapanane D, Hamanaka S, Nozawa I;
XX WPI; 1998-272129/24.
XX
XX Oligomer capable of inhibiting expression of an interleukin gene - is
XX used to alleviate inflammatory poly-arthritis, especially rheumatoid
XX arthritis.
XX
XX Claim 19; Page 7; 19pp; English.
XX
XX An oligomer has been developed which is capable of inhibiting expression
XX of an interleukin gene. The interleukin gene is preferably an interleukin
XX -15 (IL-15) gene. The oligomer can be an oligonucleotide or an
XX oligonucleotide analogue. When it is an oligonucleotide analogue it is
XX selected from protein nucleic acid, morpholino, methylene linkage,
XX boronated, and pteridine oligonucleotide analogues. The analogue is
XX linked at its 5' end or 3' end to an intercalator. The intercalator is a
XX poralen or acridine derivative. The oligomer is preferably an
XX oligonucleotide made of DNA. The oligonucleotide is a phosphodiester,
XX phosphorothioate, methylphosphonate, or methylphosphonothioate
XX oligonucleotide derivative, especially a phosphodiester oligonucleotide.
XX The oligonucleotide is at least 5 (preferably 5-50) nucleotides, in
XX length. The present sequence represents a specifically claimed
XX oligonucleotide of the present invention. The oligomer can be used to
XX alleviate inflammatory polyarthritis, especially that associated with
XX rheumatoid arthritis. The oligomer can also be used to alleviate
XX eosinophilic inflammation, especially that associated with chronic asthma
XX

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SQ Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 5412 AAGAAATATAAGCAAGAGAA 5432
 DB 21 AAGAAATATAAGCAAGAGAA 1
 RESULT 3242
 AAV37793
 ID AAV37793 standard; DNA; 21 BP.
 AC AAV37793;
 DT 09-SEP-1998 (first entry)
 DE Interleukin-15 gene inhibitor oligonucleotide 4.
 XX Interleukin gene; IL-15; inhibitor; oligomer; expression;
 KM transcription-inhibiting complex; polypurine-polypyrimidine region;
 KM inflammatory poly-arthritis; rheumatoid arthritis; asthma; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9818812-A1.
 PD 07-MAY-1998.
 PF 29-AUG-1997; 97WO-US015397.
 PR 25-OCT-1996; 96US-00740215.
 PA (HISM) HISAMITSU PHARM CO LTD.
 PI Veerapanane D, Hamanaka S, Nozawa I;
 DR WPI; 1998-272129/24.
 PT Oligomer capable of inhibiting expression of an interleukin gene - is
 PT used to alleviate inflammatory poly-arthritis, especially rheumatoid
 PT arthritis.
 PS Claim 20; Page 8; 19pp; English.
 CC An oligomer has been developed which is capable of inhibiting expression
 CC of an interleukin gene. The interleukin gene is preferably an interleukin
 CC -15 (IL-15) gene. The oligomer can be an oligonucleotide or an
 CC oligonucleotide analogue. When it is an oligonucleotide analogue it is
 CC selected from protein nucleic acid, morpholino, methylene linkage,
 CC boronated, and pteridine oligonucleotide analogues. The analogue is
 CC linked at its 5' end or 3' end to an intercalator. The intercalator is a
 CC pteralene or acridine derivative. The oligomer is preferably an
 CC oligonucleotide made of DNA. The oligonucleotide is a phosphodiester,
 CC phosphorothioate, methylphosphonate, or methylphosphonothioate
 CC oligonucleotide derivative, especially a phosphodiester oligonucleotide.
 CC The oligonucleotide is at least 5 (preferably 5-50) nucleotides, in
 CC length. The present sequence represents a specifically claimed
 CC oligonucleotide of the present invention. The oligomer can be used to
 CC alleviate inflammatory polyarthritis, especially that associated with
 CC rheumatoid arthritis. The oligomer can also be used to alleviate
 CC eosinophilic inflammation, especially that associated with chronic asthma
 SQ Sequence 21 BP; 15 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 5412 AAGAAATATAAGCAAGAGAA 5432

DB 1 AAGAAATATAAGCAAGAGAA 21
 RESULT 3243
 AAV10466/c
 ID AAV10466 standard; DNA; 21 BP.
 AC AAV10466;
 DT 17-JUN-1998 (first entry)
 DE Human osteosarcoma PCR primer #2.
 XX Osteosarcoma; haematopoietic cell; osteoblast; human; immature; antibody;
 KM immunoreactive; cell antigen; CD34; blood; bone marrow; treatment;
 KM disorder; PCR primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN US5733541-A.
 PD 31-MAR-1998.
 PF 21-APR-1995; 95US-00426792.
 PR 21-APR-1995; 95US-00426792.
 PA (UNMI) UNIV MICHIGAN.
 PI Emerson SG, Taichman RS;
 DR WPI; 1998-229763/20.
 PT Maintenance of haematopoietic cells in culture - by co-culturing with
 PT osteoblast(s).
 PS Example 4; Col 19; 38pp; English.
 CC Primers AAV10465-V10492 are used to amplify regions of the human
 CC osteosarcoma cell lines MC-63 and SAOS-2 which contain ligands and growth
 CC factors and have been designed to cross intron/exon boundaries. The
 CC products are used in a process for propagating and maintaining the
 CC immature morphology of mammalian haematopoietic cells. The process
 CC involves obtaining an enriched population of mammalian haematopoietic
 CC cells having the immature morphology of CD34+, HLA-DR+, Thy-1+ and Lin-
 CC and co-culturing this population in the presence of osteoblast cells for
 CC between 2 weeks and 8 weeks. The immature cells can be detected by
 CC exposing them to an anti-CD34 antibody immunoreactive with the
 CC haematopoietic cell antigen CD34, and removing cells that do not immuno-
 CC react with the antibody. Such haematopoietic cells can be infused into
 CC the blood stream or bone-marrow cavity to treat blood disorders
 SQ Sequence 21 BP; 0 A; 11 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 3638 AGGAGGTAGATGGGAGAGAA 3658
 DB 21 AGGAGGTAGATGGGAGAGAA 1
 RESULT 3244
 AA226171
 ID AA226171 standard; DNA; 21 BP.
 AC AA226171;
 DT 30-NOV-1999 (first entry)

DE Human polymorphic region 360.
 XX polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 XX Homo sapiens.
 OS
 XX MO9841648-A2.
 PN
 XX 24-SEP-1998.
 PD
 XX 19-MAR-1998; 98WO-US005419.
 PF
 XX 20-MAR-1997; 97US-0041057P.
 PR
 XX (VARI-) VARIAGENICS INC.
 PA
 XX Housman D, Ledley FD, Stanton VP;
 PI
 XX WPI; 1998-521232/44.
 DR
 XX
 PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 PS
 XX Disclosure; Fig 7; 605pp; English.
 CC This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA25812-226825 represent
 CC human polymorphic sites described in the method of the invention
 CC
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 10 G; 0 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Db 7414 AGCAGCAGCAGCAGCAGC 7434
 1 AGCAGCAGCAGCAGCAGC 21
 RESULT 3245
 AA226812/c
 ID AA226812 standard; DNA; 21 BP.
 AC
 XX AA226812;
 XX
 DE 30-NOV-1999 (first entry)
 DT
 XX Human polymorphic region 1001.
 DE
 XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;

KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 XX Homo sapiens.
 OS
 XX MO9841648-A2.
 PN
 XX 24-SEP-1998.
 PD
 XX 19-MAR-1998; 98WO-US005419.
 PF
 XX 20-MAR-1997; 97US-0041057P.
 PR
 XX (VARI-) VARIAGENICS INC.
 PA
 XX Housman D, Ledley FD, Stanton VP;
 PI
 XX WPI; 1998-521232/44.
 DR
 XX
 PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 PS
 XX Disclosure; Fig 7; 605pp; English.
 CC This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA25812-226825 represent
 CC human polymorphic sites described in the method of the invention
 CC
 XX
 SQ Sequence 21 BP; 3 A; 14 C; 0 G; 4 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Db 2876 GGGAGGTGGGTGGAGGAG 2896
 21 GGGAGGTGGGTGGAGGAG 1
 RESULT 3246
 AA226398
 ID AA226398 standard; DNA; 21 BP.
 AC
 XX AA226398;
 XX
 DE 30-NOV-1999 (first entry)
 DT
 XX Human polymorphic region 587.
 DE
 XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.

XX OS Homo sapiens.
 XX PN WO9841648-A2.
 XX PD 24-SEP-1998.
 XX PF 19-MAR-1998; 98WO-US005419.
 XX PR 20-MAR-1997; 97US-0041057P.
 XX PA (VARI-) VARIAGENICS INC.
 XX PI Housman D, Ledley FD, Stanton VP;
 XX DR WP1; 1998-521232/44.
 XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 XX PS Disclosure; Fig 7; 605pp; English.
 CC This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA25812-226825 represent
 CC human polymorphic sites described in the method of the invention
 XX SQ Sequence 21 BP; 9 A; 2 C; 1 G; 9 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5473 TTTTGTGTAAGATTAAT 5493
 Db 1 TTTTTCGCAAAAGCTTAAT 21
 RESULT 3247
 AA226192/c
 ID AA226192 standard; DNA; 21 BP.
 XX AC AA226192;
 XX DT 30-NOV-1999 (first entry)
 XX DE Human polymorphic region 381.
 XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 XX OS Homo sapiens.
 XX PN WO9841648-A2.

XX PD 24-SEP-1998.
 XX PF 19-MAR-1998; 98WO-US005419.
 XX PR 20-MAR-1997; 97US-0041057P.
 XX PA (VARI-) VARIAGENICS INC.
 XX PI Housman D, Ledley FD, Stanton VP;
 XX DR WP1; 1998-521232/44.
 XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
 PT dysplastic lesions, endometriosis or graft versus host disease.
 XX PS Disclosure; Fig 7; 605pp; English.
 CC This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is active
 CC on a gene vital for cell growth or viability, and where the gene is
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to the patient a first allele
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA25812-226825 represent
 CC human polymorphic sites described in the method of the invention
 XX SQ Sequence 21 BP; 2 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7415 GCAGCAGCAGCAGCAGCA 7435
 Db 21 GCAGCAGCAGCTGTGAGCA 1
 RESULT 3248
 AA226714/c
 ID AA226714 standard; DNA; 21 BP.
 XX AC AA226714;
 XX DT 30-NOV-1999 (first entry)
 XX DE Human polymorphic region 903.
 XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 XX OS Homo sapiens.
 XX PN WO9841648-A2.
 XX PD 24-SEP-1998.
 XX PF 19-MAR-1998; 98WO-US005419.

[illegible]

XX	Housman D,	Ledley FD,	Stanton VP;
PI	WPI; 1998-521232/44.		
XX			
XX	Identifying target genes for allele-specific drugs - used for diagnosis,		
PT	prevention and treatment of, e.g. cancers, atherosclerotic plaque,		
PT	dysplastic lesions, endometriosis or graft versus host disease.		
XX			
P5	Disclosure; Fig 7; 605pp; English.		
XX			
CC	This invention describes a novel method for identifying an inhibitor		
CC	potentially useful for treatment of cancer, where the inhibitor is active		
CC	on a gene vital for cell growth or viability, and where the gene is		
CC	subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is		
CC	used for preventing the development of cancer in a patient having a		
CC	precancerous condition, by administering to the patient a first allele		
CC	specific inhibitor (ASI) targeted to an allele of a first essential gene		
CC	present in cells of the precancerous condition, where the normal somatic		
CC	cells of the patient are heterozygous for the first gene, the inhibitor		
CC	is active on at least one but less than all allelic forms of the gene		
CC	present in a population and targets only one allelic form present in the		
CC	normal somatic cells, and the first gene. The products and methods can be		
CC	used in the diagnosis, prevention and treatment of LOH disorders, e.g.		
CC	cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic		
CC	lesions, benign tumors, endometriosis, polycystic kidney disease, and		
CC	graft versus host disease. The method can also be used to remove		
CC	malignant cells from bone marrow transplants. AA25812-226825 represent		
CC	human polymorphic sites described in the method of the invention		
XX			
SQ	Sequence 21 BP; 3 A; 12 C; 2 G; 4 T; 0 U; 0 Other;		
	Query Match	0.2%; Score 14.6; DB 1; Length 21;	
	Best Local Similarity	81.0%; Pred. No. 2.3e+03;	
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
QY	2865 AGCAAGGAGGAGCGACGTGGC 2885		
DB	21 AGCGAGGAGACGGTGTGTG 1		
	RESULT 3250		
	AAK17912/C		
ID	AAK17912 standard; DNA; 21 BP.		
XX			
AC	AAK17912;		
XX			
DT	11-MAY-1999 (first entry)		
XX			
DE	Anti-CMV oligonucleotide #4847.		
XX			
KM	Antisense; oligonucleotide; immediate early; DNA polymerase; CMV;		
KX	cytomegalovirus; inhibition; replication; sugar modification;		
KW	phosphorochioate; infection; retinits; ss.		
XX			
OS	Synthetic.		
OS	Human herpesvirus 5.		
XX			
FH	Key	Location/Qualifiers	
FT	modified_base	1..21	
FT	/tag= a		
FT	/note= "contains phosphorochioate internucleotide		
FT	linkages"		
XX			
PN	WO9845314-A1.		
PD	15-OCT-1998.		
XX			
PF	07-APR-1998; 98WO-US006895.		
XX			
PR	09-APR-1997; 97US-00838715.		
XX			
PA	(ISIS-) ISIS PHARM INC.		

XX Draper KG, Kisman DL, Anderson KP, Chapman S;
XX WPI; 1998-568330/48.
XX
XX New antisense oligonucleotides that target cytomegalovirus nucleic acid -
PT particularly including 2-methoxyethoxy sugar modifications, especially
PT for treating viral retinitis, with long-lasting retention in the retina.
XX
XX Claim 7; Page 26; 99pp; English.
XX
XX Antisense oligonucleotides (AA17861-X17924) are targeted to a nucleic
CC acid (AA17925-X17948) encoding IF (immediate early) 1 or 2, or DNA
CC polymerase of cytomegalovirus (CMV) and are able to inhibit CMV
CC replication. Optionally the oligonucleotides include at least one 2'-(2-
CC methoxyethoxy) sugar modification or phosphorothioate internucleotide
CC linkages. The oligonucleotides are used to inhibit CMV infections (by in
CC vivo or in vitro contact with cells, tissues or body fluids), especially
CC to treat or prevent CMV infections, particularly retinitis
XX
XX Sequence 21 BP; 6 A; 6 C; 9 G; 0 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3024 CATCTGGCCCTGACCCCACTG 3044
DB 21 CTCTGGCCCTGACCCCTCTG 1
RESULT 3251
AA200585
ID AA200585 standard; DNA; 21 BP.
XX
XX AA200585;
XX
XX 06-OCT-1999 (first entry)
XX
XX Human glypican sequence tag STS MW3a.
XX
XX Glypican; GPC1; GPC3; GPC4; GPC5; GPC6; human; glypican-related protein;
KM glypican-6; glypican-4; glypican-1; glypican-3; glypican-5; diagnosis;
KM treatment; abnormal; cell growth; cell behaviour; somatic overgrowth;
KM tumour formation; sequence tag; STS; MW3a; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9937764-A2.
XX
XX 29-JUL-1999.
XX
XX 20-JAN-1999; 99WO-EP000329.
XX
XX 27-JAN-1998; 98EP-00200226.
XX
XX (VLA-) VIAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Veugelers MPD, David GJF;
XX WPI; 1999-469128/39.
XX
XX New polynucleotides encoding glypican-related proteins, used to diagnose,
PT e.g. tumor formation.
XX
XX Example 2; Page 33; 79pp; English.
XX
XX This invention describes the isolation of novel human polynucleotides
CC encoding glypican-related proteins, glypican-6 (GPC6) and glypican-4
CC (GPC4). The invention also describes the polynucleotide and encoded
CC protein sequences of glypican-1 (GPC1), glypican-3 (GPC3) and glypican-5
CC (GPC5). The products of the invention can be used to diagnose and treat
CC disorders and diseases, particularly those involving abnormal cell growth

CC and behaviour, such as somatic overgrowth and tumour formation. AA200581-
CC 200586 represent novel glypican sequence tags (STS's)
XX
XX Sequence 21 BP; 3 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4305 TTCTCTTCCCTGACTGTCC 4325
DB 1 TTCTCTTCCCTGACTTAACC 21
RESULT 3252
AAV71751/c
ID AAV71751 standard; DNA; 21 BP.
XX
XX AAV71751;
XX
XX 15-MAR-1999 (first entry)
XX
XX Human V3 loop HIV receptor p30/PHAP1 sense PCR primer.
XX
XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
KM p30 protein; PHAP1; infection; therapy; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9840480-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-EP001409.
XX
XX 12-MAR-1997; 97US-0040969P.
XX
XX (INSP) INST PASTEUR.
XX
XX (CNRS) CENT NAT RECH SCI.
XX
XX Hovanesian A, Callebaut C, Krust B, Jacotot E, Muller S;
PI Briand J, Guichard G;
XX WPI; 1999-034588/03.
XX
XX
XX New isolated V3 loop HIV receptor - comprises P95/nucleolin, P40/PHAP1
PT and P30/PHAP1 proteins, used to develop products for the treatment and
PT prevention of HIV infection.
XX
XX Disclosure; Page 48; 267pp; English.
XX
XX This oligonucleotide is complementary to a portion of DNA sequence (see
CC AAV71743) coding for the P30/PHAP1 (see AA684053) of the newly identified
CC V3 loop HIV receptor. It is used as a sense primer, together with an
CC antisense primer (see AAV71752) in a PCR amplification of P30/PHAP1
CC reverse-transcribed mRNA. The V3 loop HIV receptor consists of an
CC association of 3 proteins, named p95/nucleolin, P40/PHAP1 and P30/PHAP1
CC (see AA684052-54). A method for screening molecules that modulate the
CC expression of the receptor comprises: cultivating cells transfected with
CC a nucleotide sequence encoding P95/nucleolin, P30/PHAP1 or P30/PHAP1,
CC placed under the control of its own promoter; bringing the cells into
CC contact with a test molecule; and quantifying expression of the
CC P95/nucleolin, P30/PHAP1 or P40/PHAP1 e.g. by quantitative PCR using the
CC primers provided (see AAV71749-54). Active molecules that have the
CC ability to alter and/or prevent the binding of the HIV receptor to the
CC HIV retrovirus can be used in pharmaceutical and diagnostic compositions
CC of the invention
XX
XX Sequence 21 BP; 1 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches	17;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	60	CGAGGCTCGCGGCGGCGG	80						
Db	21	CAGAGGCTGCGCGCGCGG	1						
RESULT 3253									
AAK32391/C									
ID	AAK32391	standard; DNA; 21 BP.							
XX	AAK32391;								
XX	17-JUN-1999	(first entry)							
DE	Ab1 variable light (VL) chain CDR2 encoding DNA.								
XX									
KM	Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;								
KM	megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;								
KM	bone marrow hypoplasia; disseminated intravascular coagulation; anemia;								
KM	myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MDS; CDR;								
KM	neurovascular; muscular dystrophy; complementarity determining region;								
KM	variable heavy chain; variable light chain; VH; VL; 88.								
XX									
OS	Homo sapiens.								
XX									
FN	W09910494-A2.								
PD	04-MAR-1999.								
XX	21-AUG-1998;	98WO-US017364.							
PF	25-AUG-1997;	97US-00918148.							
PR	(GETH) GENENTECH INC.								
PA	Adams CW, Carter PJ, Fendly BM, Gurney AL;								
PI	WPI; 1999-204666/17.								
DR	P-PSDB; AAT06691.								
XX									
XX	New thrombopoietin receptor agonist antibodies - useful for treating								
PT	immunological or hematological disorders.								
XX									
PS	Claim 10; Page 75; 86pp; English.								
XX									
CC	The invention relates to an agonist antibody (Ab) which binds to a								
CC	thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can								
CC	be used in the same way and for the same indications as thrombopoietin								
CC	(TPO). They can stimulate proliferation, differentiation or growth of								
CC	megakaryocytes. They may also be able to stimulate megakaryocytes to								
CC	increase platelet production. They can be used for treating immunological								
CC	or hematopoietic disorders, especially thrombocytopenia. Thrombocytopenia								
CC	-associated bone marrow hypoplasia (e.g. aplastic anemia following								
CC	chemotherapy or bone marrow transplant) may be effectively treated with								
CC	intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and								
CC	non HIV-induced), chronic idiopathic thrombocytopenia, congenital								
CC	thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They								
CC	can also be used in e.g. myelotoxic chemotherapy for treatment of solid								
CC	tumours or leukaemia, myeloblastic chemotherapy for autologous or								
CC	allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic								
CC	anemia, congenital thrombocytopenia, and immune thrombocytopenia. The								
CC	antibodies which bind to the MDS receptor can be used for improving								
CC	neutromuscular function in a patient, e.g. in muscular dystrophy. The								
CC	products can also be used for detection and diagnosis. The antibodies								
CC	have a longer half-life than the natural ligand for the TPO-R. Sequences								
CC	AAK32387-AX22413 represent DNA fragments encoding the CDR1, CDR2, and CDR3								
CC	regions of variable heavy (VH) chains and variable light (VL) chains of								
CC	antibodies Ab1 to Ab6								
XX									
Sequence	21BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;								

Query Match	0.2%	Score 14.6	DB 1	Length 21
Best Local Similarity	81.0%	Freq. No. 2.3e+03		
Matches 17	Conservative 0	Mismatches 4	Indels 0	Gaps 0
0y	2785	TGAAGGCGAAGCGGTGACC	2805	
Db	21	TGAGGCGCGATTGCTTTACC	1	
RESULT 3254				
AAZ06694/C				
ID	AAZ06694	standard; DNA; 21 BP.		
XX				
AC	AAZ06694;			
XX				
DT	02-DEC-1999	(first entry)		
XX				
DE	Reverse PCR primer DLX7R, for amplification of DLX7.			
XX				
XX	PCR primer; DLX7; Distal-less homeobox gene 3; DLX3; dentition;			
KM	craniofacial development; Tricho-dento-osseous syndrome; TDO;			
KM	abnormal hair; teeth; bone; osseous structure repair; bone defect;			
KM	bone thickness; bone density; broken bone; periodontal disease;			
KM	osteoporosis; BS.			
XX				
OS	Synthetic.			
OS	Homo sapiens.			
XX				
PN	MO9943784-A2.			
XX				
PD	02-SEP-1999.			
XX				
XX	26-FEB-1999;	99WO-US004237.		
XX				
PR	27-FEB-1998;	98US-00031962.		
XX				
PA	(UYWA-) UNIV WAKE FOREST.			
XX				
XX	Hart TC, Price JA;			
XX				
XX	WPI, 1999-527612/44.			
DR				
XX				
XX	PCR primers AAZ06693-206694 are used to amplify the coding sequence of			
XX	DLX7. DLX7 is a member of the distal-less homeobox gene family. DLX7 is			
CC	used in the isolation of DLX3 (AAZ06690). The DLX3 gene consists of three			
CC	exons with the homeobox contained in exons 2 and 3. Exons 1 and 2 are			
CC	separated by a 1.1 kb intron, and exons 2 and 3 are separated by a 1.6 kb			
CC	intron. The DLX3 gene has been localised to chromosome 17q20-21. The DLX3			
CC	protein has a molecular weight of 32kD. The dlx genes are thought to			
CC	function in the normal craniofacial development and the development of			
CC	normal dentition. Tricho-Dento-Osseous syndrome (TDO) is an autosomal			
CC	dominant disorder characterised by abnormal hair, teeth and bone. Studies			
CC	on TDO patients show that they have a mutated form of DLX3 called			
CC	DLX3delta (AAZ06691). DLX3delta has a deletion of 4 guanine nucleotide			
CC	residues, this results in a frame shift causing the DLX3delta protein			
CC	(AAV39227) to be a truncated form of DLX3. The nucleotide and amino acid			
CC	sequences of both DLX3 and DLX3delta can be used in the development of			
CC	products for enhancing growth, development and repair of osseous			
CC	structures, particularly for treating bone defects especially in TDO			
CC	sufferers. Addition of DLX3delta proteins and DLX3delta-encoding nucleic			
CC	acids should serve to enhance bone thickness and increase bone density at			
CC	the sites of application. Exogenously added DLX3delta proteins and			
CC	DLX3delta-encoding nucleic acids should have utility in the treatment of			
CC	bone/osseous defects secondary to trauma, such as broken bones. Finally,			
CC	the DLX3delta proteins and nucleic acids should also have utility in the			
CC	treatment of defects secondary to certain pathologies, such as			
CC	periodontal disease defects or congenital/acquired defects such as			

CC osteoporosis. The products can also be used for detection and diagnosis
 XX Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4570 CCCCCCTGCTTTTCTTG 4590
 |||||
 DB 21 CCACCAGCATTTTCTTG 1

RESULT 3255

ID AAX17984 standard; DNA; 21 BP.

AC AAX17984;

DT 11-MAY-1999 (first entry)

DE Primer D399S to generate variant humanised anti-CD3 heavy chain.

KM Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
 diagnosis; cancer; primer; PCR; amplification; ss.

OS Synthetic.

PN MO9850431-A2.

PD 12-NOV-1998.

PF 30-APR-1998; 98WO-US008762.

PR 02-MAY-1997; 97US-00850058.

PR 24-JUN-1997; 97US-0050661P.

PA (GETH) GENENTECH INC.

PI Arathoon R, Carter PJ, Merchant AM, Presta LG;

DR WPI; 1999-070091/06.

PT Selective preparation of multispecific antibodies - with heteromultimeric
 heavy chain and common light chain components, useful for, e.g. in vivo
 diagnosis of cancer.

PS Example 1; Page 43; 69pp; English.

CC This oligonucleotide was used to generate a variant anti-CD3 antibody
 (Ab) heavy chain in a new method for preparing a multispecific Ab
 comprising a first polypeptide (PP) and at least 1 extra PP, where: (1)
 the first PP comprises a multimerisation domain (MD) forming an interface
 positioned to interact with an interface of a MD of the extra PP; and
 (ii) the first and extra PPs each have a binding domain, which comprises
 a heavy chain and a light chain, where the variable light chains of the
 first and extra PPs comprise a common sequence. The method comprises: (a)
 culturing a host cell comprising nucleic acid encoding the first PP and
 extra PP, and the variable light chain, such that the nucleic acid is
 expressed; and (b) recovering the multispecific Ab from the culture. The
 method prepares heteromultimeric PPs, such as bispecific Abs, bispecific
 immunoadhesins and Ab-immunoadhesin chimeras. The method allows for the
 enhanced formation of the desired heteromultimer relative to the
 undesired heteromultimers and homomultimers. The Abs can be used in
 immunoassays and for the in vitro or in vivo diagnosis of various
 diseases, such as cancer

SO Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 185 GCCGCTGACCTCGACAGG 205
 |||||
 DB 1 GCCGTGAGCTCAGCAGG 21

RESULT 3256

ID AAX84089/c

AC AAX84089;

DT 27-AUG-1999 (first entry)

DE PCR primer for TCV S1 protein coding sequence.

KM TCV; S1 protein; turkey enteritis coronavirus; turkey coronavirus; SMT;
 spiking mortality of turkeys; vaccine; immunogenic composition;

KM poult enteritis and mortality syndrome; diarrhoea; turkey poult;
 diagnosis; PCR primer; ss.

OS Synthetic.

OS Turkey coronavirus.

PN MO925838-A1.

PD 27-MAY-1999.

PF 13-NOV-1998; 98WO-US024313.

PR 14-NOV-1997; 97US-0065556P.

PR 10-NOV-1998; 98US-00188979.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

PA (BROW/) BROWN T P.

PA (VILL/) VILLEGAS P.

PI Brown TP, Villegas P, Contreras A;

DR WPI; 1999-347478/29.

PT Turkey coronavirus isolates associated with spiking mortality of turkeys.

PS Example 7; Page 7; 90pp; English.

CC This sequence represents a PCR primer for DNA encoding a turkey
 coronavirus (TCV) S1 protein. The invention relates to an isolate of TCV
 obtained from a turkey having spiking mortality of turkeys (SMT) or
 obtained from an animal exposed to the turkey, which isolate is adapted
 to cell culture. The TCV and bovine coronavirus isolates are useful for
 forming vaccines or immunogenic compositions useful for preventing or
 inhibiting SMT. SMT is a form of poult enteritis and mortality syndrome
 and causes diarrhoea in turkey poults. The methods are useful in
 diagnosis and detection of turkey coronavirus associated with SMT. The
 oligonucleotides are useful as primers for amplification of the
 coronavirus, which is useful for detecting the replication or presence
 of a virus in a sample. N.B. The protein encoded by the amplified
 sequence is referred to in the specification, but is not given in the
 specification

SO Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2679 TGGAGAGGGAGGCACATATC 2699
 |||||
 DB 21 TGGAGAGGCACCATATATC 1

RESULT 3257

ID AAX54710/c

ID AAX54710 standard; DNA; 21 BP.

XX AAX54710;
AC
XX
XX 05-JUL-1999 (first entry)
XX
XX Human fibronectin antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
XX
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JM;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
XX
XX PS Disclosure; Page 55; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAX52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the junction between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAX55180-271. These multiple target oligonucleotides
XX (specifically AAX55180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
XX Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX AAX83847/C
XX ID AAX83847 standard; DNA; 21 BP.
XX
XX AAX83847;
XX
XX 09-SEP-1999 (first entry)
XX
XX Mouse ligand polypeptide PCR primer SEQ ID NO:9.
XX
XX G protein-coupled receptor protein; APJ; central nervous system;
XX circulation; immune function; gastrointestinal function; reproduction;
XX metabolic function; HIV; infection; AIDS; PCR primer; ss.
XX
XX Synthetic.
XX
XX Mus sp.
XX
XX WO9933976-A1.
XX
XX 08-JUL-1999.
XX
XX 22-DEC-1998; 98WO-JP005805.
XX
XX 24-DEC-1997; 97JP-00353955.
XX
XX 16-FEB-1998; 98JP-00032577.
XX
XX 04-AUG-1998; 98JP-00220853.
XX
XX 25-SEP-1998; 98JP-00271645.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Talemoto K, Hosoya M, Habata Y, Fujii R, Kitada C;
XX WPI; 1999-405507/34.
XX
XX New ligand polypeptide for the G protein-coupled receptor, APJ, useful
XX for modulating central nervous system.
XX
XX Example 11; Page 93; 169pp; English.
XX
XX The present invention describes a ligand polypeptide for the G protein-
XX coupled receptor, APJ. The APJ ligand can modulate central nervous system
XX function, circulatory function, immune function, gastrointestinal
XX function, metabolic function and reproductive function. An antibody
XX against the APJ ligand can be used in diagnosis. The APJ ligand can be
XX used in an assay to screen for compounds that change its binding activity
XX to its receptor. The ligand can also be used for treating HIV infection
XX and AIDS. The present invention represents a PCR primer used in an example
XX from the present invention
XX
XX Sequence 21 BP; 6 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3866 TTCTCTTACTTCTCCGCGCG 3866
DB 21 TTCTCTTACTTCTCCGCGCG 1

RESULT 3259
AAX09053
ID AAX09053 standard; DNA; 21 BP.
XX
XX AAX09053;
XX
XX 14-JUN-1999 (first entry)
XX
XX Tumour necrosis factor alpha antisense oligonucleotide.
XX
XX Tumour necrosis factor alpha; TNF-alpha; antisense oligonucleotide; ASO;
XX inhibition; expression; treatment; disease; disorder; ss.
XX
XX Synthetic.

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OS      Rattus rattus.
XX      WO9901139-A1.
XX      14-JAN-1999.
XX      02-JUL-1998; 98WO-US013711.
XX      03-JUL-1997; 97US-0051705P.
XX      (UYJE-) UNIV JEFFERSON THOMAS.
XX      Tu G, Israel Y;
XX      WPI; 1999-105767/09.
XX      Generation of antisense oligonucleotides - by specifically targeting a
PT      GGGA motif found in mRNA sequences.
XX      Example 1; Page 32; 55pp; English.
XX      Antisense oligonucleotides (ASO) for inhibiting a tumour necrosis factor-
CC      alpha (TNF-alpha) gene in an animal, preferably a human, comprise 12-50
CC      nucleotides, 90% of which are complementary to a region of mRNA
CC      containing a GGGA sequence motif. The ASO is used to inhibit expression
CC      of a gene in an animal and for treating the animal when afflicted with a
CC      disease or disorder characterised by the presence of an mRNA from a gene
CC      containing a GGGA motif. The ASO are specifically targeted to a GGGA
CC      sequence motif found in mRNA from a gene. A study of known ASO has shown
CC      that at least half of the most efficacious ASO's contain one or more TCCC
CC      motifs. This ASO was designated TNU-2826 and corresponds to a region of
CC      the 3' untranslated region of the primary transcript of rat TNF-alpha
XX      SO
XX      Sequence 21 BP; 8 A; 1 C; 11 G; 1 T; 0 U; 0 Other;
XX      Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY      566 CTGGGGAAGGAGGATCGAA 586
DB      1 CTGAGGGAGGAGGAGGAGAA 21
XX      AAA34157/c
XX      AAA34157 standard; DNA; 21 BP.
XX      AAA34157;
XX      28-JUL-2000 (first entry)
XX      Human adenosine receptor related polynucleotide SEQ ID NO:1846.
XX      Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM      phosphorothioate; impaired respiration; inflammation; allergy;
KM      allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM      antiallergic; antiaesthetic; cytostatic; analgesic; impaired airway;
KM      lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM      respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM      pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM      cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX      Homo sapiens.
XX      WO200009525-A2.
XX      24-FEB-2000.
XX      03-AUG-1999; 99WO-US017712.
XX      03-AUG-1998; 98US-0095212P.
XX

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PA      (UYEC-) UNIV EAST CAROLINA.
XX      Wye JW;
XX      WPI; 2000-205971/18.
XX      New antisense oligonucleotides useful for treating e.g. pulmonary
PT      vasoconstriction, inflammation, allergies, asthma, hypertension,
PT      bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT      cancers.
XX      Disclosure; Page 496; 1343pp; English.
XX      The present invention describes a new composition comprising an antisense
CC      oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC      nucleic acids involved in bronchoconstriction, allergies, and/or
CC      inflammation. The ON can have antiinflammatory, antiallergic,
CC      antiaesthetic, cytostatic and analgesic activities. The compositions are
CC      useful for the treatment of diseases associated with inflammation,
CC      impaired airways, including lung disease and diseases whose secondary
CC      effects afflict the lungs of a subject. They can be used for treating
CC      e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC      impaired respiration, respiratory distress syndrome, pain, cystic
CC      fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC      pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC      carcinomas, and cancers which may metastasise to the lungs, including
CC      breast and prostate cancer. The reduction of the adenosine content of the
CC      ONs reduces side effects. The A-containing ONs break down with the
CC      release of deoxyadenosine which activates adenosine receptors causing
CC      bronchoconstriction and inflammation. AAA32313 to AAA35112 represent the
CC      nucleotide sequences given in the sequence listing from the present
CC      invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC      sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC      from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC      AAA33992) are specifically claimed ONs from the present invention. N.B.
CC      Sequences given in the disclosure of the present invention do not match
CC      up with their corresponding SEQ ID NO: sequences given in the sequence
CC      listing
XX      SO
XX      Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;
XX      Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY      3384 CTTCCCCAGCTGCCACCCCC 3404
DB      21 CCGCCGACAGGCGCCACCCCC 1
XX      AAA34157/c
XX      AA288382 standard; DNA; 21 BP.
XX      AA288382;
XX      04-MAY-2000 (first entry)
XX      Oligonucleotide PCR primer #10.
XX      PCR primer; polymerase chain reaction; amplification; probe; detection;
KM      Trachoma chlamydia; Mycobacterium tuberculosis; Hepatitis B virus;
KM      Hepatitis C virus; ss.
XX      Synthetic.
XX      CN1232182-A.
XX      20-OCT-1999.
XX      13-APR-1998; 98CN-00106616.
XX      13-APR-1998; 98CN-00106616.
XX

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XX PA (FUXI-) FUXING HIGH SCI & TECH GROUP CO LTD SHAN.
XX PI Xia Y, Xie W, Ding Y;
XX DR WPI; 2000-098541/09.
XX PT Polymerase chain reaction test method and reagent box.
XX PS Claim 16; Page 2; 19pp; Chinese.
XX CC A method has been developed for detecting nucleic acid molecules. The
CC method includes using coating liquid to drop the specific probe onto a
CC detecting membrane (the salt concentration of coating liquid is higher
CC than 2M and the membrane is a high-molecular polymer with average pore
CC size of 1-10 microns); putting one end of the membrane in the liquid
CC containing amplified polymerase chain reaction (PCR) product, and
CC detecting if the amplified PCR product is hybridised with the probe. A
CC reagent box is also disclosed to efficiently and quickly detect Trachoma
CC chlamydia, Mycobacterium tuberculosis, Hepatitis B virus and Hepatitis C
CC virus. AA288369 to AA288383 represent specifically claimed
CC oligonucleotides used in the exemplification of the present invention
XX SQ Sequence 21 BP; 3 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1023 TGGACAGATGAAGAGAGATGA 1043
Db 21 TGGAAAGCTGAAGGGGCAATGA 1
XX
RESULT 3262
AAA40708/c
ID AAA40708 standard; DNA; 21 BP.
XX AAA40708;
XX AC
XX AC
XX 15-AUG-2000 (first entry)
XX DT
XX DE Rat No63 primer No63r SEQ ID NO:96.
XX
KM Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis; therapy;
KM screening; polymorphism; variant; detection; mutant; blood; mutation;
KM insulin; glucose metabolism; fatty acid metabolism; catecholamine;
KM malaria; infection; parasite; antiparasitic; antidiabetic; primer; ss.
XX
OS Rattus sp.
XX OS
XX WO200019883-A2.
XX PN
XX 13-APR-2000.
XX PD
XX PF 07-OCT-1999; 99WO-US023418.
XX PR 07-OCT-1998; 98US-00167750.
XX PR 28-DEC-1998; 98US-00221222.
XX PR 17-MAR-1999; 99US-00270542.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (ATM/) ALTMAN T J.
PA (SCOT/) SCOTT J.
PA (SPAN/) STANTON L W.
XX
XX Altman TJ, Scott J, Stanton LW;
XX WPI; 2000-303596/26.
XX DR
XX Nucleic acid encoding mutant CD36 proteins useful for preventing,
XX diagnosing and treating parasitic infections, especially malaria.
XX PT

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```

XX PS Example 1; Page 111; 167pp; English.
XX CC The present invention describes isolated nucleic acid molecules (A)
XX CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
XX CC falciparum (the major cause of malaria) are unable to utilize the mutated
XX CC proteins to gain entry to, and infect cells. The mutant CD36 proteins do
XX CC not function correctly preventing parasites utilizing them to infect
XX CC cells. The nucleic acids may be used for the recombinant production of
XX CC mutant CD36 proteins according to standard methodologies. They may be
XX CC used in this way to prevent and treat parasitic infections that utilize
XX CC the CD36 protein to infect cells, such as P. falciparum, the major cause
XX CC of malaria. For example, the protein may be used to identify modulators
XX CC of CD36 expression and activity or a patient's CD36 DNA may be screened
XX CC to determine whether there are any mutations present that may confer
XX CC resistance to parasitic infections. The proteins and nucleic acids may
XX CC also be used to prevent, diagnose and treat diseases associated with
XX CC defects in insulin action and/or glucose metabolism and/or fatty acid
XX CC metabolism and/or catecholamine action in subjects possessing mutations
XX CC in the CD36 genes. AAA40606 to AAA40759, and AA802515 to AA802564,
XX CC represent nucleotide and amino acid sequences respectively which are used
XX CC in the exemplification of the present invention
XX SQ Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1673 CTGTGTTTCGCAAAATATGCAC 1693
Db 21 CATGTTTATGCACATGCAC 1
XX
RESULT 3263
AAZ73907/c
ID AAZ73907 standard; DNA; 21 BP.
XX AAZ73907;
XX AC
XX AC
XX 10-SEP-2001 (first entry)
XX DT
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:8263.
XX
KM Human genome; biallelic marker; high density disequilibrium map;
KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM haplotyping; hybridisation; identification; characterisation;
KM amplification; single nucleotide polymorphism; SNP; PCR primer;
KM diagnosis; ss.
XX
XX Homo sapiens.
XX OS
XX OS
XX WO9954500-A2.
XX PN
XX 28-OCT-1999.
XX PD
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX DR
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX PT
XX Claim 8; Page 1992; 2745pp; English.
XX AA265654 to AA269578 represent human biallelic markers from the present
XX CC

```


CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

QY Sequence 21 BP; 6 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
SQ

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4138 GACCTGTGACTGATTGTT 4158
Db 21 GAACGTGACCAAGATGTGT 1

RESULT 3264
AA275773
ID AA275773 standard; DNA; 21 BP.
AC AA275773;
XX
XX
DT 10-SEP-2001 (first entry)
DE Human biallelic marker downstream amplification primer SEQ ID NO:10129.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
PA
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
DR
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX
PS Claim 9; Page 2390; 2745pp; English.
XX
XX AA26554 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

QY Sequence 21 BP; 1 A; 6 C; 4 G; 10 T; 0 U; 0 Other;
SQ

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6237 CTGTCTTGTGATTGTTATCC 6257
Db 1 CTGCTTGTGATTGTTGCTTC 21

RESULT 3265
AA272176/C
ID AA272176 standard; DNA; 21 BP.
AC AA272176;
XX
XX
DT 10-SEP-2001 (first entry)
DE Human biallelic marker upstream amplification primer SEQ ID NO:6532.
XX
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
PA
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
DR
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX
PS Claim 9; Page 1623; 2745pp; English.
XX
XX AA26554 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

SQ : Sequence 21 BP; 2 A; 9 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6177 GAAAAGAGTGTGAGAGAG 6197
DB 21 GAAATTAAGAGAGTGTGAGAG 1

RESULT 3266

AAZ75738
ID AAZ75738 standard; DNA; 21 BP.

AC AAZ75738;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:10094.

XX Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX Homo sapiens.

OS WO954500-A2.

PN 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (BEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

PS Claim 8; Page 2382; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ6579 to AAZ7440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

CC Sequence 21 BP; 12 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3280 GAAGAAAATGAAACGAGCC 3300
DB 1 GAAGAAAATGAAACGAGCC 21

RESULT 3267
AAZ76866/c
ID AAZ76866 standard; DNA; 21 BP.

XX AAZ76866;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:11222.

XX Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX Homo sapiens.

OS WO954500-A2.

PN 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (BEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

PS Claim 9; Page 2623; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ7440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

CC Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3851 CTCCTTTTCCTTATTCCTC 3871
DB 21 CTCCTTTTCCTTATTCCTC 1

RESULT 3268
AAZ76031
ID AAZ76031 standard; DNA; 21 BP.

XX AAZ76031;

```

DT 10-SEP-2001 (first entry)
XX
DE Human diallelic marker downstream amplification primer SEQ ID NO:10387.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2445; 2745pp; English.
XX
CC AA265654 to AA269578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA265579 to AA277440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 2388 TGGTACATCCAGCTGGGAC 2408
Db 1 TGGTACATTAACCTGGGAC 21

```

```

RESULT 3269
AAA97479/c
ID AAA97479 standard; DNA; 21 BP.
XX
AC AAA97479;
XX
DT 29-JAN-2001 (first entry)
XX
DE Phytolacca americana antifungal protein Pa-AFP XbaI 5' PCR primer.
XX
KW Phytolacca americana antifungal protein; Pa-AFP; Virginian pokeweed;
KW recombinant production; Escherichia coli; PCR primer; ss.
XX
OS Phytolacca americana.

```

```

OS Synthetic.
XX
PN Cn1257918-A.
XX
PD 28-JUN-2000.
XX
PE 18-DEC-1998; 98CN-00125610.
XX
PR 18-DEC-1998; 98CN-00125610.
XX
PA (WUGG/) WU G.
XX
PI Wu G, Zhao J, Liu Y;
XX
DR WPI; 2000-544291/50.
XX
PT Recombination antifungal protein gene sequence, engineering bacterium and
PT process for preparing its products.
XX
PS Claim 2; Page 2; 12pp; Chinese.
XX
CC The invention to an antifungal protein (Pa-AFP; AAB23178) from the seeds
CC of Phytolacca americana (Virginian pokeweed), to cDNA encoding it
CC (AAA97476), to the processes and primers used to clone the AFP cDNA from
CC Virginian pokeweed seed total mRNA, and to its IPTG-inducible recombinant
CC production in Escherichia coli. Pa-AFP has activity against such fungi as
CC Rhizoglyphus solani (black scurf of potato) and may therefore be useful in
CC agriculture. Sequences AAA97477-A97482 represent PCR primers used to
CC introduce restriction sites into cDNA encoding Pa-AFP in the cloning
CC process
XX
SQ Sequence 21 BP; 2 A; 2 C; 13 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 3878 CCCCCCCCCCCAGCTCGA 3898
Db 21 CCCCCCCCCCCAGCTCTAGA 1

```

```

RESULT 3270
AAF20279/c
ID AAF20279 standard; DNA; 21 BP.
XX
AC AAF20279;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human fibronectin polynucleotide fragment #1846.
XX
KW low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; always disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;
KW respiratory distress syndrome; pulmonary vasoconstriction; asthma; RDS;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX

```

PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX NYCE JW;
 DR WPI; 2000-679539/66.
 XX
 PT Low adenomine (A) content antisense oligonucleotides which do not trigger
 PT adenomine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 220; 1592pp; English.
 XX
 CC The present invention describes low adenomine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antispasmodic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenomine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensive, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasocostriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 CC
 XX
 SQ Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3384 CCTCCCGACGCTGCACCCCG 3404
 DB 21 CCGCCACACGCGCACCCCG 1
 RESULT 3271
 AAC71664/c
 ID AAC71664 standard; DNA; 21 BP.
 XX
 AC AAC71664;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Single nucleotide polymorphism PCR primer #996.
 XX
 KW Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200058519-A2.
 PD 05-OCT-2000.

XX
 XX 30-MAR-2000; 2000MO-US008440.
 XX
 XX 31-MAR-1999; 99US-0127248P.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Altschuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;
 XX
 DR WPI; 2000-611722/58.
 XX
 PT Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.
 XX
 PS Claim 8; Fig 5; 214pp; English.
 XX
 CC The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases
 CC
 XX
 SQ Sequence 21 BP; 13 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4460 GGACTTTTCTTTTCTTTTCTT 4480
 DB 21 GGACATGTTTCTTTCTTTCTT 1
 RESULT 3272
 AAC71649/c
 ID AAC71649 standard; DNA; 21 BP.
 XX
 AC AAC71649;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Single nucleotide polymorphism PCR primer #986.
 XX
 KW Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200058519-A2.
 PD 05-OCT-2000.
 XX
 PF 30-MAR-2000; 2000MO-US008440.
 XX
 PR 31-MAR-1999; 99US-0127248P.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Altschuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;
 XX
 DR WPI; 2000-611722/58.

PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
PS Claim 8; Fig 5; 214pp; English.
XX
XX The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
XX Sequence 21 BP; 13 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4460 GGACTTTTCTTTTCTTTTCTTTT 4480
DB 21 GGACATGTTTCTTTCTTTCTTT 1
RESULT 3273
AAA10973
ID AAA10973 standard; DNA; 21 BP.
XX
XX AAA10973;
XX
XX 14-JUN-2000 (first entry)
XX
XX Interleukin-6 (IL-6) microsphere genosensor target sequence.
XX
XX Microsphere genosensor; detect target analytes; library screening;
XX potential drug; pollutant; solvent; therapeutic drug; illicit drug;
XX hormone; cytokine; cancer; Alzheimer's disease; cystic fibrosis;
XX toxic bacteria; forensic DNA fingerprinting; detect; infection; target;
XX bioactive agent; optical signature; interleukin-6; IL-6; ss.
XX
XX Unidentified.
XX
XX WO200016101-A2.
XX
XX 23-MAR-2000.
XX
XX 10-SEP-1999; 99WO-US020914.
XX
XX 11-SEP-1998; 98US-00151877.
XX
XX (TUFT) TUFTS COLLEGE.
XX
XX Walt DR, Michael KU;
XX
XX WPI; 2000-364508/31.
XX
XX Composition comprising microspheres with a bioactive agent and optical
PT signature, at discrete sites on substrate, useful for detecting target
PT analytes, e.g. nucleic acids.
XX
XX
XX Disclosure; Page 29; 58pp; English.
XX
XX This sequence represents a target sequence for a microsphere genosensor
CC created using the composition of the invention. The invention relates to
CC a composition which comprises a substrate (other than a fibre optic
CC bundle) with discrete sites on its surface, and microspheres distributed
CC at these sites. The microspheres comprise at least two subpopulations,
CC each with a bioactive agent and an optical signature that identifies the
CC bioactive agent. Microsphere genosensors are made by attaching a probe

CC (examples include AAA10964-A10968) to the microsphere surface chemistry.
CC A fluorescent dye molecule is attached to the target sequence (examples
CC include AAA10965-A10973) which is in solution. The optically
CC interrogatable signal change occurs with the binding of the target
CC sequences to the microsphere. The composition of the invention is used to
CC detect target analytes and screen large libraries of bioactive agents for
CC those (potential drugs) that bind to the target analytes e.g. pollutants;
CC solvents; therapeutic or illicit drugs; hormones; cytokines; nucleic
CC acids (detecting genes associated with cancer, Alzheimer's disease or
CC cystic fibrosis); antigens; whole cells; to screen foods and water for
CC toxic bacteria; for forensic DNA fingerprinting; for sequencing and for
CC detecting mutations; and detecting viral or bacterial infections
XX
XX Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3653 AAGAAATACCCGAGCCCAAC 3673
DB 1 AATACCAACCCCTGACCCAC 21
RESULT 3274
AAA94225
ID AAA94225 standard; DNA; 21 BP.
XX
XX AAA94225;
XX
XX 12-JAN-2001 (first entry)
XX
XX Human testosterone-repressed prostate message-2 antisense oligo #1.
XX
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200049937-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX
XX WPI; 2000-531132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
XX Example 5; Page 36; 38pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
XX
SQ Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      674 TGGAGTCTGTGCAAGCCCTGG 694
      |||||
DB      1 TGGAGTCTTTCAGCGCTCTCG 21

RESULT 3275
AAA97685/c
ID      AAA97685 standard; DNA; 21 BP.
XX
AC      AAA97685;
XX
DT      15-FEB-2001 (first entry)
XX
DE      Interleukin-6 (IL-6) array probe #5.
XX
KM      Analyte detection; microsphere array; self-encoding sensor array;
XX      nucleic acid detection; biochip; disease-associated gene; probe; ss.
OS      Unidentified.
XX
FN      WO200060332-A2.
XX      12-OCT-2000.
XX
PF      06-APR-2000; 2000WO-US009183.
XX
PR      06-APR-1999; 99US-00287573.
XX
PA      (TUFT ) TUFTS COLLEGE.
XX
PI      Walt DR, Dickinson TA;
XX
DR      WPI; 2000-656240/63.
XX
PT      Method for detecting target analyte in sample involves, providing array
PT      with several sub population of sensor elements, measuring optical
PT      response of each sensor element and statistically analyzing optical
PT      response.
XX
XX      Example 19; Fig 22; 99pp; English.
XX
PS      The invention relates to a method for detecting a target analyte in a
XX      sample using a self-encoding sensor array comprising a population of
XX      microspheres on discrete locations on the surface of a substrate. The
XX      array has several subpopulations of microspheres, each of which provides
XX      a characteristic optical response signature when illuminated by
XX      excitation light energy in the presence of a reference analyte, which may
XX      in some cases be the target analyte. The method involves contacting the
XX      array with a sample, measuring the optical response of each microsphere
XX      sensor element, and performing statistical analysis on the measured
XX      optical response of the subpopulations. The method is used for detecting
XX      target analytes such as nucleic acids, proteins, hormones, lipids,
XX      carbohydrates, whole cells, environment pollutants and drugs. The method
XX      is inexpensive when compared to conventional methods. The array once
XX      loaded can be decoded or used after testing. The present sequence
XX      represents a probe used to detect the presence of a disease- associated
XX      gene fragment in an exemplification of the invention
XX
SQ      Sequence 21 BP; 2 A; 1 C; 10 G; 8 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3653 AAGAAATATCCCGACGCCAAC 3673
      |||||
DB      21 AATTAACACCCCTGACCCAAC 1

RESULT 3276
AAA97679
ID      AAA97679 standard; DNA; 21 BP.

```

```

XX      AAA97679;
AC      15-FEB-2001 (first entry)
XX
DT      Interleukin-6 (IL6) target sequence.
XX
DE      Analyte detection; microsphere array; self-encoding sensor array;
XX      nucleic acid detection; biochip; target; ss.
OS      Unidentified.
XX
FN      WO200060332-A2.
XX      12-OCT-2000.
XX
PF      06-APR-2000; 2000WO-US009183.
XX
PR      06-APR-1999; 99US-00287573.
XX
PA      (TUFT ) TUFTS COLLEGE.
XX
PI      Walt DR, Dickinson TA;
XX
DR      WPI; 2000-656240/63.
XX
PT      Method for detecting target analyte in sample involves, providing array
PT      with several sub population of sensor elements, measuring optical
PT      response of each sensor element and statistically analyzing optical
PT      response.
XX
XX      Disclosure; Page 39; 99pp; English.
XX
PS      The invention relates to a method for detecting a target analyte in a
XX      sample using a self-encoding sensor array comprising a population of
XX      microspheres on discrete locations on the surface of a substrate. The
XX      array has several subpopulations of microspheres, each of which provides
XX      a characteristic optical response signature when illuminated by
XX      excitation light energy in the presence of a reference analyte, which may
XX      in some cases be the target analyte. The method involves contacting the
XX      array with a sample, measuring the optical response of each microsphere
XX      sensor element, and performing statistical analysis on the measured
XX      optical response of the subpopulations. The method is used for detecting
XX      target analytes such as nucleic acids, proteins, hormones, lipids,
XX      carbohydrates, whole cells, environment pollutants and drugs. The method
XX      is inexpensive when compared to conventional methods. The array once
XX      loaded can be decoded or used after testing. The present sequence
XX      represents a target sequence which can be detected using the method of
XX      the invention
XX
SQ      Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3653 AAGAAATATCCCGACGCCAAC 3673
      |||||
DB      1 AATTAACACCCCTGACCCAAC 21

RESULT 3277
AAA97698
ID      AAA97698 standard; DNA; 21 BP.
XX
AC      AAA97698;
XX
DT      15-FEB-2001 (first entry)
XX
DE      Interleukin-6 (IL-6) array probe #18.
XX
KM      Analyte detection; microsphere array; self-encoding sensor array;
XX      nucleic acid detection; biochip; disease-associated gene; probe; ss.

```

```
XX Unidentified.
OS
XX WO200060332-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009183.
XX
XX 06-APR-1999; 99US-00287573.
XX
XX (TUFTS ) TUFTS COLLEGE.
XX
XX Walt DR, Dickinson TA;
XX
XX WPI; 2000-656240/63.
XX
XX Method for detecting target analyte in sample involves, providing array
XX PT with several sub population of sensor elements, measuring optical
XX PT response of each sensor element and statistically analyzing optical
XX PT response.
XX
XX Example 19; Fig 22; 99pp; English.
XX
XX The invention relates to a method for detecting a target analyte in a
XX CC sample using a self-encoding sensor array comprising a population of
XX CC microspheres on discrete locations on the surface of a substrate. The
XX CC array has several subpopulations of microspheres, each of which provides
XX CC a characteristic optical response signature when illuminated by
XX CC excitation light energy in the presence of a reference analyte, which may
XX CC in some cases be the target analyte. The method involves contacting the
XX CC array with a sample, measuring the optical response of each microsphere
XX CC sensor element, and performing statistical analysis on the measured
XX CC optical response of the subpopulations. The method is used for detecting
XX CC target analytes such as nucleic acids, proteins, hormones, lipids,
XX CC carbohydrates, whole cells, environmental pollutants and drugs. The method
XX CC is inexpensive when compared to conventional methods. The array once
XX CC loaded can be decoded or used after testing. The present sequence
XX CC represents a probe used to detect the presence of a disease-associated
XX CC gene fragment in an exemplification of the invention
XX
XX Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3653 AAGAAATACCCGACGCCAAC 3673
XX |||||
XX 1 AATACCAACCCCTGACCCAAC 21
XX
XX RESULT 3278
XX AAA65238
XX ID AAA65238 standard; DNA; 21 BP.
XX
XX AAA65238;
XX
XX 12-DEC-2000 (first entry)
XX
XX Meloidogyne chitwoodi species-specific oligonucleotide #1.
XX DE
XX Species-specific oligonucleotide; crop parasite; crop damage;
XX KM root-knot nematode; PCR primer; ss.
XX
XX Meloidogyne chitwoodi.
XX OS
XX WO200040754-A1.
XX
XX 13-JUL-2000.
XX
XX 28-DEC-1999; 99WO-NL000812.
XX
XX
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PR 30-DEC-1998; 98NL-01010917.
XX
XX (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX PA
XX Zijlstra C;
XX PI
XX WPI; 2000-465998/40.
XX DR
XX Novel DNA oligonucleotide specific for Meloidogyne species, used to
XX PT detect specific Meloidogyne species in a sample.
XX
XX Claim 5; Page 20; 33pp; English.
XX
XX The present sequence is a species-specific oligonucleotide for the root-
XX CC knot nematode Meloidogyne chitwoodi. This is a crop parasite which can
XX CC cause damage to crops such as potatoes, beets, black salisifies and
XX CC carrots, the damage being so great that in Europe the organism has been
XX CC given a quarantine status. The oligonucleotide was identified using
XX CC random amplified polymorphic DNA and subjecting it to a series of
XX CC selection procedures until a species-specific fragment was found. The
XX CC sequence can be used in tests to determine both the presence and species
XX CC of Meloidogyne parasites, which is useful for seed export and also in the
XX CC search for resistance to the parasite
XX
XX Sequence 21 BP; 9 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4731 TGGAGGCCAGCTGAGGAGA 4751
XX |||||
XX 1 TGGAGAGCAGCAGAGAGAGA 21
XX
XX RESULT 3279
XX AAA76069
XX ID AAA76069 standard; DNA; 21 BP.
XX
XX AAA76069;
XX
XX 08-DEC-2000 (first entry)
XX
XX beta-actin PCR primer #2.
XX DB
XX PCR primer; prostate cancer cell line; androgen independent; C1-1; C1-2;
XX KM LNCaP cell line; beta-actin; Prostate-specific antigen;
XX KM Prostate specific membrane antigen; Basic fibroblast growth factor;
XX KM Vascular endothelial cell growth factor; Interleukin-6;
XX KM Transforming Growth Factor-beta1; Transforming Growth Factor-beta2;
XX KM AR; PSA; IL-8; VEGF; bFGF; IL-6; TGF-beta1; TGF-beta2; TGF-beta-R;
XX KM EGF-R; BCL-2; E-cadherin; p53; PTEN; Caveolin; c-myc; HER-2/neu; p27;
XX KM Androgen receptor; ss.
XX
XX Homo sapiens.
XX OS
XX WO200044879-A1.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US002223.
XX PF
XX 28-JAN-1999; 99US-0117562P.
XX PR
XX (REGC ) UNIV CALIFORNIA.
XX PA
XX Belldegrun AS, Tso C;
XX PT
XX WPI; 2000-499329/44.
XX
XX Androgen independent, aggressively tumorigenic prostate cancer cell lines
XX PT designated C1-1 and C1-2, useful as tools for studying the cellular and
```

PT molecular mechanisms of prostate cancer progression.
 XX
 PS Example 2; Page 29; 90pp; English.
 XX
 CC The present invention relates to androgen independent, aggressively
 CC tumorigenic prostate cancer cell lines, CL-1 and CL-2, which are
 CC sublines of the LNCaP cell line. The present sequence is a PCR primer
 CC used to amplify a coding sequence expressed by the cell lines. The coding
 CC sequences which were amplified in the present invention by the primers in
 CC AAA76068 to AAA76107 were: beta-actin, prostate-specific antigen (PSA),
 CC Androgen receptor (AR), prostate specific membrane antigen (PSAM),
 CC Interleukin-8 (IL-8), Vascular endothelial cell growth factor (VEGF),
 CC Basic fibroblast growth factor (bFGF), Interleukin-6 (IL-6), Transforming
 CC Growth Factor-beta1 (TGF-beta1), Transforming Growth Factor-beta2 (TGF-
 CC beta2), Transforming Growth Factor-beta-R (TGF-beta-R), Epidermal growth
 CC factor receptor (EGF-R), BCL-2, E-cadherin, p53, PTEN, Caveolin, c-myc,
 CC HRR-2/nu and p27. RT-PCR was used to monitor changes in coding sequence
 CC expression, as the LNCaP parental lines progressed to the CL1 and CL2
 CC sublines. The CL-1 and CL-2 sublines can be used as tools for studying
 CC the cellular and molecular mechanisms of prostate cancer progression.
 CC such as the expression patterns of various transcripts and proteins that
 CC are associated with the progression of the non-metastatic, androgen-
 CC dependent state to the metastatic androgen-independent state
 CC
 XX Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 712 CTGCGATCATGAGGTACAC 732
 1 CTGCGATCATGAGGTACAC 21
 QY
 DB
 RESULT 3280
 AAF96869/c
 ID AAF96869 standard; DNA; 21 BP.
 XX
 AC AAF96869;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #1630.
 XX
 KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KM polymorphism; vascular disease; coronary artery disease; forensics;
 KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KM pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 FT
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX
 DR WPI; 2001-226749/23.

XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 PS Example; Page 158; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 CC
 XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
 SQ
 QY Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 7384 TGTACAGTTCCTTCGACGA 7404
 21 TGTACAGTTCCTTCGACGA 1
 QY
 DB
 RESULT 3281
 AAF97449/c
 ID AAF97449 standard; DNA; 21 BP.
 XX
 AC AAF97449;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #2210.
 XX
 KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KM polymorphism; vascular disease; coronary artery disease; forensics;
 KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KM pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 FT
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX
 DR WPI; 2001-226749/23.
 XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and


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PT atherosclerosis.
XX
XX Example; Page 199; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 1 A; 5 C; 11 G; 4 T; 0 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2721 CCCCCAGCCCTGCGCAAGC 2741
Db      21 CCCCCAGCTCCGCGCAAGC 1

RESULT 3282
AAF97249 standard; DNA; 21 BP.
XX
AC AAF97249;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #2010.
XX
KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM polymorphism; vascular disease; coronary artery disease; forensics;
KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key          Location/Qualifiers
FT Variation    replace(11,A)
FT              /*tag= a
FT              /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (MHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
XX Example; Page 185; 242pp; English.
XX
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CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      987 GGAGATCAAGGCGCTGAAGT 1007
Db      1 GGAGTTCAGGCTCTGTTGCT 21

RESULT 3283
AAF96294 standard; DNA; 21 BP.
XX
AC AAF96294;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1055.
XX
KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM polymorphism; vascular disease; coronary artery disease; forensics;
KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key          Location/Qualifiers
FT Variation    replace(11,C)
FT              /*tag= a
FT              /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (MHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
XX Example; Page 124; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
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CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
XX      SQ      Sequence 21 BP, 6 A, 4 C, 7 G, 4 T, 0 U, 0 Other;
QY      Query Match      0.2%; Score 14.6; DB 1; Length 21;
Db      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      2938 TGGGGAACAGGCGCCAGCAAG 2958
          |||||
Db      1 TGGAGTTCATGCGCCAGCAAG 21
          |||||

RESULT 3284
AA96296/c
ID      AAF96296 standard; DNA; 21 BP.
XX
AC      AAF96296;
XX
DT      06-JUN-2001 (first entry)
XX
DE      Human gene single nucleotide polymorphism #1057.
XX
KM      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM      polymorphism; vascular disease; coronary artery disease; forensics;
KM      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM      pulmonary embolism; paternity test; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Variation /replace(11,T)
FT      /*tag= a
FT      /standard_name= "single nucleotide polymorphism"
XX
PN      WO200118250-A2.
XX
PD      15-MAR-2001.
XX
PF      07-SEP-2000; 2000WO-US024503.
XX
PR      10-SEP-1999; 99US-0153357P.
PR      26-JUL-2000; 2000US-0220947P.
PR      16-AUG-2000; 2000US-0225724P.
XX
PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA      (MILL-) MILLENNIUM PHARM INC.
XX
PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX      WPI; 2001-226749/23.
XX
PT      Nucleic acids comprising single nucleotide polymorphisms, useful in
PT      applications such as forensics, paternity testing, medicine, genetic
PT      analysis and phenotype correlations to diseases such as diabetes and
PT      atherosclerosis.
XX
PS      Example; Page 124; 242pp; English.
XX
CC      The present invention provides a method of diagnosing a vascular disease
CC      in an individual, involving determining the sequence at various
CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC      genes. The sequences at a number of polymorphic sites are also provided
CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
```

```
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
XX      SQ      Sequence 21 BP, 6 A, 4 C, 9 G, 2 T, 0 U, 0 Other;
QY      Query Match      0.2%; Score 14.6; DB 1; Length 21;
Db      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      4306 TTCCTTCCCTGACTGTCTT 4326
          |||||
Db      21 TCCCTTCCCGAAGCTGCTG 1
          |||||

RESULT 3285
AA96817/c
ID      AAF96817 standard; DNA; 21 BP.
XX
AC      AAF96817;
XX
DT      06-JUN-2001 (first entry)
XX
DE      Human gene single nucleotide polymorphism #1578.
XX
KM      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM      polymorphism; vascular disease; coronary artery disease; forensics;
KM      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM      pulmonary embolism; paternity test; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Variation /replace(11,G)
FT      /*tag= a
FT      /standard_name= "single nucleotide polymorphism"
XX
PN      WO200118250-A2.
XX
PD      15-MAR-2001.
XX
PF      07-SEP-2000; 2000WO-US024503.
XX
PR      10-SEP-1999; 99US-0153357P.
PR      26-JUL-2000; 2000US-0220947P.
PR      16-AUG-2000; 2000US-0225724P.
XX
PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA      (MILL-) MILLENNIUM PHARM INC.
XX
PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX      WPI; 2001-226749/23.
XX
PT      Nucleic acids comprising single nucleotide polymorphisms, useful in
PT      applications such as forensics, paternity testing, medicine, genetic
PT      analysis and phenotype correlations to diseases such as diabetes and
PT      atherosclerosis.
XX
PS      Example; Page 154; 242pp; English.
XX
CC      The present invention provides a method of diagnosing a vascular disease
CC      in an individual, involving determining the sequence at various
CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC      genes. The sequences at a number of polymorphic sites are also provided
CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
```

Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2713 GGGCGGAGCCCGAGCCCTG 2733
Db 21 GGGTGTGACGACGAGCCCTG 1

RESULT 3286
AAF96350/c
ID AAF96350 standard; DNA; 21 BP.
AC AAF96350;
DT 06-JUN-2001 (first entry)
DE Human gene single nucleotide polymorphism #1111.
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

WO200118250-A2.
PN 15-MAR-2001.
PP 07-SEP-2000; 2000WO-US024503.
XX 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX (MHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
DR WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX Example; Page 128; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX Sequence 21 BP; 8 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

900 TGAGTTGATGTGTAGTGCT 920
Db 21 TGAGTTCTCTGTGAGTGCT 1

RESULT 3287
AAF97158
ID AAF97158 standard; DNA; 21 BP.
AC AAF97158;
DT 06-JUN-2001 (first entry)
DE Human gene single nucleotide polymorphism #1919.
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

WO200118250-A2.
PN 15-MAR-2001.
PP 07-SEP-2000; 2000WO-US024503.
XX 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX (MHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
DR WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX Example; Page 179; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX Sequence 21 BP; 7 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3777 TGACATTGACCTTCAACA 3797
||| ||||||| |||||||

Db 1 TTACTATTGCACCTTGCACCA 21

RESULT 3288

AAF95280/c
ID AAF95280 standard; DNA; 21 BP.

XX AAF95280;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #41.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

XX polymorphism; vascular disease; coronary artery disease; forensics;

XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Variation /tag= a

XX /standard_name= "single nucleotide polymorphism"

XX NO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000MO-US024503.

XX 10-SEP-1999; 99US-0153357P.

XX 26-JUL-2000; 2000US-0220947P.

XX 16-AUG-2000; 2000US-0225724P.

XX (MHED) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis.

XX Example; Page 49; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism and

XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

XX the human gene SNPs shown in the specification

XX Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX QY 719 CCATGAGTACACCCCTGTGG 739

XX Db 21 CCTTCAGGTACACCACTGGGG 1

XX RESULT 3289

AAF95372
ID AAF95372 standard; DNA; 21 BP.

XX AAF95372;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #133.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

XX polymorphism; vascular disease; coronary artery disease; forensics;

XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Variation /tag= a

XX /standard_name= "single nucleotide polymorphism"

XX NO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000MO-US024503.

XX 10-SEP-1999; 99US-0153357P.

XX 26-JUL-2000; 2000US-0220947P.

XX 16-AUG-2000; 2000US-0225724P.

XX (MHED) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis.

XX Example; Page 57; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism and

XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

XX the human gene SNPs shown in the specification

XX Sequence 21 BP; 4 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX QY 603 CAAAGTGGCTGCGCATTTGTAG 623

XX Db 1 CAAAGTGGCTGCGCATTTGTAG 21

XX RESULT 3290

XX AAF62434

XX ID AAF62434 standard; DNA; 21 BP.

XX AAF62434;

[illegible]

XX	Key	Location/Qualifiers
FH	Variation	replace(11,A)
FT		/tag= a
FT		/standard_name= "single nucleotide polymorphism"
FN	WO200138576-A2.	
PD	31-MAY-2001.	
XX	17-NOV-2000; 2000WO-US031639.	
XX	24-NOV-1999; 99US-0167334P.	
XX	(WHD) WHITEHEAD INST BIOMEDICAL RES.	
PI	Cargill M, Ireland JS, Lander ES;	
XX	WPI; 2001-367705/38.	
XX	New nucleic acid segments of the human genome, particularly from genes	
PT	including polymorphic sites,for phenotype correlation, forensics,	
PT	paternity testing, medicine and genetic analysis.	
XX	Claim 1; Page 43; 80pp; English.	
PS	DNA sequences AAH62100 - AAH62688 represent segments of human genes which	
CC	contain single nucleotide polymorphisms (SNPs). A method is included in	
CC	the invention for analysing a nucleic acid sample, which consists of	
CC	determining the base occupying any one of the polymorphic sites given in	
CC	the SNP containing sequences. The nucleotide sequences can be used in the	
CC	diagnosis or monitoring of diseases, such as cancer, inflammation, heart	
CC	diseases, diseases of the cardiovascular system, and infection by	
CC	microorganisms. The oligonucleotides are also useful in the manufacture	
CC	of a medicament for the treatment or prophylaxis of the diseases, and as	
CC	a pharmaceutical. SNP containing oligonucleotides are useful in	
CC	applications such as phenotype correlation, forensics, paternity testing,	
CC	medicine and genetic analysis	
SQ	Sequence 21 BP; 1 A; 10 C; 8 G; 2 T; 0 U; 0 Other;	
	Query Match 0.2%; Score 14.6; DB 1; Length 21;	
	Best Local Similarity 81.0%; Pred.No. 2.3e+03;	
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
OY	30 GAGCTGCTGCAGGCTCGCGG 50	
DB	1 GAGCTGCCCTGGCCCGCGG 21	
	RESULT 3292	
	AAH62422	
ID	AAH62422 standard; DNA; 21 BP.	
AC	AAH62422;	
XX	12-SEP-2001 (first entry)	
DT	SLC18A3 polymorphism containing DNA fragment #323.	
DE	Single nucleotide polymorphism; SNP; human; cancer; inflammation;	
KM	heart disease; paternity testing; forensic science; de.	
KX	Homo sapiens.	
OS		
XX	Key Location/Qualifiers	
FH	Variation replace(11,T)	
FT	/tag= a	
FT	/standard_name= "single nucleotide polymorphism"	
FN	WO200138576-A2.	
PD	31-MAY-2001.	

```
XX 17-NOV-2000; 2000MO-US031639.
XX
XX 24-NOV-1999; 99US-0167334P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES,
XX
XX WPI; 2001-367705/38.
XX
XX
XX New nucleic acid segments of the human genome, particularly from genes
XX including polymorphic sites, for phenotype correlation, forensics,
XX paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 55; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH6268 represent segments of human genes which
XX contain single nucleotide polymorphisms (SNPs). A method is included in
XX the invention for analysing a nucleic acid sample, which consists of
XX determining the base occupying any one of the polymorphic sites given in
XX the SNP containing sequences. The nucleotide sequences can be used in the
XX diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX diseases, diseases of the cardiovascular system, and infection by
XX microorganisms. The oligonucleotides are also useful in the manufacture
XX of a medicament for the treatment or prophylaxis of the diseases, and as
XX a pharmaceutical. SNP containing oligonucleotides are useful in
XX applications such as phenotype correlation, forensics, paternity testing,
XX medicine and genetic analysis
XX
XX Sequence 21 BP; 0 A; 8 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5778 GCCTGCTGCTGCTGCTGCTG 5798
XX 1 GCCTGCTGCTGCTGCTGCTG 21
XX
XX
XX RESULT 3293
XX ID AAA91034/c
XX AAA91034 standard; DNA; 21 BP.
XX
XX AAA91034;
XX
XX 05-APR-2001 (first entry)
XX
XX PCR primer for Human secreted protein PRO7476 coding sequence.
XX
XX Secreted protein; human; PRO protein; neoplastic cell growth; tumour;
XX proliferation; leukaemia; lymphoid malignancy; inflammatory disorder;
XX angiogenic disorder; immunologic disorder; PRO7476; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200075317-A2.
XX
XX 14-DEC-2000.
XX
XX
XX 15-MAY-2000; 2000MO-US013358.
XX
XX 09-JUN-1999; 99US-0138365P.
XX 20-JUL-1999; 99US-0144790P.
XX 03-AUG-1999; 99US-0146843P.
XX 10-AUG-1999; 99US-0148188P.
XX 17-AUG-1999; 99US-0149320P.
XX 17-AUG-1999; 99US-0149327P.
XX 17-AUG-1999; 99US-0149366P.
XX 20-AUG-1999; 99US-0150114P.
XX 31-AUG-1999; 99US-0151700P.
XX 31-AUG-1999; 99US-0151734P.
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XX (GETH ) GENENTECH INC.
XX
XX Botstein DA, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI; 2001-071075/08.
XX
XX
XX Antibodies against PRO polypeptides, useful for diagnosing and treating
XX tumors are associated with gene amplification, neoplastic cell growth and
XX proliferation in mammals.
XX
XX Example 10; Page 92; 143pp; English.
XX
XX This sequence represents a PCR primer used to isolate DNA encoding human
XX PRO7476 protein of the invention. The PRO proteins are secreted proteins.
XX Antagonists or antibodies of PRO polypeptides are useful for diagnosing
XX and treating tumours are associated with gene amplification, neoplastic
XX cell growth and proliferation in mammals, and those conditions
XX characterised by overexpression and/or activation of the amplified genes.
XX Such conditions include benign or malignant tumours (e.g. renal, liver,
XX kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
XX pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
XX glioblastomas and various head and neck tumours); leukaemias and lymphoid
XX malignancies; neuronal, glial, astrocytal, hypothalamic, and other
XX glandular, macrophageal, epithelial, stromal and blastocoele disorders;
XX and inflammatory, angiogenic and immunologic disorders. These may further
XX be used to qualitatively or quantitatively detect the expression of
XX proteins encoded by the amplified genes, and in tumour diagnostics or
XX prognostics. The PRO polypeptide or its antagonist may be used for the
XX preparation of a medicament in the treatment of a condition, which is
XX responsive to the PRO polypeptide, its antagonist or anti-PRO antibody
XX
XX Sequence 21 BP; 3 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5166 CTGGACAGTGGGCTGTCAT 5186
XX 21 CAGGCGCAGTGGAGCTGCAT 1
XX
XX
XX RESULT 3294
XX ID AAF76187/c
XX AAF76187 standard; DNA; 21 BP.
XX
XX AAF76187;
XX
XX 05-JUN-2001 (first entry)
XX
XX Human interleukin-6 (IL-6) PCR primer, SEQ ID NO:53.
XX
XX Transgenic mouse; immunodeficient; tissue recipient;
XX lymphocyte deficient; human cytokine; interleukin; IL-7; IL-6; SCF; LIF;
XX stem cell factor; leukaemia inhibitory factor; GM-CSF; M-CSF;
XX granulocyte macrophage-colony stimulating factor;
XX macrophage-colony stimulating factor; human MHC class II; DR3;
XX major histocompatibility complex; allergenicity determination;
XX human monoclonal antibody generation; haematopoietic cell development;
XX human immune system animal model; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200115521-A1.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000MO-US023971.
XX
XX 31-AUG-1999; 99US-0151688P.
XX
XX (GENV ) GENENCOR INT INC.
```

XX Huang MA, Harding FA;
PI WPI; 2001-169001/17.
XX
XX New transgenic mice, useful as non-human mammalian models of human
PT disease, comprise recombination activation gene mutations and donor
PT specific transgenes encoding cytokines.
XX
XX Example 2; Page 38, 68pp; English.
XX
XX The invention relates to a transgenic immunodeficient recipient mouse
CC which is capable of supporting the growth of donor cells. In the mouse,
CC both alleles of a gene activated in early lymphocyte development are
CC disrupted, causing it to lack mature B and T cells. In particular, both
CC alleles of the recombination activation gene-2 (RAG-2) gene are
CC disrupted, which in turn prevents VDJ recombination. The mouse also
CC comprises donor (e.g., human) specific transgenes encoding the cytokines
CC interleukin-7 (IL-7), stem cell factor (SCF), leukemia inhibitory factor
CC (LIF), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC macrophage-colony stimulating factor (M-CSF), and IL-6, which enable it
CC to support the growth of transplanted donor cells. In another embodiment
CC of the invention, the mouse comprises DNA encoding the human major
CC histocompatibility complex (MHC) class II DR3 molecule, where the
CC transgene has naturally linked DRab and DQab alleles. The transgenic
CC mouse may be used as a model for determining the allergenicity of non-
CC donor, e.g., non-human, macromolecules; to determine the effect compounds
CC have on a human immune system; to generate fully human polyclonal or
CC monoclonal antibodies to specific antigens; to determine whether
CC humanised or other monoclonal antibodies will raise a response in a human
CC immune system; to investigate the human cell mediated response to
CC pathogens and other immunomodulatory compounds; and to determine the
CC factors involved in regulating the development and function of human
CC haematopoietic cells. The transgenic mouse supports the functional
CC properties of human haematopoietic cells, unlike previous animal models
CC which produce functionally impaired haematopoietic cells or are
CC immunologically dysfunctional. In addition the transgenic mouse provides
CC a unique model system which supports T cell development in a manner which
CC more closely resembles normal ontogeny, as they possess CD4+ T cells in
CC the periphery that exhibit MHC-restricted antigen- specific responses.
CC Sequences AAF6133-AAF6192 represent human cytokine PCR primers used in
CC the development of human cytokine-expressing transgenic mice
XX
XX Sequence 21 BP; 0 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 7406 GCAACATGACGAGCAGCAGCA 7426
Db 21 GCAACACGAGGAGCAGCCCA 1
AAH23038/C
ID AAH23038 standard; DNA, 21 BP.
XX AAH23038;
AC
XX 17-SEP-2001 (first entry)
DT
XX
XX PlGF gene fragment.
DE
XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
KW antisense therapy; PlGF, ds.
XX
OS Homo sapiens.
XX
XX WO200152904-A2.
PN
XX 26-JUL-2001.
PD

XX 19-JAN-2001; 2001WO-US000019.
PE
XX 19-JAN-2000; 2000US-00487023.
PR
XX (GILL/) GILL P S.
XX
XX GILL PS, Masood R;
PI WPI; 2001-451898/48.
XX
XX
XX Novel antisense oligonucleotides useful for inhibiting vascular
PT endothelial growth factor expression, angiogenesis and for treating
PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostate cancer.
XX
XX Example; Fig 17b; 105pp; English.
XX
XX The invention provides a composition comprising one or more antisense
CC oligonucleotides directed against vascular endothelial growth factor
CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
CC cells exhibiting autocrine VEGF activity at an 10^{-5} to 10^{-6} concentration of
CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
CC Preferably the oligonucleotide AAH23032 (a modified version of AAH23984)
CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
CC prostate cancer, pancreatic cancer or melanoma. The present sequence
CC represents a PlGF gene fragment
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 5175 TGCGCTGCATGTTCTCCAC 5195
Db 21 TGCGCTGACATGCTCCAC 1
AAH62077/C
ID AAH62077 standard; DNA, 21 BP.
XX
XX AAH62077;
AC
XX 10-SEP-2001 (first entry)
DT
XX
XX PDGF B hairpin/hammerhead ribozyme recognition site SEQ ID NO:4501.
DE
XX
XX Human, ribozyme therapy, hairpin ribozyme, hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulvular;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiproliferative; dermatological; antiseborrheic; antidiabetic; vitinide;
KW anticaking; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200130362-A2.
PN
XX 03-MAY-2001.
PD
XX 26-OCT-2000; 2000WO-US029500.
PE
XX 26-OCT-1999; 99US-0161532P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX

CC 1liposome-mediated transfection, polybrene-mediated transfection, receptor
 CC -mediated uptake or Ca-PO4-mediated transformation
 CC
 SQ Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 712 CTGCGATCATGAGGTACACC 732
 |||||
 1 CTCGCGTTCATGAGGACACCC 21

RESULT 3299
 AAS22024/c
 ID AAS22024 standard; DNA; 21 BP.
 AC AAS22024;
 XX
 XX 24-OCT-2001 (first entry)
 DE Human COL1A1 PCR primer for Exon 19 #2.
 XX
 XX Human; collagen; COL1A1; COL1A2; COL9A2; COL9A3; ss;
 KM osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;
 KM shortness of stature; low bone density; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN US6265157-B1.
 XX
 PD 24-JUL-2001.
 XX
 PF 03-OCT-1997; 97US-00943731.
 XX
 PR 03-DEC-1991; 91US-00803628.
 PR 13-MAR-1994; 94US-00212322.
 XX
 PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
 PA (UYUE-) UNIV JEFFERSON THOMAS.
 PA (UYOU-) UNIV OULU.
 XX
 PI Prockop DJ, Spotila LD, Deltas CD, Sereda L;
 PI Westenhansen Larson A, Pack M, Collige A, Early J, Koerkhoe J;
 PI Ala-Kokko L, Annunen S, Pihlajamaa T, Vuoristo M, Paasasilta P;
 PI WPI; 2001-432201/46.
 DR
 XX
 PT Detecting collagen gene alteration, useful for diagnosing osteoporosis,
 PT multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of
 PT stature and low bone density in humans.
 XX
 PS Example 4; Fig 21; 617pp; English.

CC The invention relates to Detecting a collagen gene alteration associated
 CC with a pathological condition in a human subject by obtaining from the
 CC subject a sample nucleic acid containing a portion of at least 15
 CC consecutive nucleotides of the segment of the COL1A1 gene extending in
 CC the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent
 CC exon 28 through the 3' end of intron 51, where the portion contains an
 CC intronic nucleotide and a first and second site, determining the sequence
 CC of the portion and comparing the sequence of the portion with the
 CC corresponding consensus sequence of the COL1A1 gene where a difference
 CC between the sequence of the portion and the consensus sequence indicates
 CC the presence of the collagen alteration in the subject. The method is
 CC used for detecting abnormalities in a COL1 or COL3 gene is useful for
 CC determining whether a subject is afflicted with pathological conditions
 CC associated with an altered collagen gene such as osteoporosis, multiple
 CC epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and
 CC low bone density. Identification of an abnormality in a collagen gene is
 CC also useful for designing a therapeutic nucleotide or gene therapy agent
 CC which can be administered to the subject to correct or alleviate the

CC abnormality. The method is useful for detecting mutations in both the
 CC coding and non-coding sequences of any of the COL1 or COL3 genes.
 CC Therefore the method can be used to detect collagen gene alterations
 CC which affect either the primary sequence of a collagen protein chain,
 CC or the splicing of the mRNA encoding such chains or regulation of expression of
 CC the genes encoding such chains. The present sequence is a PCR primer
 CC which amplifies a nucleic acid from a collagen gene of the invention
 XX
 SQ Sequence 21 BP; 7 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 961 GACTCTCAGCGCTTCCTTC 981
 |||||
 21 GACTCTCAGCTCATCTCTTC 1

RESULT 3300
 ABR13278
 ID ABR13278 standard; DNA; 21 BP.
 AC ABR13278;
 XX
 XX 30-JAN-2003 (first entry)
 DE Fanconi anaemia FANCD exon amplifying PCR primer SEQ ID No 181.
 XX
 KM Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;
 KM Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;
 KM cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;
 KM Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;
 KM Xeroderma pigmentosum; PCR; primer; ss.
 XX
 OS Undefined.
 XX
 PN W0200236761-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 02-NOV-2001; 2001WO-US045561.
 XX
 PR 03-NOV-2000; 2000US-0245756P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA
 PI D'andrea AD, Taniguchi T, Timmers C, Grome M;
 PI WPI; 2002-519251/55.
 DR
 XX
 PT Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,
 PT useful for treating Fanconi anemia pathway defect in cell target or for
 PT treating patient with defective FANCD2 gene.
 XX
 PS Claim 8; Page 56; 103pp; English.

CC The invention relates to an isolated Fanconi anaemia protein complex
 CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472
 CC amino acids fully defined in the specification, its 90% identical
 CC sequence, a sequence encoded by a polynucleotide that is at least 90%
 CC identical to sequences given in specification such as a 517 base pair
 CC sequence, or a fragment which is at least 50 amino acids in length. The
 CC FANCD2 protein is useful for treating an FA pathway defect in a cell
 CC target or for treating a patient with a defective FANCD2 gene. The FANCD2
 CC gene is useful for making a recombinant expression vector. The FANCD2
 CC protein and its gene are useful as a novel target for therapeutic
 CC development, and in diagnostic test and screening assays for diseases
 CC associated with DNA repair and cell cycle abnormalities such as Fanconi
 CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis
 CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2
 CC gene is useful in producing probes and primers for screening patients in
 CC genetic based test, for diagnosing Fanconi anaemia and cancer, for

CC preparing an experimental mouse model for use in screening new
CC therapeutics for treating conditions involving defective DNA repair, and
CC in gene therapy methods. A recombinant vector containing the FAMC2 gene
CC of the invention is useful in gene therapy. This polynucleotide sequence
CC represents a PCR primer for amplifying a FAMC2 exon relating to the
CC invention
XX
SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2742 CGTGCAGTTCACGAGATAC 2762
DB 1 CATTCAATTCACGAGAC 21
RESULT 3301
ABS60160/c
ID ABS60160 standard; DNA, 21 BP.
XX
AC ABS60160;
XX
DT 05-NOV-2002 (first entry)
DE Human polymorphism associated DNA sequence #54.
XX
XX Aminopeptidase P, XPNP2; bradykinin receptor B1; ds; BDKRB1;
KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;
KM KXK1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KM autoimmune disease; inflammatory arthritis; cancer; wound;
KM viral infection; bacterial infection; fungal infection; COPD;
KM Chronic obstructive pulmonary disease; enterocolitis.
XX
OS Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0253678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX
PS Disclosure; Page 707; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein
CC 1 (KXK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachoma, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antinodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is included in the sequence
CC listing but is not referred to anywhere else in the specification
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2395 ATCCGAGTGGGACGACAGTG 2415
DB 21 ATACGAGTGGGAGACAGTG 1
RESULT 3302
ABS60171
ID ABS60171 standard; DNA, 21 BP.
XX
XX
XX ABS60171;
XX
XX 05-NOV-2002 (first entry)
DE Human polymorphism associated DNA sequence #55.
XX
XX
XX Aminopeptidase P, XPNP2; bradykinin receptor B1; ds; BDKRB1;
KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;
KM KXK1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KM autoimmune disease; inflammatory arthritis; cancer; wound;
KM viral infection; bacterial infection; fungal infection; COPD;
KM Chronic obstructive pulmonary disease; enterocolitis.
XX
XX
XX Homo sapiens.
XX
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.

PF 03-DEC-2001; 2001WO-US047235.
 XX
 XX 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM /) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 PI
 DR WPI: 2002-619265/66.
 XX
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 709; 977pp; English.
 XX
 XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDRKB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRKB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is included in the sequence
 CC listing but is not referred to anywhere else in the specification
 XX
 SQ Sequence 21 BP; 1 A; 10 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5317 TCTGCTTTCTGCTTTGC 5337
 |||||
 1 TCTCTACTTCCCTCCTTGC 21

RESULT 3303
 ABS68528/c
 ID ABS68528 standard; DNA; 21 BP.

XX
 AC ABS68528;
 XX
 DT 19-NOV-2002 (first entry)
 XX
 DE Clock gene Bmal2 (brain-muscle-Arnt-like protein 2)-related primer #17.
 XX
 KW Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia;
 KW sleeping disorder; non-24-hour sleep; sleep-phase forward; primer;
 KW retrain syndrome; time-zone variation syndrome; PCR; ss.
 XX
 OS Unidentified.
 OS
 PN WO200264785-A1.
 PD
 PD 22-AUG-2002.
 PD
 PF 23-AUG-2001; 2001WO-JP007197.
 XX
 XX 13-FEB-2001; 2001JP-00035743.
 PR
 XX (MISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 PI Fukada Y, Okano T;
 PI
 DR WPI: 2002-667007/71.
 XX
 XX Clock gene Bmal2 and expressed clock protein BMAL2 important in clock
 PT oscillation mechanism and relating to circadian rhythm, used in diagnosis
 PT of and developing drugs for insomnia and other sleeping disorders.
 XX
 PS Example 4; Page 35; 187pp; Japanese.
 XX
 XX The invention relates to a DNA sequence encoding clock protein BMAL2
 CC (brain-muscle-Arnt-like protein 2). The gene and protein are applicable
 CC in diagnosis of and development of drugs for insomnia and other sleeping
 CC disorders e.g. non-24-hour sleep, sleep-phase forward or retrain syndrome
 CC and time-zone variation syndrome. ABS68501-ABS68552 represent BMAL2
 CC coding sequences and PCR primers of the invention
 CC
 XX
 SQ Sequence 21 BP; 4 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4996 CCAGCTGAGACGAATGGA 5016
 |||||
 21 CCAGCTGAGACGAATGCTGGA 1

RESULT 3304
 ABK70498
 ID ABK70498 standard; DNA; 21 BP.

AC ABK70498;
 XX
 DT 15-JUL-2002 (first entry)
 XX

DE In-situ analysis synthetic probe #63.

XX
 KW Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
 KW Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
 KW kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
 KW Epstein-Barr early RNA; probe; ss.

OS Synthetic.

PN WO200222874-A2.

PD 21-MAR-2002.

PF 06-SEP-2001; 2001WO-US028014.

XX 15-SEP-2000; 2000US-0233177P.
PR (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
XX Uermohlen JG, Connaughton J;
PI
XX WPI; 2002-371972/40.
DR
XX Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT probes useful for detecting or localizing nucleic acid target genes
PT within a cell or tissue sample.
XX
XX Example 4; Page 19; 71pp; English.
XX
XX The present invention relates to a new oligonucleotide label-domain
CC comprising the sequence (CTATT)n and its complement (AAATAG)n, where
CC n is 1. The probe sets of the invention are useful for detecting kappa or
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC sequences. The invention is a useful genetic sequence for incorporation
CC into oligonucleotide probes for detecting gene-specific sequences within
CC cells or tissue samples in situ hybridization analysis and for
CC attaching a label to immunoglobulin or other proteins for detecting
CC haptens and antigens in immunohistochemical analyses. The present nucleic
CC acid sequence represents one of a collection (ABK70376-ABK70501) of
CC oligonucleotide probes that were used in the invention for detecting or
CC localizing a plurality nucleic acid target gene or antigen within a cell
CC or tissue sample
XX
SQ Sequence 21 BP; 2 A; 3 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4463 CTTTCTTTCTTTCTTTCTTTCTTT 4483
DB 1 CTATTTCTATTTCTTTCTTT 21
RESULT 3305
ABK87131/C
ID ABK87131 standard; DNA; 21 BP.
XX
XX ABK87131;
AC
XX
XX 07-OCT-2002 (first entry)
DT
XX
XX Human connective tissue growth factor, RT-PCR primer #1.
DE
XX Human; endothelial cell-specific molecule 4; EC5M4; neovascularization;
XX imaging vascular endothelium; proliferative disease; cancer; psoriasis;
XX diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;
XX tumor neovascularization; cardiac disease; endometriosis; hypoxic condition;
XX angiogenesis; cytoskeletal; RT-PCR; connective tissue growth factor;
XX reverse transcription-PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200236771-A2.
PN
XX
XX 10-MAY-2002.
PD
XX
XX 06-NOV-2001; 2001WO-GB004906.
PF
XX
XX 06-NOV-2000; 2000US-0245566P.
PR
XX 07-MAR-2001; 2001US-0273662P.
PR
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA
XX Bicknell R, Huminiecki L;
PI

XX WPI; 2002-508120/54.
DR
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
XX
XX Example 1; Page 165; 248pp; English.
XX
XX The present invention relates to endothelial cell-specific molecule 4
CC (EC5M4), and the polynucleotide sequences encoding it. The EC5M4 proteins
CC are useful for imaging vascular endothelium in the body of an individual,
CC and for diagnosing and treating a proliferative disease or condition
CC involving the vascular endothelium (preferably, neovascularization) such as
CC cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
CC The EC5M4 proteins are also useful in the manufacture of diagnostic or
CC prognostic agent for such conditions. The proteins are also useful for
CC detecting endothelial damage or activation, detecting a tumor or tumor
CC neovascularization, cardiac disease, or endometriosis by detecting the amount
CC of EC5M4 present in a sample. The polynucleotide sequences encoding EC5M4
CC are useful in gene therapy for treating a hypoxic condition such as
CC cancer, cardiac disease, endometriosis or atherosclerosis and in the
CC manufacture of medicaments for treating the above disease. The sequences
CC are useful for modulating angiogenesis in an individual. The present
CC sequence represents a RT-PCR primer for RNA encoding human connective
CC tissue growth factor
XX
SQ Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6568 TTTTGACCTCGAATCATGTG 6588
DB 21 TTTTCACCTCGAAGCATTTG 1
RESULT 3306
AAD22642
ID AAD22642 standard; DNA; 21 BP.
XX
XX AAD22642;
AC
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Antisense PCR primer #3, used as diagnostic marker for MAGE subtypes 1-6.
DE
XX PCR primer; melanoma antigen gene; MAGE; GAGE; cancer; RT-PCR;
XX reverse transcription polymerase chain reaction; ss.
XX
XX Unidentified.
OS
XX
XX WO200181575-A1.
PN
XX
XX 01-NOV-2001.
PD
XX
XX 24-APR-2001; 2001WO-KR000681.
PF
XX
XX 25-APR-2000; 2000KR-00021837.
PR
XX (ICGI-) IC & G CO LTD.
PA
XX
XX Park J, Jeon C;
PI
XX
XX WPI; 2002-026166/03.
DR
XX
XX Novel common primer useful for diagnosing cancer, is made from highly
PT homologous areas of twelve melanoma antigen gene subtypes and eight GAGE
PT subtypes.
XX
XX Claim 1; Page 4; 38pp; English.
PS
XX

CC The present invention relates to primers useful for diagnosis of one or
CC more kinds of cancer and a diagnostic kit comprising the primers of the
CC invention. The primers are derived from highly homologous areas of twelve
CC melanoma antigen gene (MAGE) subtypes or eight GAGE subtypes. The primers
CC of the invention are useful for diagnosing cancer by performing
CC polymerase chain reaction (PCR), reverse transcription (RT)-PCR, and
CC nested PCR. The kit of the invention is used to detect six MAGE subtypes
CC and eight GAGE subtypes. The present DNA sequence is an antisense PCR
CC primer which is used as a diagnostic marker for MAGE subtypes 1-6
XX
SQ Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5803 CCTGCGCTGTGCTGCTTGTGA 5823
DB 1 CCAGCATTTCTGCTTGTGA 21
RESULT 3307
AAD33020/c
ID AAD33020 standard; DNA; 21 BP.
XX
AC AAD33020;
XX
DT 01-JUL-2002 (first entry)
XX
DE HCV-S1 overlapping cDNA region amplifying antisense PCR primer. H15.
XX
KW Nucleic acid construct; expression cassette; non-coding region; NCR;
KW untranslated region; UTR; anti-viral drug; drug resistance; primer; PCR;
KW HCV-S1; Hepatitis C virus; ss.
XX
OS Hepatitis C virus.
XX
PN WO200208447-A2.
XX
PD 31-JAN-2002.
XX
PF 20-JUL-2001; 2001WO-IL000669.
XX
PR 24-JUL-2000; 2000US-0220248P.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (EHRL/) EHRLICH G.
XX
PI Tan YH, Lim SP, Lim SG, Hong WJ;
XX WPI; 2002-280605/32.
DR
XX
PT Novel nucleic acid construct useful for detecting the presence of RNA
PT virus, comprises an expression cassette and a promoter operably linked to
PT expression cassette for minus strand RNA transcription of the cassette.
XX
PS Example 1; Page 24; 81pp; English.
XX
CC The invention relates to nucleic acid construct which comprises an
CC expression cassette including a first polynucleotide region including a
CC 5' non-coding region (NCR) sequence of an RNA virus and at least an N-
CC terminal portion of a coding sequence of RNA virus, a second
CC polynucleotide region including a 3' untranslated region (UTR) sequence
CC of the RNA virus and at least a C-terminal portion of a coding sequence
CC of the virus and a third polynucleotide region encoding a reporter
CC molecule, flanked by first and second polynucleotide regions; and a
CC promoter sequence being operatively linked to expression cassette in a
CC manner so as to enable a transcription of a minus strand RNA molecule
CC from the expression cassette. Nucleic acid construct of the invention is
CC useful for detecting the presence of an RNA virus in a cell. It is also
CC useful for screening anti-viral drugs and determining drug resistance of
CC an RNA virus. The present sequence is a PCR primer used to amplify the
CC overlapping cDNA regions of the genome of Hepatitis C virus (HCV) isolate

CC HCV-S1
XX
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3094 TGACTCAGTGCTTAAGACT 3114
DB 21 TGCTCTCACAGCGCTAAAGCCT 1
RESULT 3308
AAL46645/c
ID AAL46645 standard; DNA; 21 BP.
XX
AC AAL46645;
XX
DT 05-AUG-2002 (first entry)
XX
DE A thaliana AKIN11 coding sequence PCR primer #3.
XX
KW AKIN11; pathogen resistance; transgenic; plant; antibacterial; virucide;
KW fungicide; nematocide; PCR; primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200238780-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-FR003457.
XX
PR 08-NOV-2000; 2000FR-00014354.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Roby D, Balague C, Godard F, Lumerzhelm M;
XX WPI; 2002-426954/45.
DR
XX
PT Inducing or increasing resistance to pathogens in plants e.g. industrial
PT scale flowers and vegetables, by introducing a nucleic acid that encodes
PT the AKIN11 peptide.
XX
PS Example 2; Page 74; 76pp; French.
XX
CC The present invention relates to the use of a nucleic acid that causes
CC the synthesis of the AKIN11 protein, to induce or increase the resistance
CC to pathogen attack in plants. The nucleic acid and its encoded protein
CC can be used to impart resistance to bacteria, viruses, fungi and
CC nematodes, especially necrotrophic pathogens such as Xanthomonas
CC campestris, in large-scale crops, vegetables and flowers. Probes and
CC primers that hybridise with the AKIN11 gene can be used to detect
CC resistance against pathogens, and antisense sequences can be used to
CC modulate resistance. The present sequence is a PCR primer used to isolate
CC the AKIN11 coding sequence of the invention
XX
SQ Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 26 GTGGAGCTGCTGCAAGCTCC 46
DB 21 GTGGAGCTGCTGCAAGTTC 1
RESULT 3309
ABK52977

```
ID      ABK52977 standard; DNA; 21 BP.
XX
XX      ABK52977;
AC
XX
XX      22-AUG-2002 (first entry)
DT
XX
XX      Human interleukin 6 target sequence #2.;
DE
XX      Human; interleukin 6; microsphere; genosensor; target; 88; microarray;
KW      optical signature.
XX
XX      Homo sapiens.
OS
XX
XX      Key      Location/Qualifiers
FH      modified_base      1
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "A is covalently linked to a fluorescein moiety"
XX
XX      WO200228530-A2.
XX
XX      11-APR-2002.
XX
XX      09-OCT-2001; 2001WO-US031581.
XX
XX      06-OCT-2000; 2000US-0238866P.
XX
XX      (TUFT ) TUFTS COLLEGE.
XX
XX      Walt DR;
XX
XX      WPI; 2002-463219/49.
XX
XX      Detecting target analyte comprises providing a first classifier of a
PT      first population of sensors, distributing a second population of sensors
PT      and determining the response of the second population of sensors.
XX
XX      Example 19; Fig 22; 104pp; English.
XX
XX      The invention relates to detecting a target analyte (TA) comprising: (a)
XX      providing first classifier (I) for the response of a first population of
XX      sensors (II) from a first pool of sensors (III) to a first TA; (b)
XX      distributing a second population of sensors (IV) from (III) on an array;
XX      and (c) determining response of (IV) to the sample, where response
XX      resembles (I) for a first TA, indicating the presence of the first TA in
XX      the sample. Also included is making an array comprising: (a) providing a
XX      population of microspheres comprising an optical signature; (b)
XX      recording the response of the microspheres to the target analyte; (c)
XX      generating a classifier for the response of the microspheres to the
XX      target analyte; and (e) distributing the microspheres on a substrate with
XX      a surface comprising discrete sites. The new method detects a target
XX      analyte in a sample by contacting the sample with a sensor array. The
XX      method allows the synthesis of the bioactive agents i.e., nucleic acids
XX      and antibodies, to be separated from their placement on an array. The
XX      bioactive agents may be synthesised on the beads which are then randomly
XX      distributed on a patterned surface. The beads are self-encoded with dyes
XX      allowing a correlation of the location of an individual site on the
XX      array. The self-encoding feature eliminates the need for a more complex,
XX      multi-step encoding system. The identities of the individual sensors in
XX      the array are self-encoded by exposing the array to a reference analyte
XX      while illuminating the array with excitation light energy. The light
XX      sensor array may carry thousands of discrete sensing elements whose
XX      combined signal provides for substantial improvements in sensor detection
XX      limits, response times and signal-to-noise ratios. The present sequence
XX      is a target sequence which is detected by a probe attached to a
XX      microsphere genosensor and used to illustrate the method of the invention
XX
XX      Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 14.6; DB 1; Length 21;
XX      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3653 AAGAAATACCGACGACCCGAC 3673
XX      ||| ||| ||| ||| ||| |||
DB      1 AATTACGACCCCTGACCCGAC 21
XX
XX      RESULT 3310
XX      ABK52958
XX      ID      ABK52958 standard; DNA; 21 BP.
XX
XX      ABK52958;
AC
XX
XX      22-AUG-2002 (first entry)
DT
XX
XX      Human interleukin 6 target sequence, IL6-CF.
DE
XX      Human; interleukin 6; IL6-CF; microsphere; genosensor; target; 88;
KW      microarray; optical signature.
XX
XX      Homo sapiens.
OS
XX
XX      Key      Location/Qualifiers
FH      modified_base      1
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "A is covalently linked to a fluorescein moiety"
XX
XX      WO200228530-A2.
XX
XX      11-APR-2002.
XX
XX      09-OCT-2001; 2001WO-US031581.
XX
XX      06-OCT-2000; 2000US-0238866P.
XX
XX      (TUFT ) TUFTS COLLEGE.
XX
XX      Walt DR;
XX
XX      WPI; 2002-463219/49.
XX
XX      Detecting target analyte comprises providing a first classifier of a
PT      first population of sensors, distributing a second population of sensors
PT      and determining the response of the second population of sensors.
XX
XX      Disclosure, Page 38; 104pp; English.
XX
XX      The invention relates to detecting a target analyte (TA) comprising: (a)
XX      providing first classifier (I) for the response of a first population of
XX      sensors (II) from a first pool of sensors (III) to a first TA; (b)
XX      distributing a second population of sensors (IV) from (III) on an array;
XX      and (c) determining response of (IV) to the sample, where response
XX      resembles (I) for a first TA, indicating the presence of the first TA in
XX      the sample. Also included is making an array comprising: (a) providing a
XX      population of microspheres comprising an optical signature; (b)
XX      recording the response of the microspheres to the target analyte; (c)
XX      generating a classifier for the response of the microspheres to the
XX      target analyte; and (e) distributing the microspheres on a substrate with
XX      a surface comprising discrete sites. The new method detects a target
XX      analyte in a sample by contacting the sample with a sensor array. The
XX      method allows the synthesis of the bioactive agents i.e., nucleic acids
XX      and antibodies, to be separated from their placement on an array. The
XX      bioactive agents may be synthesised on the beads which are then randomly
XX      distributed on a patterned surface. The beads are self-encoded with dyes
XX      allowing a correlation of the location of an individual site on the
XX      array. The self-encoding feature eliminates the need for a more complex,
XX      multi-step encoding system. The identities of the individual sensors in
XX      the array are self-encoded by exposing the array to a reference analyte
XX      while illuminating the array with excitation light energy. The light
XX      sensor array may carry thousands of discrete sensing elements whose
XX      combined signal provides for substantial improvements in sensor detection
XX      limits, response times and signal-to-noise ratios. The present sequence
```

```
CC is a target sequence which is detected by a probe attached to a
CC microsphere genosensor and used to illustrate the method of the invention
XX
SQ Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3653 AAGAAATATCCCGAGCCCAAC 3673
Db 1 AATACCGACCCCTGACCCCAAC 21
RESULT 3311
ABK52964/C
ID ABK52964 standard; DNA; 21 BP.
AC ABK52964;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human interleukin 6, IL6, probe sequence #2.
XX
XX Human; interleukin 6; IL6; microsphere; genosensor; probe; ss;
XX microarray; optical signature.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /mod_base= OTHER
XX /note= "G is covalently linked to an NH2-(CH2)8 moiety"
XX
XX WO200228530-A2.
XX
XX 11-APR-2002.
XX
XX 09-OCT-2001; 2001WO-US031581.
XX
XX 06-OCT-2000; 2000US-0238866P.
XX
XX (TUFT ) TUFTS COLLEGE.
XX
XX Walt DR;
XX
XX WPI; 2002-463219/49.
XX
XX
XX Detecting target analyte comprises providing a first classifier of a
XX first population of sensors, distributing a second population of sensors
XX and determining the response of the second population of sensors.
XX
XX Example 19; Fig 22; 104pp; English.
XX
XX The invention relates to detecting a target analyte (TA) comprising: (a)
XX providing first classifier (I) for the response of a first population of
XX sensors (II) from a first pool of sensors (III) to a first TA; (b)
XX distributing a second population of sensors (IV) from (III) on an array;
XX and (c) determining response of (IV) to the sample, where response
XX resembles (I) for a first TA, indicating the presence of the first TA in
XX the sample. Also included is making an array comprising: (a) providing a
XX population of microspheres comprising an optical signature; (b)
XX contacting the microspheres with a sample of the target analyte; (c)
XX recording the response of the microspheres to the target analyte; (d)
XX generating a classifier for the response of the microspheres to the
XX target analyte; and (e) distributing the microspheres on a substrate with
XX a surface comprising discrete sites. The new method detects a target
XX analyte in a sample by contacting the sample with a sensor array. The
XX method allows the synthesis of the bioactive agents i.e., nucleic acids
XX and antibodies, to be separated from their placement on an array. The
XX bioactive agents may be synthesised on the beads which are then randomly
XX distributed on a patterned surface. The beads are self-encoded with dyes
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CC allowing a correlation of the location of an individual site on the
CC array. The self-encoding feature eliminates the need for a more complex,
CC multi-step encoding system. The identities of the individual sensors in
CC the array are self-encoded by exposing the array to a reference analyte
CC while illuminating the array with excitation light energy. The light
CC sensor array may carry thousands of discrete sensing elements whose
CC combined signal provides for substantial improvements in sensor detection
CC limits, response times and signal-to-noise ratios. The present sequence
CC is a probe which is attached to a microsphere genosensor and used to
CC illustrate the method of the invention
XX
XX Sequence 21 BP; 2 A; 1 C; 10 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3653 AAGAAATATCCCGAGCCCAAC 3673
Db 21 AATACCGACCCCTGACCCCAAC 1
RESULT 3312
ABS97563
ID ABS97563 standard; DNA; 21 BP.
AC ABS97563;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human epoxide hydrolase 2 polymorphic sequence #54.
XX
XX
XX Human; de; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
XX adenylyl receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile; STM;
XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; URA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200257410-A2.
XX
XX 25-JUL-2002.
XX
XX 28-NOV-2001; 2001WO-US044838.
XX
XX 28-NOV-2000; 2000US-00724389.
XX
XX (DNAS-) DNA SCI LAB INC.
XX
XX Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX
XX Example 10; Page 119; 714pp; English.
```


CC This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon receptor (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

XX Sequence 21 BP; 8 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

SO Query Match 0.2%; Score 14.6; DB 1; Length 21; Best Local Similarity 81.0%; Pred. No. 2.3e+03; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2858 CAGGCAAGCAAGGAGGCG 2878
 |||||
 1 CAGGCAAGCAATGAGTGAG 21

Db

RESULT 3313
 ABS98273 standard; DNA; 21 BP.

XX ABS98273;
 AC 23-DEC-2002 (first entry)

DE Human lactoferrin (LTF) gene polymorphic sequence #35.

XX Human; db; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF; adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2; aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS; cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; NADPH quinone oxidoreductase 2; NQO2; sulfoxtransferase thermolabile; STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7; UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPA; multidrug resistance 1; lactotransferrin; orphan nuclear receptor; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; SNP;
 KM single nucleotide polymorphism.

OS Homo sapiens.
 XX MO200257410-A2.
 PN 25-JUL-2002.
 PD 28-NOV-2001; 2001WO-US044838.
 PF 28-NOV-2000; 2000US-00724389.
 PR 28-NOV-2000; 2000US-00724389.
 XX (DNAS-) DNA SCI LAB INC.
 PA Guida M, Hall J;
 XX WPI, 2002-698522/75.

PT Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and catepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

PS Example 23; Page 148; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (NNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), uridine kinase receptor (UPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

XX Sequence 21 BP; 2 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

SO Query Match 0.2%; Score 14.6; DB 1; Length 21; Best Local Similarity 81.0%; Pred. No. 2.3e+03; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 337 TACTTGAGGTGAGCATCCCT 357
 |||||
 337 TACTTGAGGTGAGCATCCCT 357

PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 XX
 XX Example 26; Page 157; 714pp; English.
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADBR1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diasepm binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered serine
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC sequencing primer used to sequence the polymorphic genes of the invention
 XX
 XX
 XX Sequence 21 BP; 2 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 SO
 Query Match 0.23; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5161 TTCTCTGGGACACTGGGCTC 5181
 1 TGTCTCATGGCCACTGGGCTC 21
 RESULT 3316
 ABS98319/c
 ID ABS98319 standard; DNA; 21 BP.
 AC
 XX ABS98319;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 XX Human lactoferrin (LTF) gene polymorphic sequence #82.
 DE
 XX Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxygenase 2; COX2; diasepm binding inhibitor; DBI; haematological;
 KM epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KM NADPH quinone oxidoreductase 2; NQO2; sulfoxtransferase thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; SNP;
 KM single nucleotide polymorphism.
 XX
 XX Homo sapiens.
 XX
 XX MO200257410-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 28-NOV-2001; 2001WO-US044838.
 XX
 XX 28-NOV-2000; 2000US-00724389.
 XX
 XX (DNAS-) DNA SCI LAB INC.
 XX
 XX Guida M, Hall J;
 XX
 XX WPI; 2002-698522/75.
 XX
 XX Isolated nucleic acid molecules having polymorphisms in known human genes
 XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 XX for locating, identifying and characterizing the genes responsible for
 XX disorder-related traits.
 XX
 XX Example 23; Page 149; 714pp; English.
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADBR1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diasepm binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 XX Sequence 21 BP; 8 A; 1 C; 10 G; 2 T; 0 U; 0 Other;
 SO

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

4573 CCTGCCCCCTTTCTTCTGACT 4593
 21 CCTGCCCCCTTTCTTCTGACT 1

RESULT 3317
 ABS97961/c
 ID ABS97961 standard; DNA; 21 BP.
 AC ABS97961;
 DT 23-DEC-2002 (first entry)
 XX Human UDP-glucuronosyl transferase 2B15 polymorphic sequence #5.
 DE
 XX Human; de; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02B; CYP45002B1; LTP;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
 KW aryl hydrocarbon receptor nuclear translocator; AHRNT; catepsin S; CTSS;
 KW cyclooxigenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological; SNP;
 KW single nucleotide polymorphism.
 KM
 KM
 OS Homo sapiens.
 XX
 PN WO200257410-A2.
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 PR 28-NOV-2000; 2000US-00724389.
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome P450 and catepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 PS
 PS Example 20; Page 137; 714p; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (AHRNT), catepsin S (CTSS), cyclooxigenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1

(MDR1), lactotransferrin (LTP), multidrug resistance associated protein 3
 (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1,
 CC AHRNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTP for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central
 CC and peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention

Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

749 TCTTCTACCGCCTGAGGCT 769
 21 TCTTCTACCGCCTGAGGCT 1

RESULT 3318
 ABR94085/c
 ID ABR94085 standard; DNA; 21 BP.
 AC ABR94085;
 DT 27-AUG-2002 (first entry)
 XX
 XX Endothelin-1 (EDN-1) SNP detection PCR primer #29.
 DE
 XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
 KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
 KW hyperension; atherosclerosis; angiogenesis; fatty acid metabolism;
 KW diabetes; familial hypercholesterolaemia; forensic marker;
 KW transgenic animal; solid support; cardiovascular regulator; SNP;
 KW single nucleotide polymorphism; PCR; primer; ss.
 KM
 KM
 OS Synthetic.
 XX
 PN WO200224747-A2.
 PD 28-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-EP010087.
 PR 19-SEP-2000; 2000EP-00120123.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Brinkmann U, Hoffmeyer S;
 XX
 DR WPI; 2002-435060/46.
 XX
 PT Novel polymorphisms of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme signaling
 PT system associated with cardiovascular disease, useful for treating the
 PT disease.

XX Claim 1, Page 55, 190pp; English.

PS The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

XX signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolaemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

XX

SQ Sequence 21 BP, 12 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3722 TCCTCATTCATTGAGCTTTT 3742

DB 21 TCCTGATTAGTATCTTTT 1

RESULT 3319

ABK94086

ID ABK94086 standard; DNA; 21 BP.

XX

AC ABK94086;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #30.

XX

XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolaemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Brinkmann U, Hoffmeyer S;

XX

DR WPI; 2002-435060/46.

XX

PT Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

PS Claim 1, Page 55, 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

XX signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolaemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

XX

SQ Sequence 21 BP, 3 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3722 TCCTCATTCATTGAGCTTTT 3742

DB 1 TCCTGATTAGTATCTTTT 21

RESULT 3320

ABK94081/c

ID ABK94081 standard; DNA; 21 BP.

XX

AC ABK94081;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #25.

XX

XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolaemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Brinkmann U, Hoffmeyer S;

XX

DR WPI; 2002-435060/46.

XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

XX Example 6; Page 55; 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC polynucleotide variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

CC

XX Sequence 21 BP; 12 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

SO

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3722 TCCTCATTCATTCAGCTTTT 3742

Db 21 TCCTGATTATGATCTTTT 1

RESULT 3321

ABK94242

ID ABK94242 standard; DNA; 21 BP.

XX

AC ABK94242;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #30.

XX

KM Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX Brinkmann U, Hofmeyer S;

PI

XX WPI; 2002-435060/46.

DR

XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

XX Claim 1; Page 62; 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

CC

XX Sequence 21 BP; 5 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

SO

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5355 GTTTTCAGCTGGGCTTGA 5375

Db 1 GATTCATCTGTCCTTGA 21

RESULT 3322

ABK94082

ID ABK94082 standard; DNA; 21 BP.

XX

AC ABK94082;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #26.

XX

KM Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

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PR 19-SEP-2000; 2000EP-00120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling
PT system associated with cardiovascular disease, useful for treating the
PT disease.
XX
XX
XX Example 6; Page 55; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a
CC molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of the
CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway
XX
SQ Sequence 21 BP; 4 A; 3 C; 2 G; 12 T; 0 U; 0 Other:
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3722 TCCTCATTGATGAGCTTTT 3742
Db 1 TCCTGATTATGATCTTTT 21
RESULT 3323
ABN86025
ID ABN86025 standard; DNA; 21 BP.
XX
XX ABN86025;
XX
XX 06-SEP-2002 (first entry)
XX
XX Mutagenic primer D399S.
XX
XX Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
XX antiviral; vaccine; tumour; PCR primer; ss.
XX
XX Synthetic.
XX
XX US2002062010-A1.
XX
XX 23-MAY-2002.
XX
XX 23-MAY-2001; 2001US-00863693.
XX
XX 02-MAY-1997; 97US-0046816P.
XX

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PR 30-APR-1998; 98US-00070166.
XX
XX (GETH ) GENENTECH INC.
XX
XX Arachoon WR, Carter PU, Merchant AM, Presta LG;
XX
XX WPI; 2002-499676/53.
XX
XX
PT New multispecific antibodies having heteromultimeric and common
PT components are useful to direct treatment to a target site such as a
PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
PT treat infectious disease.
XX
XX
XX Example 2; Page 23; 36pp; English.
XX
CC The invention relates to a new multispecific antibody, comprising at
CC least two polypeptides (P1 and P2) which meet at a multiface, where P1
CC has a multimerisation domain forming an interface positioned to interact
CC with an interface of a multimerisation domain of P2, and both
CC polypeptides each comprise a binding domain consisting a heavy chain and
CC a variable light chain, where the light chain has a sequence common to
CC both polypeptides. Heteromultimers of the invention include bispecific
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin
CC chimeras. The activity of antibodies of the invention may be described
CC as, cytostatic, antibacterial and antiviral. The heteromultimer can be
CC used for redirected cytotoxicity, for example to kill tumour cells, as a
CC vaccine adjuvant, for delivering thrombolytic agents to clots, for
CC converting enzyme activated prodrugs at a target site such as a tumour,
CC for treating infectious diseases, for targeting immune complexes to cell
CC surface receptors or for delivering immunotoxins to tumour cells. The
CC current sequence represents the mutagenic primer D399S for introducing a
CC mutation into the CH3 domain of a humanised anti-CD3 heavy chain or CD4-
CC IgG by site directed mutagenesis
XX
SQ Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other:
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 185 GCCGCTGACCTCCGACGGG 205
Db 1 GCCGTCGAGACTCAGCAGGG 21
RESULT 3324
AAL49183/C
ID AAL49183 standard; DNA; 21 BP.
XX
XX AAL49183;
XX
XX 30-OCT-2002 (first entry)
XX
XX Porcine CD 151 coding sequence PCR primer #7.
XX
XX CD 151; porcine reproductive and respiratory syndrome virus; PRRSV; pig;
XX selective breeding; xenotransplant; anti-RNA entry protein; anti-REP;
XX anti-viral; vaccine; PCR; primer; ss.
XX
XX Sus scrofa.
XX
XX WO2002060924-A2.
XX
XX 08-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-US002868.
XX
XX 29-JAN-2001; 2001US-00772044.
XX
XX 28-JAN-2002; 2002US-00772044.
XX
XX (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
XX Kapil S, Shanmukhapra K;
XX

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XX DR WP1; 2002-619225/66.
XX PT Determining susceptibility and resistance to porcine reproductive and
PT respiratory syndrome virus (PRRSV), useful for improving swine breeding,
PT by assaying for CD 151 in a sample of cellular material of known origin
PT from the animal.
XX PS Example 17; Page 35; 77pp + Sequence Listing; English.
XX CC The present invention relates to a method of determining the
CC susceptibility or resistance of an animal to porcine reproductive and
CC respiratory syndrome virus (PRRSV). This involves assaying for CD 151 in
CC a sample of cellular material of known origin from the animal. In
CC addition, coding sequences of CD 151 are described, and anti-viral
CC compounds designated anti-RNA entry proteins (anti-RSPs). The method is
CC useful for determining susceptibility and resistance to PRRSV in an
CC animal. This is particularly useful for improving swine breeding or for
CC screening different pig breeding lines. The method is also useful for
CC developing non-simian recombinant cell lines for propagating the virus,
CC for producing anti-viral compounds or vaccines for inducing immunity
CC against PRRSV, and for diagnosing PRRSV infection in a swine. The present
CC sequence is a PCR primer used to isolate the porcine CD 151 coding
CC sequence. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 21 BP; 1 A; 8 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7406 GCAACATCAGCAGCAGCA 7426
DB 21 GAAAGATGAGCAGCAGCAGA 1
RESULT 3325
ABZ95973/C
ID ABZ95973 standard; DNA; 21 BP.
XX AC ABZ95973;
XX DT 17-OCT-2003 (first entry)
XX DE Human fibronectin antisense fragment no.1833.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquitinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PP 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIGENESIS PHARM INC.
XX PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahabuddin S,
XX WP1; 2003-229219/22.
XX DR Pharmaceutical composition for treating ailments associated with impaired
PT

PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquitinone.
XX PS Disclosure; SEQ ID NO 11215; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquitinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquitinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3384 CTTCCCCAGCTGCACCCCC 3404
DB 21 CCGCCGACAGCGCGCACCCCC 1
RESULT 3326
ABX94380
ID ABX94380 standard; DNA; 21 BP.
XX AC ABX94380;
XX DT 18-JUN-2003 (first entry)
XX DE Human endothelial cell differentiation gene-4, Edg-4 PCR primer #1.
XX KW Human; se; PCR; primer; Edg-4; prostatic disease; Edg-7 receptor;
KW benign prostatic hyperplasia; intracellular signal transduction;
KW endothelial cell differentiation gene; prostate cancer; LPA;
KW lysophosphatidic acid.
XX OS Homo sapiens.
XX PN WO2003013605-A1.
XX PD 20-FEB-2003.
XX PP 06-AUG-2002; 2002WO-JP008016.
XX PR 07-AUG-2001; 2001JP-00239306.
XX PR 31-JUL-2002; 2002JP-00224215.
XX PA (NISB) JAPAN TOBACCO INC.
XX PI Furuno M, Naito T, Yamamoto Y, Noki J, Arai H, Kakehi Y,
XX WP1; 2003-248240/24.
XX DR Composition for preventing or treating prostatic diseases e.g. benign
PT prostatic hyperplasia and prostate cancer containing inhibitors of
PT interaction between lysophosphatidic acid (LPA) and its receptor to
PT

PT prevent cell proliferation.
XX
PS Example 2; Page 53; 59pp; Japanese.
XX
CC The invention relates to drug compositions for preventing, treating and/
CC or inhibiting progression of prostatic diseases, e.g. benign prostatic
CC hyperplasia or their accompanying diseases, comprises substances with an
CC activity of inhibiting intracellular signal transduction induced by a
CC stimulus mediated by Edg-7 (endothelial cell differentiation gene-7)
CC receptor (interacting with LPA, lysophosphatidic acid), and
CC pharmaceutically-acceptable carriers. The remedies are for prostatic
CC diseases e.g. benign prostatic hyperplasia and prostate cancer. The
CC present sequence is a PCR primer for human Edg-4 used in the
CC exemplification of the invention
XX
SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 818 AGTCTGTGCGCCCTGCATGT 838
1 AGCGTGTGAGTCCCTGCATGT 21
|||||
|

RESULT 3327
ABX90522/C
ID ABX90522 standard; DNA; 21 BP.
XX
AC ABX90522;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human PlGF A antisense target region.
XX
KW Antisense; sg; human; VEGF; vascular endothelial growth factor; cancer;
KW angiogenesis; neoplastic proliferation; cellular proliferation.
XX
OS Homo sapiens.
XX
PN US2002165174-A1.
XX
PD 07-NOV-2002.
XX
PF 13-MAR-2001; 2001US-00805761.
XX
PR 31-JAN-1997; 97US-0037004P.
PR 30-JAN-1998; 98US-00016541.
PR 19-JAN-2000; 2000US-00487023.
PR 19-JAN-2001; 2001WO-US000019.
XX
PA (GILL/) GILL P S.
PA (MASO/) MASOOD R.
XX
PI G111 PS, Masood R;
XX
DR WPI; 2003-255224/25.
XX
PT New composition comprising an antisense oligonucleotide directed against
PT vascular endothelial growth factor, useful for preparing a composition
PT for treating cancer.
XX
PS Example 13; Fig 17B; 54pp; English.
XX
CC The invention relates to a composition comprising an antisense
CC oligonucleotide directed against vascular endothelial growth factor
CC (VEGF). The antisense oligonucleotide is useful for preparing a
CC composition treating cancer, neoplastic proliferation, abnormal cellular
CC proliferation and preventing angiogenesis. The present sequence is a VEGF
CC cDNA target region for the antisense oligonucleotides of the invention
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5175 TGGGCTCTGCAGTCTCCAC 5195
21 TGGGCTGAGACATGTCTCCAC 1
|||||
|

RESULT 3328
ACC49738/C
ID ACC49738 standard; DNA; 21 BP.
XX
AC ACC49738;
XX
DT 03-JUL-2003 (first entry)
XX
DE Mouse CRH-R1 PCR primer P163 SEQ ID NO:30.
XX
KW Mouse; corticotropin releasing hormone receptor type 1; CRH-R1;
KW antipsoriatic; anti-allergic; immunosuppressive; anti-inflammatory;
KW dermatological; pathophysiological state; neuroendocrine disorder;
KW hyperproliferative epidermal disorder; allergic contact dermatitis;
KW autoimmune disorder; epidermal carcinogenesis; malignant transformation;
KW epidermal melanocyte; dermal melanocyte; chromosome 11; PCR primer; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO2003024990-A2.
XX
PD 27-MAR-2003.
XX
PF 13-SEP-2002; 2002WO-US029117.
XX
PR 14-SEP-2001; 2001US-0322195P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
XX
PI Pisarchik A, Slominski A;
XX
DR WPI; 2003-313342/30.
XX
PT Novel DNA encoding corticotropin releasing hormone receptor type 1 which
PT is useful for creating pathophysiological state such as inflammatory skin
PT disease e.g. psoriasis and allergic contact dermatitis.
XX
PS Example 3; Page 26; 110pp; English.
XX
CC The present invention describes DNA (I) encoding a corticotropin
CC releasing hormone receptor type 1 (CRH-R1) protein comprising an amino
CC acid sequence given in ABR43055 to ABR43071. Also describe: (1) a vector
CC (II) capable of expressing (I) or its degenerate variant, and comprising
CC (1) or its degenerate variant, and regulatory elements necessary for
CC expression of the DNA in a cell; (2) a host cell (III) transfected with
CC (II); (3) an isolated CRH-R1 protein (IV) encoded by (I); (4) an antibody
CC (V) directed against (IV); (5) a pharmaceutical composition (VI)
CC comprising (IV), and a carrier; and (6) protecting (W) skin cells against
CC damage induced by an environmental factor, by inducing the expression of
CC CRH-R type 1g in the skin cells, where the expression of the receptor
CC protects the skin cells against the damage. CRH-R1 has antipsoriatic,
CC anti-allergic, immunosuppressive, anti-inflammatory and dermatological
CC activities. (VI) can be used for treating a pathophysiological state such
CC as hyperproliferative epidermal disorder, neuroendocrine disorder,
CC allergic contact dermatitis, autoimmune disorder, epidermal
CC carcinogenesis, malignant transformation of epidermal or dermal
CC melanocytes. (W) is useful for protecting (W) skin cells against damage
CC induced by an environmental factor such as solar radiation. Human CRH-R1
CC is located on chromosome 17, and mouse CRH-R1 is located to chromosome
CC 11. The present sequence represents a PCR primer for mouse CRH-R1, which
XX is used in an example from the present invention

SO Sequence 21 BP; 4 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 823 GTGGCCCTGCGCATGTGAG 843
DB 21 GTCCGCTGTGCGCATGCGGAG 1
RESULT 3329
ABT34056
ID ABR34056 standard; DNA; 21 BP.
AC ABR34056;
XX 29-MAY-2003 (first entry)
DT
XX Human pigmentation trait-related PCR primer - SEQ ID No 155.
DE
XX Human; single nucleotide polymorphism; SNP; ss; melanocortin-1 receptor;
KW genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KM hair colour; eye colour; forensic tool; PCR; primer.
XX
OS Homo sapiens.
XX
FN WO200297047-A2.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016789.
XX
PR 25-MAY-2001; 2001US-0293560P.
PR 21-JUN-2001; 2001US-0300187P.
PR 07-AUG-2001; 2001US-0310781P.
PR 17-SEP-2001; 2001US-0323662P.
PR 26-OCT-2001; 2001US-0344418P.
PR 15-NOV-2001; 2001US-0334674P.
PR 02-JAN-2002; 2002US-0346303P.
XX
XX (DNAP-) DNAPRINT GENOMICS INC.
XX
PI Frudakis T;
XX
DR WPI; 2003-239091/23.
XX
PT Inferring genetic pigmentation trait such as hair/eye color or shade from
PT nucleic acid sample of human subject, by identifying a pigmentation-
PT related haplotype allele of a pigmentation gene in the sample.
XX
XX Example 17; Page 246; 396pp; English.
XX
XX The invention comprises a method for inferring a genetic pigmentation
XX trait of a human. The method involves identifying a single nucleotide
XX polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
XX is not melanocortin-1 receptor (MC1R) and agouti signaling protein
XX (ASIP). The method of the invention is useful for inferring the race of a
XX human subject. The method is useful for inferring a genetic pigmentation
XX trait such as hair shade or colour, or eye shade or colour of a human
XX subject. The method may be used as a forensic tool for obtaining
XX information relating to physical characteristics of a potential crime
XX victim or a perpetrator of a crime from a nucleic acid sample present at
XX the invention scene. The present PCR primer is used in the exemplification of
XX
XX Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1851 GGTGAAGACGTGTGTCAGAC 1871
DB 1 GATGAAGACGTGTGTCAGAC 21
RESULT 3330
ABX10723/c
ID ABR10723 standard; DNA; 21 BP.
XX
AC ABR10723;
XX
XX 15-APR-2003 (first entry)
DT
XX Human glycoprotein hormone Zluth1 PCR primer #11.
DE
XX Human; ss; PCR; Zluth1; glycoprotein hormone; hyperthyroidism;
KW antithyroid; chromosome 14q23.3; primer.
KM
XX
OS Homo sapiens.
XX
XX US2002160953-A1.
FN
XX 31-OCT-2002.
XX
PF 30-AUG-2001; 2001US-00943388.
XX
XX 25-APR-2000; 2000US-0199498P.
PR 20-APR-2001; 2001US-00839706.
XX
XX (HOLL/) HOLLOWAY J L.
PA (WEBB/) WEBSTER P J.
PA (THAY/) THAYER E C.
XX
XX Holloway JL, Webster PJ, Thayer EC;
PI
XX WPI; 2003-209228/20.
XX
XX
XX New Zluth1 polypeptides and polynucleotides, useful for manufacturing a
XX medicament for treating hyperthyroidism.
PT
XX
XX Example 8; Page 48; 51pp; English.
XX
XX The invention relates to an isolated glycoprotein hormone Zluth1 sequence,
XX the mature protein or antigenic peptides derived from Zluth1. Also
XX included are an isolated polynucleotide encoding Zluth1, an isolated
XX antibody that specifically binds to Zluth1, treating hyperthyroidism in
XX female mammals by administering Zluth1 and a pharmaceutical composition
XX comprising Zluth1. Zluth1 is useful for manufacturing a medicament for
XX treating hyperthyroidism. Anti-Zluth1 antibodies can be used to detect
XX Zluth1 in tissue sections from a biopsy specimen or to screen biological
XX samples in vitro for the presence of Zluth1. Zluth1 is useful for treating
XX women with hyperthyroidism. The nucleic acid molecules are useful for
XX detecting the expression of a Zluth1 gene in a biological sample. The
XX present sequence is a PCR primer used to detect expression of Zluth1 in
XX pituitary cells, amplifying part of the 3' untranslated region
XX
XX Sequence 21 BP; 12 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4476 TTTTCTTGTGCTGAGCATG 4496
DB 21 TTTTCTTGTGCTGAGCATG 1
RESULT 3331
ACF64056/c
ID ACF64056 standard; DNA; 21 BP.
XX
AC ACF64056;
XX

DT 13-OCT-2003 (first entry)
XX
XX IFNARI reverse PCR primer #32.
DE
XX Human; detection; computer-readable storage medium; polymorphic site;
KM signal carrying data; data processing system; multiple sclerosis;
KM PCR primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO2003014319-A2.
PN
XX 20-FEB-2003.
PD
XX 07-AUG-2002; 2002WO-US025268.
PF
XX 07-AUG-2001; 2001US-0310741P.
PR 24-SEP-2001; 2001US-0324790P.
XX
XX (DNAS-) DNA SCI INC.
PA
XX Jones HB, Xu H, White R, Rienhoff HY, Jin W, Natsoulis G;
PI WPI; 2003-268196/26.
DR
XX New polynucleotide, useful for detecting loci associated with multiple
PT sclerosis.
PT
XX Disclosure; Page 10; 93pp; English.
PS
XX
XX The present invention describes an isolated polynucleotide (PN)
CC comprising: (a) a sequence comprising at least 15 contiguous nucleotides
CC of a sequence comprising variant sequences (A) from Table 4 given in the
CC specification; or (b) a sequence that is complementary to (A). Also
CC described: (1) an array of (PN)s comprising two or more of the isolated
CC (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable
CC storage medium, where each record has a field identifying a base
CC occupying a (PN) site and a location of the polymorphic site; and (4) a
CC signal carrying data for access by an application program having executed
CC on a data processing system. The (PN) can be used for detecting loci
CC associated with multiple sclerosis. ACF64025 to ACF64424 represent
CC sequences used in the exemplification of the present invention
CC
SQ Sequence 21 BP; 10 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6449 CAGGTCTTTGGATACCTTTT 6469
DB 21 CGGTGTGTGGATGCTTTAT 1
RESULT 3332
ACF64052/C
ID ACF64052 standard; DNA; 21 BP.
XX
XX ACF64052;
AC
XX
XX 13-OCT-2003 (first entry)
DE
XX ESRI reverse PCR primer #28.
DE
XX Human; detection; computer-readable storage medium; polymorphic site;
KM signal carrying data; data processing system; multiple sclerosis;
KM PCR primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO2003014319-A2.
PN

XX
PD 20-FEB-2003.
XX
XX 07-AUG-2002; 2002WO-US025268.
PF
XX 07-AUG-2001; 2001US-0310741P.
PR 24-SEP-2001; 2001US-0324790P.
XX
XX (DNAS-) DNA SCI INC.
PA
XX Jones HB, Xu H, White R, Rienhoff HY, Jin W, Natsoulis G;
PI WPI; 2003-268196/26.
DR
XX New polynucleotide, useful for detecting loci associated with multiple
PT sclerosis.
PT
XX Disclosure; Page 10; 93pp; English.
PS
XX
XX The present invention describes an isolated polynucleotide (PN)
CC comprising: (a) a sequence comprising at least 15 contiguous nucleotides
CC of a sequence comprising variant sequences (A) from Table 4 given in the
CC specification; or (b) a sequence that is complementary to (A). Also
CC described: (1) an array of (PN)s comprising two or more of the isolated
CC (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable
CC storage medium, where each record has a field identifying a base
CC occupying a (PN) site and a location of the polymorphic site; and (4) a
CC signal carrying data for access by an application program having executed
CC on a data processing system. The (PN) can be used for detecting loci
CC associated with multiple sclerosis. ACF64025 to ACF64424 represent
CC sequences used in the exemplification of the present invention
CC
SQ Sequence 21 BP; 6 A; 0 C; 13 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5328 CTCTCTTGGCTACCTCTTC 5348
DB 21 CTCTCTTGGCTACCTCTTC 1
RESULT 3333
AAL53918
ID AAL53918 standard; DNA; 21 BP.
XX
XX AAL53918;
AC
XX
XX 18-FEB-2003 (first entry)
DT
XX
XX Interleukin 6 target sequence.
DE
XX Target analyte; array; substrate; microsphere; non-cleavable linker;
KM enzymatic reaction; forensic DNA fingerprinting; pesticide; herbicide;
KM detecting environmental pollutant; pregnancy test; target; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /note= "Nucleotide is modified by fluorescein"
XX
XX WO200277291-A1.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 25-MAR-2002; 2002WO-US009126.
PF
XX
XX 23-MAR-2001; 2001US-00816651.
PR
XX
XX (TUFT) TUFTS COLLEGE. PA

```
XX PI Walt DR, Michael KL;
XX XX
DR WPI: 2003-092858/08.
XX
PT Detecting a target analyte or an enzymatic reaction useful for forensic
PT DNA fingerprinting or detecting environmental pollutants, comprises
PT providing an array comprising an array substrate, first and second sites,
PT and micropheres.
XX
PS Disclosure; Page 28; 61pp; English.
XX
CC The invention relates to a novel method for detecting a target analyte in
CC the sample. The novel method comprises providing an array comprising an
CC array substrate, at least first and second sites, and a population of
CC micropheres, where first and second reaction components are attached
CC with a non-cleavable linker to the first and second micropheres that are
CC randomly distributed on the sites. The methods are useful for detecting
CC the presence of a particular target analyte, or for detecting an
CC enzymatic reaction, such as the presence or absence of, or mutations on a
CC particular nucleotide sequence or protein, e.g. an enzyme, antibody or
CC antigen. They are also useful in forensic DNA fingerprinting, detecting
CC environmental pollutants such as pesticides or herbicides, and in
CC bacterial, fungal, protozoal, Mycoplasma, Rickettsial diagnostic tests,
CC as well as in pregnancy tests. This polynucleotide represents a target
CC sequence of the microsphere genosensors of the invention
XX
SQ Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3653 AAGAAATATACCCGACGCCAAC 3673
DB 1 AATAACGACCCCTGACCCCAAC 21
XX
RESULT 3334
ACCA2623/c
ID ACCA2623 standard; DNA; 21 BP.
XX
AC ACCA2623;
XX
DT 26-AUG-2003 (first entry)
XX
DE Human interleukin-6, IL-6, PCR primer hIL6-F2.
XX
KW Human; PCR; primer; transgenic mouse; lymphocyte maturation; IL-3; IL-7;
KW cytokine; interleukin-3; interleukin-6; IL-6; interleukin-7; M-CSF; SCF;
KW macrophage-colony stimulating factor; stem cell factor; oncostatin M; OM;
KW granulocyte-colony stimulating factor; GM-CSF; LIF;
KW leukaemia inhibitory factor; ss.
XX
OS Homo sapiens.
XX
PN WO2003018744-A2.
XX
PD 06-MAR-2003.
XX
PE 05-AUG-2002; 2002WO-US024807.
XX
PR 23-AUG-2001; 2001US-00938689.
XX
PA (GENV ) GENENCOR INT INC.
XX
PI Harding PA, Huang M;
XX
DR WPI: 2003-278650/27.
XX
PT New recipient mammal, preferably a mouse, useful as a model of human
PT disease to assess efficacy of therapeutic or prophylactic treatments, or
PT for facilitating production of donor-specific functional immunity.
```

```
XX PS Example; Page 36; 70pp; English.
XX
CC The present invention relates to a new transgenic mouse, which comprises
CC a disruption in both alleles of a gene such that lymphocyte maturation
CC does not occur and exogenous cytokines. The cytokines are selected from:
CC interleukin-3 (IL-3), interleukin-6 (IL-6), interleukin-7 (IL-7),
CC macrophage-colony stimulating factor (M-CSF), granulocyte-colony
CC stimulating factor (GM-CSF), stem cell factor (SCF), leukaemia inhibitory
CC factor (LIF) and oncostatin M (OM). The gene disruption is in a gene that
CC modulated VDJ recombination e.g. a RAG gene. The gene is disrupted by
CC insertion of a transgene comprising major histocompatibility complex
CC (MHC) Class II DR3 and DQ2 genes. The transgenic mouse is useful as a
CC model of human disease to assess efficacy of therapeutic or prophylactic
CC treatments, or to assess the antigenic potential of compounds. The
CC transgenic mouse is also useful for supporting donor haematopoietic stem
CC cells or facilitating production of donor-specific functional immunity.
CC PCR primers ACCA2571-ACCA2639 were used to generate the transgenic mouse
XX
SQ Sequence 21 BP; 0 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 7406 GCAACATCAGCAGCAGCAGCA 7426
DB 21 GCAACACGACGAGCAGCCCA 1
XX
RESULT 3335
ABT33411
ID ABT33411 standard; DNA; 21 BP.
XX
AC ABT33411;
XX
DT 22-MAY-2003 (first entry)
XX
DE NOVX PCR primer SEQ ID No 266.
XX
KW Hepatotropic; immunosuppressive; cardiac; hypertensive; tranquilizer;
KW vulnerrary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW antiparasitic; neuroprotective; cerebroprotective; antiparthenian;
KW anticonvulsant; antidiabetic; analgesic; dermatological; keratolytic;
KW antiseborrheic; antineumatic; antidiarrhetic; antinflammatory; anti-HIV;
KW cytosolic; antiasomatic; antipoxiatic; hypotensive; osteopathic;
KW antitumor; anorectic; antidiabetic; antiallergic; haemostatic;
KW neuroleptic; antidepressant; antifertility; NOVX; human disease;
KW NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW parasitic infection; Alzheimer's disease; stroke; forensic biology;
KW immunogen; non-human transgenic animal; gene therapy; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200281517-A2.
XX
PD 17-OCT-2002.
XX
PE 22-JAN-2002; 2002WO-US002064.
XX
PR 19-JAN-2001; 2001US-0262892P.
PR 23-JAN-2001; 2001US-0263598P.
PR 24-JAN-2001; 2001US-0263799P.
PR 25-JAN-2001; 2001US-0264117P.
PR 25-JAN-2001; 2001US-0264139P.
PR 26-JAN-2001; 2001US-0264478P.
PR 30-JAN-2001; 2001US-0263351P.
PR 02-MAR-2001; 2001US-0272870P.
PR 14-MAR-2001; 2001US-0275927P.
PR 15-MAR-2001; 2001US-0275990P.
PR 15-MAR-2001; 2001US-0276449P.
PR 20-MAR-2001; 2001US-0277358P.
PR 23-MAR-2001; 2001US-0278151P.
```


XX
PN WO2003027309-A2.
XX
PD 03-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030238.
XX
PR 24-SEP-2001; 2001US-0324421P.
XX
PS (ONEL-) ONE LAMBDA.
XX
PI Saito K, Lee J, Blair L;
XX
DR WPI; 2003-363216/34.
XX
PT Detecting the presence of a target nucleic acid sequence on a sample
PT nucleic acid strand, useful for human leukocyte antigen tissue typing,
PT comprises contacting a sample with a diagnostic probe under hybridizing
PT conditions.
XX
PS Example 3; Page 29; 62pp; English.
XX
CC The present invention relates to the detecting of a target nucleic acid
CC sequence on a sample nucleic acid strand. The methods are useful for
CC detecting the presence or absence of target nucleic acid sequences on
CC sample nucleic acid strands that are characteristic of pathogens or gene
CC variations and mutations relating to human leukocyte antigen (HLA) or T-
CC cell receptor gene sequences, e.g. for HLA tissue typing, detecting
CC genetically inherited diseases or detecting infectious organisms in
CC tissues. The diagnostic probes are useful for detecting the presence of
CC particular target nucleic acid sequences. The present invention provides
CC improved methods of detecting sample/target nucleic acid sequences, where
CC the use of diagnostic probes having increased specificity reduces the
CC number of alleles detected, which increases the resolution of the method,
CC and does so at a lower cost. The present sequence represents a probe of
CC the invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2740 GCCGTGACGGTTCACGAGAT 2760
DB 21 GCCGCGCAGGTCGCCAGGTT 1
XX
RESULT 3339
ADB78522/C
ID ADB78522 standard; DNA; 21 BP.
XX
AC ADB78522;
XX
DT 04-DEC-2003 (first entry)
XX
DE Probe sequence #25 related to the invention.
XX
KM human leukocyte antigen; HLA; probe; PCR; ss.
XX
OS Synthetic.
XX
PN WO2003027309-A2.
XX
PD 03-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030238.
XX
PR 24-SEP-2001; 2001US-0324421P.
XX
PS (ONEL-) ONE LAMBDA.
XX
PI Saito K, Lee J, Blair L;

XX
DR WPI; 2003-363216/34.
XX
PT Detecting the presence of a target nucleic acid sequence on a sample
PT nucleic acid strand, useful for human leukocyte antigen tissue typing,
PT comprises contacting a sample with a diagnostic probe under hybridizing
PT conditions.
XX
PS Example 3; Page 29; 62pp; English.
XX
CC The present invention relates to the detecting of a target nucleic acid
CC sequence on a sample nucleic acid strand. The methods are useful for
CC detecting the presence or absence of target nucleic acid sequences on
CC sample nucleic acid strands that are characteristic of pathogens or gene
CC variations and mutations relating to human leukocyte antigen (HLA) or T-
CC cell receptor gene sequences, e.g. for HLA tissue typing, detecting
CC genetically inherited diseases or detecting infectious organisms in
CC tissues. The diagnostic probes are useful for detecting the presence of
CC particular target nucleic acid sequences. The present invention provides
CC improved methods of detecting sample/target nucleic acid sequences, where
CC the use of diagnostic probes having increased specificity reduces the
CC number of alleles detected, which increases the resolution of the method,
CC and does so at a lower cost. The present sequence represents a probe of
CC the invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2740 GCCGTGACGGTTCACGAGAT 2760
DB 21 GCCGCGCAGGTCGCCAGGCT 1
XX
RESULT 3340
ADC16367
ID ADC16367 standard; RNA; 21 BP.
XX
AC ADC16367;
XX
DT 18-DEC-2003 (first entry)
XX
DE Short interfering double-stranded RNA oligonucleotide SEQ ID NO:92.
XX
KM expression interference; expression inhibition; target gene;
KM short interfering double stranded RNA; cyostatic; gene therapy;
XX
OS Synthetic.
XX
PN WO2003012052-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002WO-US024226.
XX
PR 30-JUL-2001; 2001US-0308640P.
XX
PR 08-APR-2002; 2002US-0370970P.
XX
PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CARN-) CARNEGIE INST WASHINGTON.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Caplen NJ, Morgan RA, Fire A, Parrish S, Moussee S;
PI Kallionlemi O, Cornelison JR, Alton EW, Griesendach U;
XX
DR WPI; 2003-248169/24.
XX
PT New RNA comprising double stranded RNA and a 3' or 5' overhang having a
PT length of 0-nucleotide to 5-nucleotide on each strand, useful as reverse
PT genetic and/or therapeutic tools for interfering or inhibiting expression

PT of a target gene.
 XX
 PS Claim 71; SEQ ID NO 92; 176pp; English.
 CC The present invention describes an RNA (1) used for the interference or
 CC inhibition of expression of a target gene, where (1) comprises double
 CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang
 CC having a length of 0-nucleotide to 5-nucleotides on each strand, where
 CC the sequence of the double stranded RNA is substantially identical to a
 CC portion of a mRNA or transcript of the target gene. Also described: (1)
 CC interfering with or inhibiting the expression of a target gene in a cell
 CC by exposing the cell to an amount of (1); (2) a gene silencing array
 CC comprising a substantially flat substrate, and addressably arrayed
 CC different double-stranded RNAs; (3) an array-based method of assessing a
 CC phenotypic effect of a double-stranded RNA on a target gene; (4)
 CC validating a gene as a potential drug target for a disease or condition;
 CC (5) selecting an optimised sequence of a double-stranded RNA for
 CC interference with or inhibition of expression of a target gene in a cell;
 CC and (6) a short double-stranded RNA effective for interfering with or
 CC inhibiting expression of a target gene comprising any of 311 20-78
 CC nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic
 CC activity, and can be used in gene therapy. The RNAs are useful as reverse
 CC genetic and/or therapeutic tools for interfering or inhibiting expression
 CC of a target gene. They are useful for treating proliferative diseases,
 CC e.g. cancer.
 CC
 SQ Sequence 21 BP; 3 A; 7 C; 4 G; 0 T; 7 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 52.4%; Pred. No. 2.3e+03;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 2761 ACTCTGCCGACCACTACTTC 2781
 Db 1 AGCTCCCGCAGCGGACGAC 21
 RESULT 3341
 ADC42515
 ID ADC42515 standard; DNA; 21 BP.
 AC ADC42515;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE FANCD2 PCR primer MG763 SEQ ID NO:181.
 XX
 KW cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;
 KW chemosensitising; ss; PCR; primer.
 XX
 OS Synthetic.
 XX
 PN MO2003039327-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 06-JUN-2002; 2002WO-US018153.
 XX
 PR 02-NOV-2001; 2001US-00998027.
 XX
 PR 02-NOV-2001; 2001WO-US045561.
 XX
 PA (DAND) DANA FARRER CANCER INST.
 PA (UTOR-) UNIV OREGON HEALTH SCI.
 XX
 PI D'andrea AD, Taniguchi T, Timmers C, Grome M, Fox EA;
 DR WPI; 2003-441436/41.
 XX
 PT Diagnosing or determining cancer or increased risk of cancer in a
 PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
 PT cancer-associated defect, that indicates cancer or increased risk of
 PT cancer.
 XX

PS Claim 11; SEQ ID NO 181; 160pp; English.
 XX
 CC The invention relates to a novel method of diagnosing or determining if a
 CC patient has cancer or is at increased risk of cancer, involving testing a
 CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
 CC cancer-associated defect, where the presence of one or more cancer-
 CC associated defects is indicative of cancer or an increased risk of cancer
 CC in the patient. The method of the invention has cytostatic activity. The
 CC method is useful for determining if a patient has cancer, or is at
 CC increased risk of developing cancer, e.g. breast, ovarian or prostate
 CC cancer. A microarray of the invention is useful for determining if a
 CC patient has cancer, or is at increased risk of developing cancer, by
 CC hybridising a nucleic acid sample to the nucleic acid sequences from the
 CC array, and detecting the presence of mutations in FA/BRCA pathway genes
 CC in the nucleic acid sample from the patient, where detecting the presence
 CC of mutations is indicative of a patient who has cancer, or is at
 CC increased risk of developing cancer. A method of the invention is useful
 CC for screening a chemosensitising agent, and the agent obtained is useful
 CC for treating a patient having a cancer. The present sequence is used in
 CC the exemplification of the invention.
 CC
 SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2742 CGTGCAGTTCACCAGGATAC 2762
 Db 1 CATTGACATTCCACGAGAC 21
 RESULT 3342
 ADC64837/C
 ID ADC64837 standard; DNA; 21 BP.
 AC ADC64837;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE RNaseA PCR primer SEQ ID NO:2.
 XX
 KW atopic dermatitis; steroid; RNaseA; RNase K6 precursor; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN JP2002291485-A.
 XX
 PD 08-OCT-2002.
 XX
 PF 03-APR-2001; 2001JP-00104621.
 XX
 PR 03-APR-2001; 2001JP-00104621.
 XX
 PA (GENO-) GENOX SOYAKU KENKUSHO KK.
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
 XX
 DR WPI; 2003-375782/36.
 XX
 PT Examination of responsiveness to steroids in patients with atopic
 PT dermatitis for improved treatment of patients suffering from allergic
 PT diseases.
 XX
 PS Example 2; Page 14; 24pp; Japanese.
 XX
 CC The present invention describes a method for examining the response of
 CC patients with atopic dermatitis to steroids. The method comprises: (a)
 CC determining the expression levels of an RNaseA gene or an RNase K6
 CC precursor gene in a living sample; and (b) comparing the response level
 CC with that of healthy subjects and steroid responsive patients, determined
 CC by PCR of cDNA. The present sequence represents an RNaseA PCR primer,
 CC which is used in an example from the present invention.
 CC

Matches	17	Conservative	0	Mismatches	4	Indels	0	Gaps	0
Qy	4708	TTACTTAGACCTAGCCAGG	4728						
Db	21	TTCCCTTAGAGCTAGCCAGG	1						

RESULT 3345
ADC84417
ID ADC84417 standard; DNA; 21 BP.

Detector for identifying human papilloma virus subtypes, comprises carrier having two parts carrying first and second oligonucleotides that respectively hybridize with DNA contained in first and second subtypes of the virus.

RESULT: 3346
ADD20200/C
ID ADD20200 standard; DNA; 21 BP.
XX
XX
AC ADD20200;
XX
DT 15-JAN-2004 (first entry)
XX
DE Oreochromis niloticus microsatellite primer SEQ ID NO:835.
XX
XX single nucleotide polymorphism; SNP; fish; Salmo salar;
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod

KM polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
 KM detection; primer; ss.
 XX
 XX
 OS Synthetic.
 OS Oreochromis niloticus.
 OS

Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic acids.

PS Claim 18; SEQ ID NO 835; 233pp; English.

The present invention describes an isolated nucleic acid (I) comprising a single nucleotide (SNP) chosen from: (1) a nucleic acid of *Salmo salar* SNPs, *Oreochromis niloticus* SNPs or Atlantic halibut SNPs; and (11) a nucleic acid having nucleotide sequence that hybridises to (1), or its complement under highly stringent hybridisation conditions. Also described: (1) an isolated oligonucleotide (II) comprising at least 17 contiguous nucleotides of a nucleotide sequence of *S. salar* SNPs, *O. niloticus* SNPs, *O. niloticus* microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or their complement; (2) a primer pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from *S. salar* SNPs and, *O. niloticus* SNPs, *O. niloticus* microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites; and determining (M1) the origin of fish sample comprising providing a parentage genotype database comprising a collection of candidate parent genotypes, where each of the candidate parent genotype represents a distinct origin, and comparing a sample genotype to the parentage genotype database, where a match between the sample genotype and one of the candidate parent genotype identifies to the origin of the sample. (M1) is useful for determining the origin of a fish sample such as family salmonidae, *S. salar*, *Tilapia*, *O. niloticus*, rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for detecting nucleic acid molecule comprising SNP in a sample, which involves contacting the sample containing nucleic acids with one or more (II) derived from nucleotide sequence of *S. salar* SNPs and *O. niloticus* SNPs, and identifying nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid molecule comprising a polymorphic sequence in a sample, comprising contacting the sample containing nucleic acids with one or more (II) which is derived from *O. niloticus* microsatellite, *O. niloticus* SNPs, Atlantic halibut SNPs, cod polymorphic sites or seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II). (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is used in the exemplification of the present invention.

```

RESULT 3347
ADD95120/c
ID ADD95120 standard; DNA; 21 BP.
XX
AC ADD95120;
XX
DT 29-JAN-2004 (first entry)
XX
DE BMP receptor type 1B upstream primer #SEQ ID 4.
XX
KM Pigmentation; skin; hair; wool; fur; bone morphogenetic protein 4; BMP-4;
KM PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2003086313-A2.
XX
PD 23-OCT-2003.
XX
PF 11-APR-2003; 2003WO-US011376.
XX
PR 12-APR-2002; 2002US-0372523P.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Year M, Park H, Botchkarev V, Gilchrist BA;
XX
DR WPI; 2003-903051/82.
XX
PT Decreasing skin, hair, wool or fur pigmentation in a mammal comprising
PT administering a composition comprising bone morphogenetic protein 4 (BMP-
PT 4), an active fusion protein or fragment of BMP-4, a BMP-4 mimic or its
PT combination.
XX
PS Example 8; SEQ ID NO 4; 42bp; English.
XX
CC The invention relates to decreasing pigmentation in the skin, hair, wool
CC or fur of a vertebrate or a mammal. This method comprises administering a
CC composition comprising bone morphogenetic protein 4 (BMP-4), an active
CC fusion protein of BMP-4, an active fragment of BMP-4, a BMP-4 mimic or a
CC combination of any of those. The method is useful for lightening or
CC decreasing pigmentation in the skin, hair, wool or fur of a vertebrate or
CC a mammal. The current sequence represents a PCR primer for the
CC amplification of BMP receptor type 1B DNA.
XX
SQ Sequence 21 BP; 6 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1915 AAACTTGTCGCAATTACAC 1935
DB 21 AATGCTGTCGCAATTACAC 1
XX
RESULT 3348
ADE16100/c
ID ADE16100 standard; DNA; 21 BP.
XX
AC ADE16100;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related forward PCR primer, SEQ ID NO 130.
XX
KM G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KM vincide; fungicide; cytostatic; nootropic; neuroprotective;
KM antiparkinsonian; haemostatic; antihypertensive; neurogenesis;
KM cell differentiation; cell proliferation; hematopoiesis; wound healing;
KM angiogenesis; gene therapy; chromosome mapping; tissue typing;
KM preventive medicine; pharmacogenomics; human; PCR; primer; ss.
XX

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OS Homo sapiens.
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 24-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zernhusen BD;
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boidog FL;
PI Voss EZ, Vermet CAM, MacDougall JR, Kestell L, Anderson DW;
PI Zhong M, Mezes PD, Futrak K, Paturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
DR WPI; 2003-067574/06.
XX
PT New isolated NOX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
PS Example 27; SEQ ID NO 130; 320bp; English.
XX
CC The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC vincide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antihypertensive. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorder,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
XX

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CC tissue typing, preventive medicine, and pharmacogenomics. This
 CC polynucleotide sequence represents a primer relating to the novel G-
 CC coupled protein receptor related polypeptides of the invention.

XX Sequence 21 BP; 1 A; 8 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2859 AGAGGAGCAAGAGAGGGA 2879
 Db 21 AAAGCAGCAAGAGAGACTGA 1

RESULT 3349
 AAQ14243
 ID AAQ14243 standard; DNA; 22 BP.

XX AAQ14243;

AC 20-JAN-1992 (first entry)

XX Primer CMLI.

DE Acute lymphocytic leukaemia; chimeric; mRNA; ABL; breakpoint; cluster;
 KW BCR; ABL; exon junction; PCR; ss.

XX Synthetic.

OS US5057410-A.

XX 15-OCT-1991.

XX 05-AUG-1988; 88US-00229604.

XX 05-AUG-1988; 88US-00229604.

XX (CERTU) CERTUS CORP.

XX KAWASAKI ES, McCormick EP, Witto OO;

XX WPI; 1991-324515/44.

PT Method for detecting chimeric mRNA - useful e.g. for distinguishing
 PT between acute lymphocytic leukaemia and chronic myeloid leukaemia.

PS Claim 5; Page 13; 14pp; English.

CC The primer is used with primer CMLII (AAQ14244) to amplify chimeric mRNA
 CC contg. a specific exon-exon junction associated with chronic myeloid
 CC leukaemia (CML). It is complementary to cDNA sequences within the break
 CC point cluster region (BCR) exon 2. It can distinguish between ABL BCR-ABL
 CC chimeric mRNA and CML BCR-ABL mRNA. The CML DNA sequences used to design
 CC the primer are reported by Heisterkamp, N., et al. Nature 315:758 (1985)
 CC ; Grosvel, G., et al Mol. Cell Biol. 6:607 (1987); and Shivelman, E.,
 CC et al Cell 47:277 (1986). See also AAQ14241-47

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2539 GAGCTCCAGATCTGACCTAC 2559
 Db 2 GAGCTGCAGATCTGACCAAC 22

RESULT 3350
 AAQ32173/C
 ID AAQ32173 standard; DNA; 22 BP.

AC AAQ32173;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 30-MAR-1993 (first entry)

DE Reverse PCR primer for novel nematode active genes eg BT toxins.
 KW nematode worms; nematicide; nematicidal toxin; agriculture; plants;
 KW crops; pests; CryV proteins.

OS Bacillus thuringiensis.

XX EP517367-A1.

XX 09-DEC-1992.

XX 01-MAY-1992; 92EP-00303969.

XX 03-MAY-1991; 91US-00693018.

XX 31-JAN-1992; 92US-00830050.

XX 23-APR-1992; 92US-00871510.

XX (MYCO) MYCOGEN CORP.

XX Schinepf HE, Schwab GE, Payne JM, Narva KE, Foncerrada L;

XX WPI; 1992-408829/50.

XX Nematocidal toxins from *Bacillus thuringiensis* - useful for control of
 XX animal or plant parasites, and DNA acid coding sequences, transformed
 XX hosts and transgenic plants.

XX Claim 1(f); Page 53; 57pp; English.

XX This degenerate sequence represents a reverse PCR primer for the cloning
 CC of a novel nematocidal toxin from BT as in AAQ32172. (Updated on 25-MAR-
 CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 22 BP; 7 A; 2 C; 2 G; 7 T; 0 U; 4 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4405 TTACCAAAATGCAATTTTCC 4425
 Db 22 TWGAYMDAATTGAATTATTC 2

RESULT 3351

AAQ30933/C
 ID AAQ30933 standard; DNA; 22 BP.

XX AAQ30933;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 30-MAR-1993 (first entry)

DE Reverse PCR primer for novel nematode active genes eg BT toxins.

KW nematode worms; nematicide; nematicidal toxin; agriculture; plants;
 KW crops; pests; CryV proteins.

OS *Bacillus thuringiensis*.

XX W09219739-A1.

XX 12-NOV-1992.

XX 01-MAY-1992; 92WO-US003624.

```
PR 03-MAY-1991; 91US-00693018.  
PR 31-JUN-1992; 92US-00830050.  
PR 23-APR-1992; 92US-00871510.  
XX  
XX (MYCO ) MYCOGEN CORP.  
XX  
PI Schnopf HE, Schwab GE, Payne JM, Narva KB, Foncecrada L,  
XX WPI; 1992-398866/48.  
XX  
XX New genes and toxins against nematodes - obt'd. from Bacillus  
PT Thuringiensis isolates with nematocidal activity.  
XX  
XX  
PS Claim 1(f); Page 12; 77pp; English.  
XX  
XX This degenerate sequence represents a reverse PCR primer for the cloning  
CC of a novel nematocidal toxin from BT as in AAQ0943. (Updated on 25-MAR-  
CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 22 BP; 7 A; 2 C; 2 G; 7 T; 0 U; 4 Other;  
  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 66.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4405 TTTACAAAATGAAATTTTTC 4425  
DB 22 TWGAYMRAATTGAATTATTC 2  
  
RESULT 3352  
AAQ0300  
ID AAQ0300 standard; DNA; 22 BP.  
XX  
XX AAQ0300;  
XX  
XX 25-MAR-2003 (revised)  
DT 11-JUL-1995 (first entry)  
XX  
XX Human plasmin cDNA PCR primer.  
DE  
XX Human plasmin; haemopoietic cells; neoplastic; PCR primers;  
KM nucleotide probes; anti-plasmin antibodies; ss.  
XX  
XX Synthetic.  
OS  
XX US5360715-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 10-JAN-1991; 91US-00642983.  
PF  
XX 07-JUN-1988; 88US-00203434.  
PR 16-MAR-1990; 90US-00495256.  
XX  
XX (CALY ) CALIFORNIA INST OF TECHN.  
PA  
XX Lin C, Hebersold RH, Leavitt JC;  
PI WPI; 1994-349444/43.  
XX  
XX DNA encoding leukocyte-plasmin and tissue-plasmin - used to develop  
PT prods. for distinguishing human haemopoietic cells, normal tissue cells  
PT and neoplastic cells.  
XX  
XX Example 2; Col 19; 17pp; English.  
XX  
XX AAQ0239 and AAQ0300 are a pair of upstream and AAQ0301 and AAQ0302  
CC are a pair of downstream primers for the PCR amplification of AAQ3001  
CC and AAQ73002, which encode AAR62657 and AAR62658 human tissue plasmin (t-  
CC plasmin) and human leukocyte plasmin (l-plasmin) respectively. The  
CC plasmin cDNA and amino acid sequences were used to develop isoform  
CC specific plasmin nucleotide probes, and isoform specific anti-plasmin
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CC antibodies. Using the fact that human cells that express only l-plasmin  
CC are haemopoietic cells, and human cells that express both l-plasmin and t-  
CC plasmin are neoplastic, the above probes and antibodies could be used to  
CC distinguish between the above cell types. (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 22 BP; 1 A; 18 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 3388 CCCGAGCTCCACCCCCACC 3408  
DB 1 CTCGAGCTCCCCCCCCCCC 21  
  
RESULT 3353  
AAQ61522/c  
ID AAQ61522 standard; cDNA; 22 BP.  
XX  
XX AAQ61522;  
XX  
XX 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 21-OCT-1994 (first entry)  
XX  
XX TCR delta B5 enhancer element comprising Ikaros binding site.  
DE  
XX Ikaros; zinc finger; protein; immune disorder; therapy; treatment;  
KM corpus striatum; regulatory gene; enhancer; regulatory element;  
KM gene expression; ss.  
XX  
XX Mus sp.  
OS  
XX WO9406814-A1.  
PN  
XX 31-MAR-1994.  
PD  
XX 14-SEP-1993; 93WO-US008743.  
PF  
XX 14-SEP-1992; 92US-00946233.  
PR  
XX (GEHO ) GEN HOSPITAL CORP.  
PA  
XX Georgopoulos K;  
PI  
XX WPI; 1994-118387/14.  
XX  
XX I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc  
PT finger proteins, useful for treating immune system disorders.  
XX  
XX Disclosure; Page 28; 112pp; English.  
XX  
XX The Ikaros gene encodes a zinc finger protein which can be used in a  
CC therapeutic composition to treat animals with an immune system disorder.  
CC It may also be used for assessing whether a subject is at risk for an  
CC immune disorder. It is of particular use in treating a disorder of the  
CC corpus striatum. Heterologous genes may be expressed by placing them  
CC under the control of an Ikaros responsive control element and contacting  
CC the element with an Ikaros protein. Potential high affinity binding sites  
CC for the Ikaros proteins were found in the enhancer and promoter regions  
CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma  
CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains  
CC of other T cell restricted antigens. Related sequences to the Ikaros  
CC motif were also found in the purine boxes of the IL2 gene in the  
CC LTF site of the TDT promoter as well as in the NFkB variant sites of the  
CC HIV long terminal repeat. See also AAQ61504-061543. (Updated on 10-MAR-  
CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN  
CC field.)  
SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
```

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5690 TACCACTGTTTGGCTTCCTT 5710
 |||||
 DB 21 TTCCCTGTTTGGTTTCCTT 1

RESULT 3354
 AA086634
 ID AA086634 standard; DNA; 22 BP.
 XX
 AC AA086634;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-NOV-1995 (first entry)
 XX
 DE Non-promoter primer for the CML major breakpoint region.
 XX
 KM Primer; autocatalytic; PCR; target; sequence; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 XX
 PD 21-MAR-1995.
 XX
 PF 19-MAR-1992; 92US-00855732.
 XX
 PR 11-JUL-1989; 89US-00379501.
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse transcriptase
 PT with RNase H activity and a RNA polymerase at constant temp.
 XX
 PS Example 18; Col 47; 58pp; English.
 XX
 CC The oligonucleotide AA086634 is a non-promoter primer for the CML major
 CC breakpoint amplification region. It is used to illustrate that small
 CC changes in the NA sequence result in large changes in the amplification
 CC efficiency. AA086634 is capable of serving as a primer for the synthesis
 CC of autocatalytic oligonucleotides which require no change in the PCR
 CC conditions i.e. constant temperature, pH and ionic strength. This sequence
 CC is useful in generating multiple copies of specific nucleic acid target
 CC sequences. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2539 GAGCTCGAGATCGTACGTAC 2559
 |||||
 DB 2 GAGCTCGAGATCGTACCAAC 22

RESULT 3355
 AA086627
 ID AA086627 standard; DNA; 22 BP.
 XX
 AC AA086627;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-NOV-1995 (first entry)
 XX

DE CML chromosomal translocation plus strand primer.
 XX
 KM Primer; autocatalytic; target; CML; translocation; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 XX
 PD 21-MAR-1995.
 XX
 PF 19-MAR-1992; 92US-00855732.
 XX
 PR 11-JUL-1989; 89US-00379501.
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse transcriptase
 PT with RNase H activity and a RNA polymerase at constant temp.
 XX
 PS Disclosure; Col 9; 58pp; English.
 XX
 CC AA086626-28 are primers and a probe for the CML chromosomal
 CC translocation. They are used to produce autocatalytic oligonucleotides
 CC which require no change in the experimental conditions i.e. constant
 CC temperature, pH and ionic strength. These sequences are useful in
 CC generating multiple copies of specific nucleic acid target sequences.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2539 GAGCTCGAGATCGTACGTAC 2559
 |||||
 DB 2 GAGCTCGAGATCGTACCAAC 22

RESULT 3356
 AAT15572
 ID AAT15572 standard; DNA; 22 BP.
 XX
 AC AAT15572;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-JUL-1996 (first entry)
 XX
 DE CML-2 chromosomal translocation major breakpoint t(9;22) (+) primer.
 XX
 KM CML-2 chromosomal translocation major breakpoint; t(9; 22); primer;
 KM auto-catalytic; synthesis; RNA target sequence; assay; detection;
 KM quantification; ss.
 XX
 OS Synthetic.
 XX
 PN US5480784-A.
 XX
 PD 02-JAN-1996.
 XX
 PF 10-JUL-1990; 90US-00550837.
 XX
 PR 11-JUL-1989; 89US-00379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4149 CTGATTGTTCTCTGACCTCG 4169
 |||||
 DB 2 CTGATTGTTCTCTGACCTCG 22

RESULT 3359

AAK83072
 ID AAK83072 standard; DNA; 22 BP.

XX AAK83072;

XX 31-AUG-1999 (first entry)

XX Primer 5E9 to detect mutations in the human WRN gene.

XX Human; WRN; Werner's syndrome; detection; diagnosis; autosomal; mutation;
 KW recessive disorder; phenotype; primer; PCR; amplification; ss.

XX Synthetic.

XX Homo sapiens.

XX MO9724435-A1.

XX 10-JUL-1997.

XX PF 30-DEC-1996; 96WO-US020785.

XX PR 29-DEC-1995; 95US-0009409P.

XX PR 29-DEC-1995; 95US-0058053P.

XX PR 30-JAN-1996; 96US-0010835P.

XX PR 30-JAN-1996; 96US-00594242.

XX PR 12-APR-1996; 96US-00632175.

XX PA (DARW-) DARWIN MOLECULAR CORP.

XX PI Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;

XX DR WPI; 1997-363671/33.

XX Isolated nucleic acid molecule encoding the WRN gene product - useful for
 PT detection and treatment of Werner's syndrome, and related diseases.

XX PS Example 5; Page 48; 153pp; English.

XX CC Primers AAK83071-X83082 were used to PCR amplify, detect and identify
 CC mutations in the human WRN gene (AAK83003) which encodes a protein
 CC related to Werner's syndrome. The products can be used for the detection
 CC and treatment of Werner's syndrome (WS), an autosomal recessive disorder
 CC with a complex phenotype, as well as related diseases

XX SQ Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7337 AGCTGACCTGTGCAGTCCA 7357
 |||||
 DB 1 AGATGACTTGGCCATTCCA 21

RESULT 3360

AAK68896
 ID AAK68896 standard; DNA; 22 BP.

XX AAK68896;

XX 06-APR-1998 (first entry)

DE Human BCR 5' RT-PCR primer.

XX Drug-resistance; neoplastic disease; non-malignant haematopoietic cell;
 KW progenitor; gene rearrangement; RT-PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX MO9718305-A2.

XX 22-MAY-1997.

XX PF 13-NOV-1996; 96WO-US018273.

XX PR 14-NOV-1995; 95US-0006692P.

XX PA (MTNU) UNIV MINNESOTA.

XX Verfallle CM, McIvor RS, Zhao RC;

XX WPI; 1997-289281/26.

XX Expression cassette for forming drug resistant hematopoietic stem cells -
 PT decreases RNA or protein found only in malignant cells; for treating
 PT leukaemia(s), such as chronic myelogenous leukaemia.

XX Example 2; Fig 1; 52pp; English.

XX This RT-PCR 5' primer is designed to a human breakpoint cluster region
 CC (BCR) and is used in a novel method of preparing drug-resistant, non-
 CC malignant haematopoietic cells. This method involves the construction of
 CC a new expression cassette comprising a first nucleic acid molecule which
 CC encodes resistance of a host cell to a cytotoxic agent, operably linked
 CC to a first promoter which functions in the host cell and a second nucleic
 CC acid molecule operably linked to a second promoter which functions in the
 CC host cell. The second nucleic acid molecule encodes an RNA molecule or a
 CC polypeptide whose expression decreases the expression of an RNA or a
 CC polypeptide present in a malignant cell only. This method can eliminate
 CC residual neoplastic disease in a patient, where the disease has an
 CC immature hematopoietic progenitor cell with a well-defined gene
 CC rearrangement. Diseases such as chronic myelogenous leukaemia which is
 CC associated with a BCR/ABL gene rearrangement, acute lymphoblastic
 CC leukaemia and acute promyelocytic leukaemia may be treated using this
 CC method

XX SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2539 GAGCTCCAGTCTGACGTAC 2559
 |||||
 DB 2 GAGCTCCAGTCTGACGTAC 22

RESULT 3361

AAK91777
 ID AAK91777 standard; DNA; 22 BP.

XX AAK91777;

XX 25-MAR-2003 (revised)

XX DT 08-JAN-1998 (first entry)

XX DE Primer B3300b for bcr2-abl2 and bcr3-abl2 translocation regions.

XX PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;
 KW chronic myelogenous leukaemia; human; bcr2-abl2; translocation region;
 KW cytogenetic remission; Ph chromosome; bcr3-abl2; CML cell;
 KW acute lymphocytic leukaemia; ss.

XX OS Synthetic.

XX WO9708339-A1.
 XX 06-MAR-1997.
 XX 28-AUG-1995; 95WO-US010919.
 XX 25-AUG-1995; 95US-00296258.
 XX (DADE-) DADE INT INC.
 XX Brown J, LockhartDruce C;
 XX WPI; 1997-179294/16.
 XX Detection of chronic myelogenous leukemia cells - by amplification of
 PT RNA from hematopoietic cells with primers for the bcr2-ab12 and bcr3-
 PT ab12 translocation regions.
 XX
 XX Example 1; Page 10; 79pp; English.
 XX
 XX AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
 CC the invention. AAT91754-T91759 can also be used as capture
 CC oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
 CC also be used as detector agents. The method of the invention is for
 CC detecting or monitoring chronic myelogenous leukemia (CML) cells in a
 CC human patient. The method comprises obtaining RNA from hematopoietic
 CC cells of the patient, and amplifying it using a pair of primers that
 CC amplify both the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC amplified sequence is contacted with a capture agent comprising a capture
 CC ON and a binding ligand to form a capture mixture. The capture ON is
 CC specific for the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC mixture is contacted with a solid phase coupled to a receptor specific
 CC for the binding ligand. The solid phase is washed, then contacted with a
 CC detector agent comprising a detector ON specific for the bcr2-ab12 or
 CC bcr3-ab12 translocation regions and a label. The amount of labelled
 CC detector ON bound to the solid phase is then correlated with the presence
 CC or quantity of CML cells in the patient. The method is to detect or
 CC monitor CML cells in patients. It can also be used prognostically to
 CC assess cytogenetic remission in patients with CML. The method detects
 CC both the bcr2-ab12 and the bcr3-ab12 translocations associated with CML.
 CC The assay does not detect CML in the absence of the Ph chromosome, nor
 CC does it detect acute lymphoblastic leukemia (ALL) even if the ALL
 CC patient has the Ph chromosome. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 CC
 XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2539 GAGCTCCAGATCCTGACGTAC 2559
 |||||
 2 GAGCTGCAGATGTCGACCAAC 22
 RESULT 3362
 AAV29432
 ID AAV29432 standard; DNA; 22 BP.
 XX
 XX AAV29432;
 XX 31-JUL-1998 (first entry)
 XX Calcium ion channel alpha subunit exon 28 specific reverse primer.
 DE Calcium ion channel alpha subunit; human; episodic ataxia type 2;
 KW familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;
 KW PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 OS

XX EF834561-A1.
 XX 08-APR-1998.
 XX 27-SEP-1996; 96EP-00202707.
 XX 27-SEP-1996; 96EP-00202707.
 XX (UYLE-) RIJXSUNIV LEIDEN.
 XX WPI; 1998-195461/18.
 XX
 XX New human nucleic acid associated with migraine and episodic ataxia type
 PT 2 - useful for diagnosis and development of, e.g. familial hemiplegic
 PT migraine and episodic ataxia type 2.
 XX
 XX Disclosure; Page 9; 157pp; English.
 XX
 XX This primer is used for the PCR amplification of an exon of the human
 CC calcium ion channel alpha 1 subunit. The channel is related to familial
 CC hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is
 CC derived from, related to or associated with a gene present in humans on
 CC chromosome 19p13.1-13.2. The encoding nucleic acid can be used to
 CC localise or identify genes related to episodic neurological disorders,
 CC specifically migraine, FHM or EA-2, but also epilepsy. It can also be
 CC used to distinguish between alleles of the corresponding gene. Cells and
 CC animals containing recombinant expression vectors comprising the nucleic
 CC acid can be useful in study, development and treatment of migraine, FHM,
 CC EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and
 CC natural or synthetic antibodies against the proteins can be used to
 CC diagnose FHM, EA-2, migraine and other neurological conditions associated
 CC with cation channel dysfunction
 CC
 XX Sequence 22 BP; 1 A; 10 C; 2 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4602 TTTTCTGCCCCACCTGCTGG 4622
 |||||
 1 TTTCCCTGCCCCCACTCTTGG 21
 Db
 RESULT 3363
 AAV52673/c
 ID AAV52673 standard; DNA; 22 BP.
 XX
 XX AAV52673;
 XX 21-DEC-1998 (first entry)
 XX Hepatocyte nuclear factor 4 alpha gene exon 4 forward PCR primer.
 DE Hepatocyte nuclear factor 4 alpha; HNF-4 alpha; MODY1; human;
 KW Hepatocyte nuclear factor; maturity onset diabetes of the young; TCF14;
 KW diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX WO9811254-A1.
 XX 19-MAR-1998.
 XX 10-SEP-1997; 97WO-US016037.
 XX 10-SEP-1996; 96US-0025719P.
 XX 02-OCT-1996; 96US-0028056P.
 XX 30-OCT-1996; 96US-0029679P.
 XX (ARCH-) ARCH DEV CORP.
 PA

XX Bell Gi, Yamagata K, Oda N, Katsaki P, Furuta H, Menzel S;
 PI Horikawa Y;
 XX WPI, 1998-271667/24.
 XX
 PT Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-
 PT beta - useful for detecting susceptibility for non-insulin dependent
 PT diabetes, especially maturity-onset diabetes of the young.
 XX
 PS Example 3; Page 112; 363pp; English.
 XX
 CC This is a forward PCR primer designed for use with a reverse primer (see
 CC AAV52674) in the PCR amplification of exon 4 and the flanking introns
 CC (see AAV52656) of the human hepatocyte nuclear factor-4 alpha (HNF-4
 CC alpha) gene (see AAV52687). Mutations of the HNF-4 alpha gene have been
 CC identified by amplifying (see AAV5265-86) and sequencing the appropriate
 CC exon. The invention concerns the identification of genes responsible for
 CC non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostic
 CC and therapeutics. It demonstrates that the MODY1 (maturity-onset diabetes
 CC of the young) locus is the HNF-4 alpha gene. Analysis of mutations in the
 CC HNF-4 alpha gene can be diagnostic for diabetes
 CC
 SQ Sequence 22 BP; 3 A; 13 C; 1 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 4513 CAGGACTGAGAGGTGGTGG 4533
 |||||
 Db 21 CAGGATGAGTGGGCGTGG 1
 |||||
 RESULT 3364
 AAV45376/c
 ID AAV45376 standard; DNA; 22 BP.
 XX
 AC AAV45376;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Mouse T cell receptor delta enhancer binding site for Ikaros.
 XX
 KW Ikaros; mIK; transcription factor; mouse; lymphocyte;
 KW cell differentiation; T cell; cancer; immunodeficiency;
 KW Alzheimer's disease; therapy; diagnosis; T cell receptor; enhancer; ss.
 XX
 OS Mus sp.
 XX
 PN CA2194256-A.
 XX
 PD 05-MAR-1998.
 XX
 PF 02-JAN-1997; 97CA-02194256.
 XX
 PR 05-SEP-1996; 96US-00711417.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PI
 PT Georgopoulos K;
 XX
 DR WPI; 1998-378292/33.
 XX
 PT New nucleic acid encoding Ikaros protein involved in early
 PT differentiation of lymphocytes - existing in several isoforms, and
 PT related products, used to treat e.g. immune diseases or cancer and to
 PT control cell differentiation.
 XX
 PS Disclosure; Page 38; 158pp; English.
 XX
 CC This oligonucleotide from the T cell receptor delta enhancer was
 CC identified as a potential high affinity binding site for Ikaros proteins

CC (see AAW70963-71). It includes the core motif GGGAA found in consensus
 CC recognition sequences for murine Ikaros protein isoforms mIK-1, mIK-2 and
 CC mIK-3 (see AAV52830-32). High affinity binding sites for Ikaros have been
 CC found in enhancer and promoter regions of the regulatory domains of the
 CC TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal repeat
 CC and in the regulatory domains of other T cell restricted antigens (see
 CC AAV45358-402) by gel retardation assay. Ikaros is involved in early
 CC differentiation of lymphocytes. The invention provides Ikaros nucleic
 CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host
 CC cells. These are used to treat T and B cell diseases, to control
 CC expression of heterologous genes placed under control of an Ikaros-
 CC responsive element, to treat nervous system diseases and to modulate cell
 CC division, amplification or differentiation, especially in haematopoietic
 CC cells
 XX
 SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 5690 TACCACGTGTTTGGCTTCCTT 5710
 |||||
 Db 21 TTCCCGTGTGTTTCCTT 1
 |||||
 RESULT 3365
 AAV66352
 ID AAV66352 standard; DNA; 22 BP.
 XX
 AC AAV66352;
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE CML-2 chromosomal translocation major breakpoint non-promoter primer.
 XX
 KW CML-2 chromosomal translocation t(14; 18) major breakpoint;
 KW block splice template; autocatalytic RNA amplification; primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5824518-A.
 XX
 PD 20-OCT-1998.
 XX
 PF 06-JUN-1995; 95US-00469067.
 XX
 PR 11-JUL-1989; 89US-00379501.
 XX
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 PI
 PT Fultz TJ, Kacian DL;
 XX
 DR WPI; 1998-582557/49.
 XX
 PT Block splice template useful for amplification of nucleic acids -
 PT comprises two nucleic acid regions, the first region located 3' of the
 PT second region and blocked at its 3' terminus to inhibit primer extension
 PT by a DNA polymerase.
 XX
 PS Example 18; Col 43; 51pp; English.
 XX
 CC AAV66352-55 represent CML-2 chromosomal translocation t(14;18) major
 CC breakpoint amplification region non-promoter primers. The primers are
 CC used to exemplify the invention. The specification describes methods of
 CC synthesizing multiple copies of a target nucleic acid sequence
 CC autocatalytically under conditions of substantially constant temperature,
 CC ionic strength and pH are provided in which multiple RNA copies of the
 CC target sequence autocatalytically generate additional copies. The target
 CC sequence is a block splice template which comprises two nucleic acid
 CC regions. The first region is located 3' of the second region and is
 CC blocked at its 3' terminus to inhibit primer extension by a DNA

CC polymerase, and the second region comprises a promoter sequence
 CC recognised by an RNA polymerase. The methods are used to amplify nucleic
 CC acids, especially RNA, for analysis, cloning or probe production
 XX
 SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2539 GAGCTCCAGATCCTGACGTAC 2559
 DB 2 GAGCTCCAGATCCTGACGTAC 22
 RESULT 3366
 ID AAV66350 standard; DNA; 22 BP.
 XX
 AC AAV66350;
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE CML-2 chromosomal translocation t(9;22) primer.
 XX
 KM CML-2 chromosomal translocation t(9;22); block splice template;
 XX autocatalytic RNA amplification; primer; ss.
 OS
 XX Synthetic.
 XX
 PN US5824518-A.
 XX
 PD 20-OCT-1998.
 XX
 PF 06-JUN-1995; 95US-00469067.
 XX
 PR 11-JUL-1989; 89US-00379501.
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fullz TJ, Kacian DJ;
 XX
 DR WPI, 1998-582557/49.
 XX
 PT Block splice template useful for amplification of nucleic acids -
 PT comprises two nucleic acid regions, the first region located 3' of the
 PT second region and blocked at its 3' terminus to inhibit primer extension
 PT by a DNA polymerase.
 XX
 PS Example 15; Col 9; 51pp; English.
 XX
 CC AAV66349-50 represent CML-2 chromosomal translocation t(9;22) primers,
 CC for the (+) and (-) strands respectively. The primers are used to
 CC exemplify the invention, together with probe AAV66351. The specification
 CC describes methods of synthesising multiple copies of a target nucleic
 CC acid sequence autocatalytically under conditions of substantially
 CC constant temperature, ionic strength and pH are provided in which
 CC multiple RNA copies of the target sequence autocatalytically generate
 CC additional copies. The target sequence is a block splice template which
 CC comprises two nucleic acid regions. The first region is located 3' of the
 CC second region and is blocked at its 3' terminus to inhibit primer
 CC extension by a DNA polymerase, and the second region comprises a promoter
 CC sequence recognised by an RNA polymerase. The methods are used to amplify
 CC nucleic acids, especially RNA, for analysis, cloning or probe production
 XX
 SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2539 GAGCTCCAGATCCTGACGTAC 2559

DB 2 GAGCTCCAGATCCTGACGTAC 22
 RESULT 3367
 ID AAV45541 standard; DNA; 22 BP.
 XX
 AC AAV45541;
 XX
 DT 15-FEB-1999 (first entry)
 XX
 DE Helicobacter pylori babA gene PCR primer.
 XX
 KM Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;
 KM stomach cancer; babA gene; PCR; primer; ss.
 OS
 XX Synthetic.
 XX
 PN WO9844130-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 31-MAR-1998; 98WO-KR000073.
 XX
 PR 31-MAR-1997; 97KR-00011950.
 PR 31-MAR-1997; 97KR-00011951.
 XX
 PA (DAEW-) DAEWONG PHARM CO LTD.
 XX
 PI Kim B, Shin S, Yu Y, Park M, Choi D, Jung H;
 XX
 DR WPI, 1998-568279/48.
 XX
 PT New chimeric proteins for use against Helicobacter pylori - comprising an
 PT antigenic protein of H. pylori and A1 and B subunits of Vibrio cholerae
 PT toxin, preferably produced by recombinant techniques.
 XX
 PS Example 2-21; Page 15; 102pp; English.
 XX
 CC PCR primers (see AAV45541 and AAV45542) are designed for the PCR
 CC amplification of the Helicobacter pylori babA gene. The invention relates
 CC to recombinant DNA (see AAV45460-61) comprising a fusion gene prepared by
 CC ligating an antigenic determinant coding gene (e.g. the babA gene) of H.
 CC pylori and A2 and B subunit genes of Vibrio cholerae. Also claimed are
 CC chimeric proteins (see AAV80599-600) encoded by such recombinant DNA,
 CC methods for the recombinant production of the chimeric proteins, and use
 CC of the chimeric proteins in preventative and therapeutic vaccines for H.
 CC pylori and associated diseases such as gastritis, gastric ulcer, duodenal
 CC ulcer and gastric cancer
 XX
 SQ Sequence 22 BP; 9 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2015 GAGCGATGGGAAAAAACCCTT 2035
 DB 1 CCGTGGATGAAAAAACCCTT 21
 RESULT 3368
 ID AAV67083 standard; cDNA; 22 BP.
 XX
 AC AAV67083;
 XX
 DT 14-JAN-1999 (first entry)
 XX
 DE Mouse TCR-delta enhancer deltaEs.
 XX

KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
 KW differentiation marker; immune system; corpus striatum; AIDS;
 KW Alzheimer's disease; ss.
 XX Mus sp.
 OS Synthetic.
 XX US5824770-A.
 PN 20-OCT-1998.
 XX 05-JUN-1995; 95US-00465590.
 XX 14-SEP-1992; 92US-00946233.
 PR 14-SEP-1993; 93US-00121438.
 PR 02-MAY-1994; 94US-00238212.
 XX (GCHO) GEN HOSPITAL CORP.
 PA Georgopoulos K;
 PI WPI; 1998-582621/49.
 DR Ikaros poly:peptide(s) - useful for treating disorders of immune system
 XX or corpus striatum.
 PT Disclosure; Col 26; 11pp; English.
 XX The present invention describes a purified peptide having at least one of
 CC the following properties: (a) it stimulates transcription of a DNA
 CC sequence under the control of a delta A element, an NFKB element or an
 CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
 CC a delta A element, an NFKB element or an Ikaros binding oligonucleotide
 CC consensus sequence; (c) it competitively inhibits the binding of a
 CC naturally occurring Ikaros isoform to any of a delta A element, an NFKB
 CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or
 CC (e) it inhibits protein-protein interactions of transcriptional complexes
 CC formed with naturally occurring Ikaros isoform. The proteins, provided
 CC that they stimulate gene transcription under the control of delta A
 CC elements, NFKB elements and/or Ikaros-binding oligonucleotides, bind to
 CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to
 CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
 CC inhibit protein-protein interactions of transcriptional complexes with
 CC naturally occurring Ikaros isoforms, can be used to treat immune system
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
 CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides
 CC given in the present invention
 XX
 SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No.2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5690 TACCACTGTTTGGCTTCTT 5710
 DB 21 TTCCCTGTGTTGGTTCCTT 1
 RESULT 3369
 AAT9486
 ID AAT9486 standard; DNA; 22 BP.
 AC AAT9486;
 XX 21-MAY-1998 (first entry)
 DT Human ST receptor PCR primer.
 XX ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
 KW

KW metastasis; diagnosis; human; PCR; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9742506-A1.
 PN 13-NOV-1997.
 XX 02-MAY-1997; 97WO-US007467.
 XX 03-MAY-1996; 96US-0016564P.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Waldman SA, Carrithers SJ;
 PI WPI; 1998-008454/01.
 DR Determining whether an individual has metastasised colorectal cancer
 XX cells and origin of tumour cells - by detecting presence of heat-stable
 FT toxin receptor on cells in a sample.
 PT Claim 14; Page 53; 62pp; English.
 XX Claimed PCR primers (see AAT99462-199531) hybridise to sequences that
 CC encode the extracellular domain of human heat-stable toxin (ST) receptor
 CC protein (see AAM37371), a highly specific marker for metastasised
 CC colorectal cancer cells. PCR using these primers provides specific and
 CC sensitive detection of human ST receptor expression. A specific primer
 CC pair comprises the primers given in AAT99486 and AAT99487. Claimed in
 CC vitro methods for determining whether or not (i) an individual has
 CC metastasised colorectal cancer cells, or (ii) a tumour cell is a
 CC colorectal cancer cell comprise the steps of examining a sample of
 CC extraintestinal tissue and/or body fluids or tumour cells from an
 CC individual to determine whether ST receptor protein is being expressed by
 CC cells in the sample. Expression is determined by immunassay or by PCR
 CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
 CC AAT97229)
 XX
 SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No.2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3199 AGTGAGGCGCTTGGAAGTG 3219
 DB 2 AATGAGGCGCTCGAATATG 22
 RESULT 3370
 AAT9484
 ID AAT9484 standard; DNA; 22 BP.
 AC AAT9484;
 XX 21-MAY-1998 (first entry)
 DT Human ST receptor PCR primer.
 XX ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
 KW metastasis; diagnosis; human; PCR; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9742506-A1.
 PN 13-NOV-1997.
 PD 02-MAY-1997; 97WO-US007467.
 PF

PR 03-MAY-1996; 96US-0016564P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
PI Waldman SA, Carrithers SL;
XX
XX WPI; 1998-008454/01.
DR
XX Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
PS
XX Claim 14; Page 53; 62pp; English.
XX
CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AAW37371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99484 and AAT99485. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a
CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunoassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AAT97229)
XX
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3199 AGTGAGGGGCTTGAGAAAGTG 3219
Db 2 AATGAGGGGCTGGAATAGTG 22
RESULT 3371
AAT99494
ID AAT99494 standard; DNA; 22 BP.
XX
AC AAT99494;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human ST receptor PCR primer.
XX
KM ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KM metastasis; diagnosis; human; PCR; primer; 88.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W09742506-A1.
PN
PD 13-NOV-1997.
XX
XX 02-MAY-1997; 97WO-US007467.
PF
XX 03-MAY-1996; 96US-0016564P.
PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX Waldman SA, Carrithers SL;
XX
XX WPI; 1998-008454/01.
DR
XX Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.

XX
PS Claim 14; Page 53; 62pp; English.
XX
XX Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AAW37371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99494 and AAT99495. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a
CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunoassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AAT97229)
XX
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3201 TGAGGGGCTTGAGAAAGTG 3221
Db 2 TGAGGGGCTGGAATAGTG 22
RESULT 3372
AAT99490
ID AAT99490 standard; DNA; 22 BP.
XX
AC AAT99490;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human ST receptor PCR primer.
XX
KM ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KM metastasis; diagnosis; human; PCR; primer; 88.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W09742506-A1.
PN
PD 13-NOV-1997.
XX
XX 02-MAY-1997; 97WO-US007467.
PF
XX 03-MAY-1996; 96US-0016564P.
PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX Waldman SA, Carrithers SL;
XX
XX WPI; 1998-008454/01.
DR
XX Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
PS
XX Claim 14; Page 53; 62pp; English.
XX
CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AAW37371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99490 and AAT99491. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a

CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunosassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AA197229)
XX
SQ Sequence 22 BP; 8 A; 1 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3199 AGTGAGGGCTTGAGAAAGTG 3219
DB 1 AATGAGGGCTGGAATAGTG 21
RESULT 3373
AAT99496
ID AAT99496 standard; DNA; 22 BP.
XX
AC AAT99496;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human ST receptor PCR primer.
XX
KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KW metastasis; diagnosis; human; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9742506-A1.
XX
PD 13-NOV-1997.
XX
PF 02-MAY-1997; 97WO-US007467.
XX
PR 03-MAY-1996; 96US-0016564P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA, Carrithers SL;
XX
DR WPI; 1998-008454/01.
XX
PT Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
XX
PS Claim 14; Page 53; 62pp; English.
XX
CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AA197371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99496 and AAT99497. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a
CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunosassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AA197229)
XX
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3199 AGTGAGGGCTTGAGAAAGTG 3219
DB 2 AATGAGGGCTGGAATAGTG 22
RESULT 3375
AAT99492
ID AAT99492 standard; DNA; 22 BP.
XX

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3201 TGAGGGGCTTGAGAAAGTGCG 3221
DB 2 TGAGGGGCTGGAATAGTGAG 22
RESULT 3374
AAT99488
ID AAT99488 standard; DNA; 22 BP.
XX
AC AAT99488;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human ST receptor PCR primer.
XX
KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KW metastasis; diagnosis; human; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9742506-A1.
XX
PD 13-NOV-1997.
XX
PF 02-MAY-1997; 97WO-US007467.
XX
PR 03-MAY-1996; 96US-0016564P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA, Carrithers SL;
XX
DR WPI; 1998-008454/01.
XX
PT Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
XX
PS Claim 14; Page 53; 62pp; English.
XX
CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AA197371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99488 and AAT99489. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a
CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunosassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AA197229)
XX
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3199 AGTGAGGGCTTGAGAAAGTG 3219
DB 2 AATGAGGGCTGGAATAGTG 22
RESULT 3375
AAT99492
ID AAT99492 standard; DNA; 22 BP.
XX

PT Assay for detecting modulating agents of UL97 protein kinase - useful
CC for, e.g. preparation of therapeutics for treatment of cytomegalovirus
PT infections.
XX
XX Disclosure: Page 15; 57pp; English.
XX
XX The pGST97-delta-N238 primer was used with pGST97 reverse primer
CC (AAV16101) to amplify the corresponding fragments by PCR, using
CC linearised pGST-UL97 as a template. The PCR product would encode for a
CC glutathione-S-transferase (GST)- human cytomegalovirus (CMV) UL97 fusion
CC protein in which the N-terminal region of the latter protein was
CC truncated by 238 residues. Truncation of the N-terminal region of UL97
CC protein kinase (see also AAV16098 and AAV16100) was carried out to
CC investigate any changes in enzyme activity. It was determined that
CC truncation of the first 303 N-terminal residues totally abolished
CC enzymatic activity indicating that the N-terminal region was involved in
CC kinase activity. The invention provides an assay method for the detection
CC of agents that inhibit or enhance activity of the CMV UL97 protein
CC kinase. GST-UL97 fusion protein confers an advantage in this method as it
CC is more soluble, without loss of enzymatic activity, than UL97 protein.
CC The invention claims that by using an optionally modified polypeptide
CC which contains a UL97 phosphorylation consensus sequence, the assay
CC method can be extended for usage in therapeutic compositions which can be
CC used for treating CMV infections
CC
SQ Sequence 22 BP; 1 A; 11 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
CC Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 109 CGAGCCCGCGCGGATCCCG 129
Db 21 CGGCCCGGCGCGGATCCCG 1
XX
XX
XX RESULT 3378
XX AAX81911
XX ID AAX81911 standard; DNA; 22 BP.
XX AC AAX81911;
XX XX
XX 02-SEP-1999 (first entry)
XX DT
XX XX
XX PCR primer used to amplify human TCR V beta genes.
XX DE
XX Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
XX KW V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 8;
XX KW multiple sclerosis; PCR primer; ss.
XX XX
XX Synthetic.
XX OS Homo sapiens.
XX XX
XX MO9927957-A1.
XX PN
XX PD 10-JUN-1999.
XX PF 03-DEC-1997; 97WO-US023147.
XX XX
XX 03-DEC-1997; 97WO-US023147.
XX PR 03-DEC-1997; 97WO-US023147.
XX XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX XX
XX Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;
XX PI
XX WPI; 1999-404801/34.
XX DR
XX T0 cell receptor peptide-derived vaccines.
XX PT
XX Example 10; Page 41; 104pp; English.
XX PS
XX The specification describes vaccines which comprise immunologically

CC effective amounts of T cell receptor (TCR) peptides. The TCRs are present
CC on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta
CC 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta
CC TCR peptide-based vaccines are useful for prevention or treatment of
CC multiple sclerosis. The presence of V beta 6.7 appears to be particularly
CC associated with multiple sclerosis and can be used to determine an
CC individual's susceptibility to multiple sclerosis. Vaccinating, rather
CC than passively administering heterologous antibodies, allows the host's
CC own immune system to mobilize and suppress auto aggressive T cells.
CC Therefore, the suppression is persistent and may involve any and all
CC immunological mechanisms in effecting that suppression. Such a multi-
CC faceted response is more effective than the uni-dimensional suppression
CC achieved by passive administration of monoclonal antibodies or extant-
CC derived regulatory T cell clones. PCR primers AAX81882-X81914 were used
CC to amplify and analyse human TCR V beta genes, in the course of the
CC invention
CC
SQ Sequence 22 BP; 4 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
CC Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 4141 CTGTGACCTGATTGTTCTC 4161
Db 1 CAGTGACCTGAGTTGTTCTC 21
XX
XX
XX RESULT 3379
XX AA239210/C
XX ID AA239210 standard; DNA; 22 BP.
XX AC AA239210;
XX XX
XX 11-FEB-2000 (first entry)
XX DT
XX XX
XX HLA allele DRB1*0820 exon 2 amplifying primer.
XX DE
XX Human leukocyte antigen; HLA; allele; HLA-B*3913; HLA-B*1406; human;
XX KW HLA-B*51; HLA-DRB1*0820; HLA-DRB1*04; allele typing; exon;
XX KW major histocompatibility complex; MHC; PCR primer; ss.
XX XX
XX Synthetic.
XX OS Homo sapiens.
XX XX
XX MO9954496-A2.
XX PN
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-EP002614.
XX XX
XX 20-APR-1998; 98EP-00870088.
XX PR
XX XX
XX (INNO-) INNOGENETICS NV.
XX PA
XX De Canck I, Merssch G, Rousseau R;
XX PI
XX WPI; 1999-634008/54.
XX DR
XX New polynucleotides for human leukocyte antigen, HLA, allele fragments,
XX PT useful for typing HLA alleles.
XX XX
XX Claim 4; Page 7; 62pp; English.
XX PS
XX The invention provides polynucleotides corresponding to exon 2 and exon 3
CC of human leukocyte antigen (HLA) alleles HLA-B*3913, HLA-B*1406 and HLA-
CC B*51 and exon 2 of HLA alleles HLA-DRB1*0820, HLA-DRB1*04 and HLA-
CC DRB4*01. The polynucleotides are useful for typing the above HLA alleles
CC in a sample, especially by a method that comprises (a) amplifying
CC all/part of the relevant sequence using at least one primer pair; and (b)
CC hybridizing the amplified product to a set of probes specifically
CC hybridizing to target regions comprising one or more polymorphic
CC nucleotides of the sequence, to determine the absence or presence of the

CC allele in the sample. Diagnostic kits for (a) typing the alleles
CC comprising at least one preferred primer and/or at least one preferred
CC probe and (b) for detecting the protein fragment encoded by the
CC polynucleotides, comprising an antiserum or ligand (e.g. antibody)
CC binding specifically to the protein fragment are provided. The
CC polynucleotides also enable the isolation of the complete respective
CC genes from a human genomic library

XX
SQ Sequence 22 BP, 3 A, 8 C, 6 G, 5 T, 0 U, 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1611 GAACCTCAGACGACGCTGG 1631
DB 22 GAGCTTCACAGTGCAGCGCG 2

RESULT 3380
AAK8451/c
ID AAK8451 standard; DNA, 22 BP.
XX
AC AAK8451;
XX
DT 01-OCT-1999 (first entry)
XX
DE Human RANTES P2B primer.
XX
KM RANTES; chemokine; detection; primer; probe; amplification; MIP-1 alpha;
KM regulated upon activation normal T expressed and secreted; MIP-1 beta;
KM macrophage inflammatory protein; CD4+T-cell; inhibitor; prognosis;
KM primary non-synclium-inducing HIV-1 strain; therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9937815-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-US001327.
XX
PR 22-JAN-1998; 98US-00010641.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Romano JW, Shurtliff R, Williams KG;
XX
DR WPI; 1999-469145/39.
XX
PT Detection of expression levels of the cytokines RANTES, MIP-1alpha and
PT MIP-1beta used as prognostic markers of HIV-infected patients.
XX
PS Claim 1; Page 38; 48pp; English.

CC This invention describes novel oligonucleotides which are used for
CC detecting the chemokines RANTES (regulated upon activation normal T
CC expressed and secreted), macrophage inflammatory protein (MIP)-1 alpha or
CC MIP-1 beta by (a) obtaining a sample possible containing RANTES or MIP-1
CC alpha or MIP-1 beta RNA, (b) performing an isothermal transcriptional
CC amplification on the sample with 2 oligonucleotide primers, (c) detecting
CC the product of step (b) where detection of a product indicates the
CC presence of RANTES, MIP-1 alpha or MIP-1 beta in the sample. The assay is
CC used to determine the levels of the chemokines RANTES, MIP-1 alpha and
CC MIP-1 beta in samples, especially cells. These chemokines have been shown
CC to be inhibitors of CD4+T-cells by primary non-synclium-inducing HIV-1
CC strains. Thus the level of expression of these genes can be used as
CC prognostic markers for direct therapeutic management of HIV-infected
CC patients. By being isothermal, the assay requires less manipulation by
CC the experimenter. Also 'spiking' the sample with a known amount of
CC control RNA allows quantitation and qualification of the products in a
CC single assay. AAK8447-X8491 represent the primers and probes used in the

CC method of the invention

XX
SQ Sequence 22 BP, 5 A, 9 C, 5 G, 3 T, 0 U, 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 690 CCTGATGTGGCCATGAGGCA 710
DB 21 CCTGATGTGGCCACGGGCA 1

RESULT 3381
AAK23203
ID AAK23203 standard; DNA, 22 BP.
XX
AC AAK23203;
XX
DT 11-JUN-1999 (first entry)
XX
DE CML t(14; 18) non-promoter primer #1.
XX
KM Autocatalytic amplification; transcription-based amplification; CML;
KM thermalcycling; diagnostic; environmental testing; probe; detection;
KM genetic disease; infectious disease; microorganism; food; forensic;
KM paternity; primer; ss.
XX
OS Synthetic.
OS
PN US8888779-A.
XX
PD 30-MAR-1999.
XX
PF 05-JUN-1995; 95US-00461654.
XX
PR 11-JUL-1989; 89US-00379501.
PR 10-JUL-1990; 90US-00550837.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Fultz TV, Kacian DL;
XX
DR WPI; 1999-253231/21.
XX
PT Kit for autocatalytic amplification of RNA targets.
XX
PS Example 18; Col 43; 51pp; English.

CC This invention describes a novel method for the autocatalytic
CC amplification of an RNA target in a transcription-based amplification
CC system without thermalcycling. The method generates oligonucleotides for
CC diagnostic or environmental testing, for use e.g. as probes and in
CC cloning. Typical applications are the detection of genetic or infectious
CC diseases, the monitoring of responses to therapy, the quantitation or
CC detection of microorganisms in foods, forensic studies and the
CC establishment of paternity. Kits containing the products of the invention
CC provide many copies of selected RNA targets under conditions of constant
CC temperature, ionic strength and pH. Specific amplification of RNA targets
CC increases sensitivity, convenience, accuracy and the reliability of
CC assays

XX
SQ Sequence 22 BP, 6 A, 6 C, 7 G, 3 T, 0 U, 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2539 GAGCTCAGATCTCTGACGTAAC 2559
DB 2 GAGCTCAGATGCTGACCAAC 22

```
RESULT 3382
AA30126
ID AAX30126 standard; DNA; 22 BP.
XX
AC AAX30126;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human APRIL PCR primer #1.
XX
KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
KW immune disorder; cancer; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO9912965-A2.
XX
PD 18-MAR-1999.
XX
PP 11-SEP-1998; 98MO-US019191.
XX
PR 12-SEP-1997; 97US-0058786P.
XX
PR 26-MAR-1998; 98US-0079384P.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-215028/18.
XX
PT A Proliferating Inducing Agent (APRIL), a member of the Tumour Necrosis
PT Factor Family, - useful as diagnostic agents and for prevention or
PT treatment of immune disorders and cancer.
XX
PS Example 1; Page 30; 47pp; English.
XX
CC The present sequence represents a PCR primer for human APRIL (a
CC factor inducing agent). APRIL is a member of the tumour necrosis
CC factor family, and essentially free of normally associated proteins.
CC APRIL and APRIL antibodies are useful in pharmaceutical compositions for
CC preventing or reducing severity of an autoimmune disease or an immune
CC response to tissue graft. The composition is also useful for stimulating
CC or suppressing the immune system, and treating cancer. APRIL is also
CC useful for treating APRIL-related disorders by delivering via a vector
CC (preferably viral vector) (gene therapy) into a mammalian (preferably
CC human) cell. Labeled APRIL and fragments are useful for identifying APRIL
CC receptors by screening compositions. Antisense DNA and antibodies and
CC modified APRIL (preferably an anti-APRIL receptor antibody) are useful as
CC blocking agents for inducing cell death by interfering with APRIL
CC receptors. The blocking agent is preferably administered with interferon-
CC c, and treats, suppresses or alters an immune response involving a
CC signalling pathway between APRIL and its receptor (preferably involving
CC human carcinoma cells); and also treats, suppresses or alters the
CC progression of cancer (preferably at least one chemotherapeutic agent is
CC also administered, and radiation therapy is also given to the patient
XX
XX
SQ Sequence 22 BP; 2 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 5651 CCAGCCTCATCTCTTAGTG 5671
Db 1 CCAGCCTCATCTCTTCTTG 21
XX
RESULT 3383
AAX34398
ID AAX34398 standard; DNA; 22 BP.
XX
AC AAX34398;
XX
```

```
XX
DT 16-JUL-1999 (first entry)
XX
DE S. aureus 3-hydroxyacyl-CoA dehydrogenase gene hcd probe.
XX
KW 3-hydroxyacyl-CoA dehydrogenase; hcd; infection; Helicobacter pylori;
KW tissue; wound; skin; connective tissue; implant; mucous membrane; mouth;
KW throat; mammary gland; urethra; vagina; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN MO9918117-A1.
XX
PD 15-APR-1999.
XX
PP 02-OCT-1998; 98MO-US020636.
XX
PR 03-OCT-1997; 97US-0060983P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (VIRU-) VIRUS RES INST.
XX
PI Palmer L, Pratt JM, Lonetto MA, Hodgson JE, Nicholas RO;
PI Beattie DT, Deresiewicz RL, Lowe A;
XX
DR WPI; 1999-263995/22.
XX
PT New isolated 3-hydroxyacyl-CoA dehydrogenase polynucleotides.
XX
PS Example 2; Page 55; 75pp; English.
XX
CC This sequence represents a probe used to detect the coding region for a
CC novel 3-hydroxyacyl-CoA dehydrogenase (hcd) from Staphylococcus aureus
CC (AAX34393). The products can be used to prevent or treat bacterial
CC infection, e.g. S. aureus infection or Helicobacter pylori infection.
CC They can also be used for preventing invasion of bacteria in damaged
CC tissue including wounds in skin or connective tissue caused, e.g. by
CC mechanical, chemical, thermal or radiation damage or by implantation of
CC indwelling devices, or wounds in the mucous membranes, such as the mouth,
CC throat, mammary glands, urethra or vagina
XX
XX
SQ Sequence 22 BP; 5 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2158 ATCCATTCTCAAGTCCACC 2178
Db 1 AGCCATTCTGCAAGGCCACC 21
XX
RESULT 3384
AAX32149/c
ID AAX32149 standard; DNA; 22 BP.
XX
AC AAX32149;
XX
DT 14-JUN-1999 (first entry)
XX
DE BRCA2 gene specific primer.
XX
KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW CTRR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW BAP1 gene; PCR primer; ss.
XX
OS Synthetic.
XX
```

PN W0906598-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 04-AUG-1998; 98WO-US016574.
 XX
 PR 04-AUG-1997; 97US-00905772.
 XX 22-MAY-1998; 98US-00084471.
 PA (ONCO-) ONCOMED INC.
 XX
 PI Murphy PD;
 XX
 DR WPI; 1999-153820/13.
 XX
 PT Determining common functional alleles in a population - useful in the
 XX diagnosis of disease associated with allelic heterogeneity.
 PS Example 5; Page 37; 78pp; English.
 XX
 CC The invention relates to methods of determining a functional allele
 CC profile of a gene in a population. Functional allele profiles comprise
 CC the commonly occurring alleles in a population, and the relative
 CC frequencies at which such alleles of a given gene occur. The methods are
 CC used to identify and determine the frequency of the functional alleles of
 CC genes which display extensive allelic heterogeneity, particularly those
 CC implicated in disease or conditions, such as the BRCA1 gene associated
 CC with breast cancer, CTR associated with cystic fibrosis, dystrophin
 CC associated with Duchenne muscular dystrophy and Becker muscular
 CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
 CC also be employed for diseases where allelic and genetic heterogeneity
 CC exist, such as breast cancer, neurofibromatosis, and hereditary non-
 CC polyposis colorectal cancer. Identification of functional alleles is
 CC necessary for identification of mutations which may be implicated in the
 CC disease. Sequences AA32001-172 represent primers for determining the
 CC functional allele profiles of various genes. The primers are specific for
 CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
 XX
 SQ Sequence 22 BP; 13 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7307 CTTGAGATTGCTTGTGCT 7327
 DB 22 CTTGAGATTGCTTGTGCT 2
 RESULT 3385
 AA209309/c
 ID AA209309 standard; DNA; 22 BP.
 XX
 AC AA209309;
 XX
 DT 26-OCT-1999 (first entry)
 XX
 DE Human macrophage stimulating protein PCR primer 1.
 XX
 KM Macrophage stimulating protein; MSP; human; modulator; proliferation;
 KM differentiation; intestinal epithelium; colon crypt; treatment; cancer;
 KM haematopoietic disorder; megakaryocyte deficiency; gastrointestinal;
 KM chemotherapeutic agent; gut toxicity; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5948892-A.
 XX
 PD 07-SEP-1999.
 XX
 PF 16-DEC-1996; 96US-00766982.
 XX

PR 16-DEC-1996; 96US-00766982.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Wahl RC;
 XX
 DR WPI; 1999-517975/43.
 XX
 PT Analogues of macrophage stimulating protein for treating gastrointestinal
 PT or haematopoietic disorders.
 PS Example 5; Col 23-24; 23pp; English.
 XX
 CC This invention describes a novel purified and isolated analogue of mature
 CC macrophage stimulating protein (MSP) having at least one unpaired
 CC cysteine residue substituted with another amino acid which modulates the
 CC proliferation or differentiation of the intestinal epithelium. The
 CC product of the invention binds to RON (a cell membrane protein tyrosine
 CC kinase which is a member of the c-met family) to promote the formation of
 CC colon crypts. MSP analogues are useful for the treatment of conditions
 CC requiring the administration of MSP, such conditions include
 CC haematopoietic disorders such as those involving a deficiency of
 CC megakaryocytes and gastrointestinal disorders such as ulcerative colitis,
 CC Crohn's disease and infections. The MSP analogues are useful for
 CC maintaining and repairing the epithelial lining in the treatment of
 CC cancer, where the aggressive use of chemotherapeutic agents or the use of
 CC whole body radiation may lead to gut toxicity. The MSP analogues, which
 CC have a higher activity than normal human MSP are effective at smaller
 CC dosages, or optionally, they may be administered less frequently than
 CC human MSP. This sequence represents a PCR primer used to amplify the
 CC human MSP described in the method of the invention
 XX
 SQ Sequence 22 BP; 5 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2826 TTCCAGCCCGGAGCTGTG 2846
 DB 21 TTCCAGCCCGGAGCTGTG 1
 RESULT 3386
 AA27795/c
 ID AA27795 standard; DNA; 22 BP.
 XX
 AC AA27795;
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE PCR primer for human DNA marker clone G212.
 XX
 KM Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
 KM ITR sequence; pentanucleotide tandem repeat; stutter artifact;
 KM typing; DNA profiling; linkage analysis; criminal justice;
 KM paternity testing; animal lineage analysis; microsatellite loci;
 KM polymorphism detection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09940194-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 04-FEB-1999; 99WO-US002345.
 XX
 PR 04-FEB-1998; 98US-00018584.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Schumm JW; Bacher JW;
 XX

CC and/or hypermethylation of the remaining allele, leading to reduced
 CC expression of the gene. DBCR1 nucleic acid sequences are used for
 CC treatment or prevention of cancer, particularly bladder, ovarian or skin
 CC cancer, squamous carcinoma, renal cell carcinoma or squamous cell
 CC esophageal carcinoma. The DBCR1 protein can be used directly in the
 CC same way, or used to raise antibodies and to screen for modulators. The
 CC products can be used for diagnosis or prognosis of cancer, or to indicate
 CC predisposition to cancer (including prenatal testing), particularly where
 CC this is associated with loss of heterozygosity at 9q32-33. Antibodies may
 CC also be used for affinity purification, therapeutically as modulator and
 CC to detect the protein in cells etc

XX Sequence 22 BP; 7 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5904 AGAACCTGTCGCCAAGCCA 5924
 Db 2 AGAACCTGTCGCCAATCCA 22

RESULT 3389
 AAX33028/c
 ID AAX33028 standard; DNA; 22 BP.
 XX
 AC AAX33028;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Human BRCA2 gene PCR primer SEQ ID NO:41.

XX Human; BRCA2; genetic testing; protein therapy; haplotype; detection;
 KM gene therapy; breast cancer; ovarian cancer; PCR primer; ss.

XX Synthetic.
 OS Homo sapiens.

PN WO9909164-A1.

PD 25-FEB-1999.

PF 14-AUG-1998; 98WO-US016905.

PR 15-AUG-1997; 97US-0055784P.

PR 07-NOV-1997; 97US-0064926P.

PR 12-NOV-1997; 97US-0065367P.

PR 01-MAY-1998; 98US-000721715.

PR 22-MAY-1998; 98US-000844471.

XX (ONCO-) ONCOMED INC.

PI Murphy PD, White MB, Rablin MB, Olson SJ, Yoshikawa M, Jackson GM,
 PI Eskandari T, Schryer B, Park M;

DR WPI; 1999-190163/16.

XX New coding sequence haplotypes of the human BRCA2 gene - used to develop
 PT products for determining susceptibility to, detection and treatment of
 PT breast or ovarian cancer.

XX Example 1; Page 32; 226pp; English.

XX The present invention describes genomic DNA which contains a BRCA2 gene
 CC where the first 12 nucleotides beginning exon 5 are 5'-TCTGTTGTTCT-3' as
 CC in sequence (I) (see AAX03249), where nucleotides numbers 5782-5790 are
 CC GTTGTGTT as in sequence (IV) (see AAX30255), and where the last 20
 CC nucleotides encoding exon 15 are 5'-CTGCGTCTTCATAAACAG-3' as in
 CC sequence (II) (see AAX30251) and the first 20 nucleotides beginning exon
 CC 16 are 5'-CTGTATACGATAGCGCTTC-3' as in sequence (III) (see AAX30253).
 CC Products and methods from the present invention can be used for
 CC identifying mutations in the BRCA2 gene leading to predisposition or

CC higher susceptibility to breast or ovarian cancer. They can also be used
 CC for detection and gene therapy for breast and ovarian cancer. They can
 CC be used in methods for monitoring disease progression, for determining
 CC patients suited for gene and protein replacement progression, or for
 CC detecting the presence or quantifying the amount of a tumour growth
 CC inhibitor following such therapy. The BRCA2 protein, polypeptides, their
 CC functional equivalents, antibodies, and PNs may also be useful in the
 CC study of the characteristics of BRCA2 proteins, such as structure and
 CC function of BRCA2 in oncogenesis or subcellular localisation of BRCA2
 CC protein in normal and cancerous cells. AAX33001 to AAX33097 represent PCR
 CC primers used in the amplification of the human BRCA2 gene

XX Sequence 22 BP; 13 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7307 CTTTGAGATTGTTGTTGTTGT 7327
 Db 22 CTTTGAGATTGTTGTTGTTGT 2

RESULT 3390
 AAX36878
 ID AAX36878 standard; DNA; 22 BP.
 XX
 AC AAX36878;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Human XLIIS gene fragment PCR primer 2.1 F.

XX XLIIS gene; human; detection; diagnosis; prenatal diagnosis; therapy;
 KM lissencephaly; LIS; agyria-pachygyria; subcortical laminar heterotopia;
 KM SCLH; cortical dysgenesis; cryptogenic epilepsy; neurological disorder;
 KM neurodegenerative disease; Alzheimer's disease; X-linked disorder;
 KM genetic counselling; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

PN EP918091-A1.

PD 26-MAY-1999.

PF 21-NOV-1997; 97EP-00402811.

PR 21-NOV-1997; 97EP-00402811.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Chelly J, Kahn A, Des Portes V, Pinard J;

DR WPI; 1999-290318/25.

XX New gene and its gene product expressed in the brain, useful for
 PT diagnosing and treating disorders such as lissencephaly and subcortical
 PT laminar heterotopia.

XX Claim 9; Page 46; 71pp; English.

XX This sequence is a primer for the human XLIIS gene of the invention. The
 CC XLIIS fragments may be used to detect abnormalities in the expression of
 CC the XLIIS gene transcripts or to compare their sequence with that of the
 CC XLIIS transcripts from patients for in vitro especially prenatal diagnosis
 CC of lissencephaly (LIS) (or agyria-pachygyria), subcortical laminar
 CC heterotopia (SCLH), cortical dysgenesis, cryptogenic epilepsies or
 CC neurodegenerative diseases such as Alzheimer's disease. These disorders
 CC mainly affect females as the XLIIS gene is X-linked. The XLIIS fragments
 CC may also be used to administer to patients to prevent or treat the above
 CC disorders and may be used as a tool in genetic counselling.
 CC Oligonucleotides which bind to the fragments may be used to amplify the

CC XLIS gene from a sample for comparison to normal samples in the in vitro
CC diagnosis regime. This may also be performed by amplifying XLIS cDNA from
CC the mRNA in the sample. Antibodies to XLIS may be used to detect XLIS in
CC a biological sample or can be administered to patients to prevent or
CC treat the above disorders. They may also be used to purify XLIS from a
CC biological sample. XLIS may also be administered to patients to prevent
CC or treat the above neurological disorders. In addition XLIS may be used
CC as a marker of neuronal cells at an early stage of development; its
CC discovery increases understanding of both the neuronal movement which
CC leads to development of the cortical region of the brain and of the
CC pathogenesis of the group of neuronal disorders mentioned above
CC
XX
XX
SQ Sequence 22 BP; 0 A; 10 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5701 TGCCCTCTTCCTTCCTCTC 5721
1 TCCTCTCTTTTTCCTCTC 21

Db

RESULT 3391
AAx81831/c
ID AAx81831 standard; DNA; 22 BP.
XX
AC AAx81831;
XX
DT 02-SEP-1999 (first entry)
XX
DE PCR primer used to amplify human malignancy-associated gene (MAG).
XX
KW Liver neoplastic disease; malignancy-associated gene; MAG; liver disease;
KW neoplastic disease; cirrhosis; hepatocellular carcinoma; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9929859-A1.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US026461.
XX
PR 12-DEC-1997; 97US-00989750.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Black K, Ljubimova JV, Demetrio AA;
XX
DR WPI; 1999-404942/34.
XX
PT Liver-associated malignancy-associated gene (MAG), useful for screening
PT for cirrhosis and hepatocellular carcinoma.
XX
PS Example 11; Page 17; 42pp; English.
XX
CC PCR primers AAx81830-31 were used to amplify human malignancy-associated
CC gene (MAG) proteins. The polypeptide is useful for detecting antibodies
CC associated with liver disease. Probes derived from the MAG gene are
CC useful for detecting the presence of sequences associated with neoplastic
CC disease, e.g. liver diseases such as cirrhosis and hepatocellular
CC carcinoma, and therefore can be used in disease diagnosis. The sequences
CC can be used for development of therapeutics that are useful for
CC inhibition of the development of neoplastic liver disease
XX
SQ Sequence 22 BP; 4 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 616 ATTGTGAGCTGGCGAATGCTG 636
22 ATAGTAGCTGGCCAAAGCTG 2

Db

RESULT 3392
AAx81837/c
ID AAx81837 standard; DNA; 22 BP.
XX
AC AAx81837;
XX
DT 02-SEP-1999 (first entry)
XX
DE PCR primer used to amplify cDNA sequences isolated from liver tissue.
XX
KW Liver neoplastic disease; malignancy-associated gene; MAG; liver disease;
KW neoplastic disease; cirrhosis; hepatocellular carcinoma; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9929859-A1.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US026461.
XX
PR 12-DEC-1997; 97US-00989750.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Black K, Ljubimova JV, Demetrio AA;
XX
DR WPI; 1999-404942/34.
XX
PT Liver-associated malignancy-associated gene (MAG), useful for screening
PT for cirrhosis and hepatocellular carcinoma.
XX
PS Example 16; Page 23; 42pp; English.
XX
CC The specification describes a liver neoplastic disease polynucleotide and
CC malignancy-associated gene (MAG) proteins. The polypeptide is useful for
CC detecting antibodies associated with liver disease. Probes derived from
CC the MAG gene are useful for detecting the presence of sequences
CC associated with neoplastic disease, e.g. liver diseases such as cirrhosis
CC and hepatocellular carcinoma, and therefore can be used in disease
CC diagnosis. The sequences can be used for development of therapeutics that
CC are useful for inhibition of the development of neoplastic liver disease.
CC PCR primers AAx81836-37 were used in the course of the invention
XX
SQ Sequence 22 BP; 4 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 616 ATTGTGAGCTGGCGAATGCTG 636
22 ATAGTAGCTGGCCAAAGCTG 2

Db

RESULT 3393
AAx99208
ID AAx99208 standard; DNA; 22 BP.
XX
AC AAx99208;
XX
DT 23-JAN-2001 (first entry)
XX
DE Human apoptosis related protein CCR9 related primer #4.
XX
KW Human; apoptosis; CCR9; anti-tumour; tumour; cancer; diagnosis; primer;
KW ss.

```
OS Homo sapiens.
XX
XX JF2000210089-A.
XX
XX 02-AUG-2000.
XX
XX 18-NOV-1999; 99JP-00327885.
XX
XX 20-NOV-1998; 98JP-00330302.
XX
XX (ASAK ) ASAH1 BREWERIES LTD.
XX
XX WPI; 2000-614556/59.
XX
XX Gene and its encoded protein that induce apoptosis, useful for producing
XX a malignant tumor gene treating agent and for the diagnosis on the
XX resistance of cancer cells against an anticancer agent.
XX
XX Example 2; Page 5; 13pp; Japanese.
XX
XX The present invention describes the human CCR9 protein, which is an
XX apoptosis related protein having apoptosis-inducing activity. Human CCR9
XX has anti-tumour activity, and can be used to produce a malignant tumour
XX gene treating agent. The CCR9 gene and protein can be used for the
XX diagnosis of the resistance of cancer cells against an anticancer agent.
XX The present sequence represents a primer which is used in an example from
XX the present invention
XX
XX Sequence 22 BP; 10 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1296 CATGATTAAGGCCACAGCTAG 1316
XX |||||
XX 2 CAAGAAAAATGCCACAGCCAG 22
XX
XX Db
XX
XX RESULT 3394
XX AAZ39687/C
XX ID AAZ39687 standard; DNA; 22 BP.
XX
XX AAZ39687;
XX
XX 28-FEB-2000 (first entry)
XX
XX Human Vth aggregation factor gene specific FPCR-SSCP primer.
XX
XX Gene polymorphism; human; Vth aggregation factor; genetic diagnosis;
XX diabetes; FPCR; SSCP; fluorescence-based polymerase chain reaction;
XX single strand conformation polymorphism; PCR primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX JF1313676-A.
XX
XX 16-NOV-1999.
XX
XX 30-APR-1998; 98JP-00120217.
XX
XX 30-APR-1998; 98JP-00120217.
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
XX
XX WPI; 2000-057352/05.
XX
XX Discrimination of human V aggregation factor gene polymorphism.
XX
XX Disclosure; Page 10; 34pp; Japanese.
XX
XX The invention provides a method for the discrimination of the gene
```

```
CC polymorphism of human Vth aggregation factor, where one of the following
CC (1) to (6) residues/nucleotides in the aggregation gene is discriminated
CC in the patient to be tested: (1) residue 495; guanine (G) or adenine (A),
CC (2) residue 642: (G) or thymine (T), (3) residue 2663: (G) or (A), (4)
CC residue 2763: (G) or (A), (5) residue 2863: (A) or (G), (6) residue 5112:
CC (A) or (G). The method is useful in the genetic diagnosis of a diabetes
CC patient. The method uses FPCR-SSCP (fluorescence-based polymerase chain
CC reaction-single strand conformation polymorphism) for analyzing DNA
CC samples for polymorphisms. Sequences AAZ39632-717 represent primers used
CC for the FPCR-SSCP analysis of the human Vth aggregation factor gene
XX
XX Sequence 22 BP; 5 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 7398 TGAAGCAGCAGCATCAGCAG 7418
XX |||||
XX 22 TGAATCAACATCATGAGCAG 2
XX
XX Db
XX
XX RESULT 3395
XX AAZ49922
XX ID AAZ49922 standard; DNA; 22 BP.
XX
XX AAZ49922;
XX
XX 02-MAY-2000 (first entry)
XX
XX Human tumour suppressor gene IB3089A exon 4 reverse primer SSCPex4.
XX
XX Human; tumour suppressor; IB3089A; cytosolic; promoter; 9q32-33;
XX Deleted in Bladder Cancer Chromosome Region candidate 1; DBCCR1;
XX diagnostic; prophylactic; therapeutic treatment; cancer; skin; ovarian;
XX bladder; squamous carcinoma; renal cell; oesophageal; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200001816-A1.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1998; 98WO-GB001958.
XX
XX 02-JUL-1998; 98WO-GB001958.
XX
XX 02-JUL-1998; 98WO-GB001958.
XX
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
XX Knowles M, Habuchi T;
XX
XX WPI; 2000-171014/15.
XX
XX Novel promoter sequence, useful for identifying a predisposition to
XX cancer or the presence of a tumor.
XX
XX Claim 22; Page 78; 101pp; English.
XX
XX The patent relates to the identification of a novel gene IB3089A, also
XX referred as DBCCR1 (Deleted in Bladder Cancer Chromosome Region candidate
XX 1), and its promoter in a tumour suppressor region at 9q32-33 between
XX D9S1848 and AFMA239XA9 of human chromosome 9q. The DBCCR1 sequence can be
XX used in the diagnostic, prophylactic and therapeutic treatment of cancer
XX particularly bladder cancer. The promoter can be used to design DBCCR1
XX amplifying primers and screen compounds that activate production of
XX the DBCCR1 gene in a patient, where inactivation indicates the presence
XX of a tumour or a predisposition to cancer, especially a cancer associated
XX with loss of heterozygosity involving 9q32-33 e.g. bladder cancer,
XX squamous carcinoma, skin cancer, renal cell carcinoma, oesophageal and
XX ovarian cancers. The present sequence is a reverse primer SSCPex4 used to
XX amplify exon 4 of IB3089A from the genomic DNA for SSCP (single-stranded
XX conformational polymorphism) analysis
```

```
XX
SQ Sequence 22 BP; 7 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 5904 AGAACCTGTCCCAAGCCCA 5924
DB 2 AGAACCTGTCCCAATCCA 22
RESULT 3396
AAZ44367
ID AAZ44367 standard; DNA; 22 BP.
XX
AC AAZ44367;
XX
DT 06-APR-2000 (first entry)
XX
DB Human G protein-coupled receptor primer 106R1.
XX
KW G protein-coupled receptor; human; lysophosphatidic acid; diagnosis;
KW treatment; prostate cancer; prostatic hyperplasia; inflammation; primer;
XX 88.
XX Homo sapiens.
XX
XX WO967383-A1.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-JP003306.
XX
XX 22-JUN-1998; 98JP-00174731.
XX
XX (NLSB) JAPAN TOBACCO INC.
XX
XX Nozaki Y, Naito T;
XX
XX WPI; 2000-106293/09.
XX
XX G-protein coupled receptor protein binding to lysophosphatidic acid used
XX for treatment of prostate cancer.
XX
XX Example 1; Page 60; 67pp; Japanese.
XX
XX This invention describes a novel human G-protein coupled receptor protein
XX capable of binding lysophosphatidic acid, and proteins derived from it by
XX addition, deletion and/or substitution of one or more amino acid
XX residues. Antibodies to the protein are used for diagnosis of, and
XX agonists/antagonists to the protein are used for the treatment of,
XX prostatic disorders such as prostate cancer, benign prostatic
XX hyperplasia, and inflammation of the prostate. This sequence represents a
XX primer used in the isolation of the human G protein-coupled receptor
XX protein described in the method of the invention
XX
XX Sequence 22 BP; 7 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 7414 AGCAGCAGCAGCAGCAGCAGC 7434
DB 2 AGCAGCAGCAGCAGCAGCAGC 22
RESULT 3397
AAAI1724/C
ID AAAI1724 standard; DNA; 22 BP.
XX
XX AAAI1724;
```

```
XX
DT 14-JUL-2000 (first entry)
XX
DE Human prothrombin 20210 A allele PCR primer #2.
XX
KW Prothrombin; human; thrombosis; mutation; PCR primer; 88.
XX
XX Homo sapiens.
XX
XX US6043035-A.
XX
XX 28-MAR-2000.
XX
XX 03-NOV-1997; 97US-00962790.
XX
XX 03-NOV-1997; 97US-00962790.
XX
XX 03-NOV-1997; 97US-00962790.
XX
XX (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Bertina RM, Reitsma PH, Rosendaal FR, Poort SR;
XX
XX WPI; 2000-270338/23.
XX
XX Determining increased risk for thrombosis by determining prothrombin
XX level, or by detecting the presence or absence of genetic mutation
XX correlated with elevated prothrombin levels.
XX
XX Example 2; Col 11-12; 11pp; English.
XX
XX This invention describes a novel method for determining an increased risk
XX for thrombosis in an individual by determining the prothrombin level, or
XX by detecting the presence or absence of a genetic mutation correlated
XX with elevated prothrombin levels in individuals with the mutation, and
XX where an increased prothrombin level indicates increased risk for
XX thrombosis. INDEPENDENT CLAIMS are also included for the following: (1) a
XX kit for determining whether an individual is at an increased risk for
XX thrombosis comprising at least one primer which specifically hybridizes
XX adjacent to the region of the prothrombin gene that contains a G to A
XX mutation at position 20210, and suitable amplification reagents; and (2)
XX an isolated polynucleotide comprising a mutated prothrombin gene, in
XX which G at position 20210 is replaced by A, or a fragment of the gene
XX which includes the G to A transition mutation at position 20210. The
XX method is also used for screening and diagnosis of thrombophilia.
XX especially, hereditary thrombophilia. AAAI1723-A11726 represent PCR
XX primers used in the method of the invention
XX
XX Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 5842 GCTGCATGATCCCACTGTTA 5862
DB 2 GCTTCATGCTCCCACTGCTA 2
RESULT 3398
AAA95380
ID AAA95380 standard; DNA; 22 BP.
XX
XX AAA95380;
XX
XX 12-FEB-2001 (first entry)
XX
XX Rat G11 coding sequence PCR primer #1.
XX
XX Rac1; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
XX Parkinson's disease; manic depression; schizophrenia; PCR primer; 88.
XX
XX Rattus norvegicus.
XX
XX WO200058451-A1.
```

XX 05-OCT-2000.
 PD
 XX
 PF 21-MAR-2000; 2000WO-US007544.
 XX
 PR 26-MAR-1999; 99US-00277078.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Sakurada K, Palmer T, Gage FH;
 XX
 DR WPI; 2000-656165/63.
 XX
 PT Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase
 PT expression useful for treating catecholamine-related diseases such as
 PT Parkinson's disease, manic depression and schizophrenia.
 XX
 PS Example 1; Page 20; 68pp; English.
 CC The present invention describes the rat Nurrl coding and protein
 CC sequences. The Nurrl protein is involved in the induction of tyrosine
 CC hydroxylase expression in adult rat-derived hippocampal progenitor cells.
 CC The Nurrl gene and protein can be used in the treatment of catecholamine-
 CC related diseases such as Parkinson's disease, manic depression and
 CC schizophrenia. They can also be used to induce tyrosine hydroxylase
 CC expression and identify tyrosine hydroxylase related deficiencies, which
 CC are linked to the same diseases. The present sequence is a PCR primer
 CC used in a method to differentiate adult neural progenitor cells
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 6583 CATGTGTAACAAGGTTG 6603
 |||||
 1 CATGTGTAACAAGGTTG 21
 DB
 RESULT 3399
 AAA37706
 ID AAA37706 standard; DNA; 22 BP.
 XX
 AC AAA37706;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Human Rad51 antisense inhibitor AS6.
 XX
 KW Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
 KW radiation sensitivity; therapy; AS6; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200047231-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 03-FEB-2000; 2000WO-US002881.
 XX
 PR 10-FEB-1999; 99US-0119578P.
 PR 06-DEC-1999; 99US-00454495.
 XX
 PA (PANG-) PANGENE CORP.
 XX
 PI Reddy G;
 XX
 DR WPI; 2000-506091/45.
 XX
 PT Inhibiting cell proliferation useful for cancer therapy, comprises
 PT administering Rad51 inhibitor in vivo.
 XX

PS Claim 8; Page 26; 42pp; English.
 XX
 CC This sequence represents an antisense inhibitor of human Rad51,
 CC designated AS6 (also referred to as R51AS6). The antisense inhibitors can
 CC be used in a method of the invention, for inhibiting cell proliferation.
 CC They can also be used in methods for inducing sensitivity to radiation
 CC and DNA damaging chemotherapeutics in an individual and in a method for
 CC prolonging survival in an individual with cancer. The methods and
 CC antisense molecules are useful for inhibiting cell proliferation,
 CC especially cancerous cell proliferation, for inducing sensitivity to
 CC radiation and DNA damaging chemotherapeutics in individuals and for
 CC prolonging survival in an individual with cancer. Kits for carrying out
 CC the methods may be used to diagnose and/or treat cancer and for
 CC adjunctive therapy
 XX
 SQ Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3477 CCTTACTAATTCTTAAAGCAGC 3497
 |||||
 1 CCTTACTAATTCTTAAAGCAGC 21
 DB
 RESULT 3400
 AAA74138
 ID AAA74138 standard; DNA; 22 BP.
 XX
 AC AAA74138;
 XX
 DT 29-NOV-2000 (first entry)
 XX
 DE Reverse PCR primer for loblolly pine locus R1PPT815.
 XX
 KW PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
 KW microsatellite DNA repeat; genetic marker; mapping; inheritance study;
 KW population genetics study; plant breeding programme; ss.
 XX
 OS Pinus taeda.
 XX
 PN WO200042210-A2.
 XX
 PD 20-JUL-2000.
 XX
 PF 06-JAN-2000; 2000WO-US000325.
 XX
 PR 15-JAN-1999; 99US-00232884.
 PR 19-JAN-1999; 99US-00232785.
 XX
 PA (INTO) INT PAPER CO.
 PA (ECHT/) ECHT C S.
 PA (NELS/) NELSON C D.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Echt CS, Nelson CD;
 XX
 DR WPI; 2000-462836/42.
 XX
 PF Polynucleotide having simple sequence repeat useful as markers in plants
 PT for genetic characterization e.g. genetic mapping study, an inheritance
 PT study of a commercially important trait in a plant breeding program.
 XX
 PS Claim 6; Page 24; 57pp; English.
 XX
 CC The present invention relates to loblolly pine polynucleotides with one
 CC or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
 CC also known as microsatellite DNA repeats. The SSRs are useful as genetic
 CC markers for genetic mapping, population genetics studies and inheritance
 CC studies in various plant breeding programmes. The present sequence is a
 CC PCR primer used for detecting the presence of a SSR locus in a pine
 CC genomic DNA sample

```

XX SQ Sequence 22 BP; 3 A; 3 C; 6 G; 10 T; 0 U; 0 Other;
      Query Match      0.2%; Score 14.6; DB 1; Length 22;
      Best Local Similarity 81.0%; Pred. No. 2.4e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7282 TGTGACTGTTGATTTGT 7302
DB 1 TGTTCATCTGCATGATGT 21

RESULT 3401
AAS01199
ID AAS01199 standard; cDNA; 22 BP.
XX AC AAS01199;
XX DT 04-JUL-2001 (first entry)
XX DE Human RAD51 antisense oligonucleotide, AS6.
XX KW Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
XX KW arthritis; graft rejection; inflammatory bowel disease; surgery;
XX KW angioplasty; ss.
XX OS Homo sapiens.
XX PN WO200119397-A1.
XX PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-US025838.
XX PR 17-SEP-1999; 99US-0154616P.
XX PR 06-DEC-1999; 99US-00455300.
XX PA (PANG-) PANGENE CORP.
XX PI Reddy G;
XX DR WPI; 2001-244704/25.
XX PT Inhibiting cell proliferation for treating arthritis, graft rejection,
XX PT inflammatory bowel disease, cancer, proliferation induced after medical
XX PT procedure, involves administering Rad51 antibody or its fragment to cell.
XX PS Example 6; Fig 16C; 102pp; English.
XX CC The sequence represents the human Rad51 antisense oligonucleotide, AS6.
XX CC The antisense oligonucleotide is used to study down-regulation of Rad51
XX CC protein in human brain, breast and prostate cells. Rad51 protein is
XX CC defective in repair of damaged DNA, genetic recombination and the
XX CC recombinational repair of DNA lesions, and plays a central role in
XX CC cancer. Inhibiting cell proliferation involves administering to a cell a
XX CC Rad51 antibody or its fragment. The Rad51 antibody or its fragment is
XX CC useful for inhibiting cell proliferation, for treating disease states
XX CC such as cancer, autoimmune disease, arthritis, graft rejection,
XX CC inflammatory bowel disease, proliferation induced after medical
XX CC procedures such as surgery, angioplasty etc. in humans and animals
XX SQ Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
      Query Match      0.2%; Score 14.6; DB 1; Length 22;
      Best Local Similarity 81.0%; Pred. No. 2.4e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3477 CCTAGTAATCTTAAGGCAC 3497
DB 1 CCCAAGTCATCTCTAAGGCAC 21

RESULT 3402

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AAD14949
ID AAD14949 standard; DNA; 22 BP.
XX AC AAD14949;
XX DT 01-NOV-2001 (first entry)
XX DE Oligo #20 used for mutagenesis of humanised KS antibody-IL-2 fusion DNA.
XX KW Fusion protein; immunoglobulin; serum half-life; FcR; Fc receptor;
XX KW Fc protection receptor; FcR; cancer; viral infection; immune disorder;
XX KW cell proliferation; human; KS antibody; BCGAM;
XX KW Epithelial cell adhesion molecule; mutagenesis; interleukin-2; IL-2; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT mlec_feature 22 /*tag= a
FT /label= Cohesive_end
FT /note= "The 5' end of the complementary strand overhangs
FT the 3' end of this sequence by 5'-CGC-3'."
XX PN WO200158957-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004455.
XX PR 11-FEB-2000; 2000US-0181768P.
XX PA (LEXT-) LEXIGEN PHARM CORP.
XX PI Gallies SD, Burger C, Lo KM;
XX DR WPI; 2001-514646/56.
XX PT Antibody-based fusion protein comprises mutations near the fusion
XX PT junction for enhancing circulating half-life.
XX PS Example 3; Page 17; 48pp; English.
XX CC The invention relates to antibody-based fusion proteins having one or
XX CC more mutations in the junction between an immunoglobulin (Ig) and a non-
XX CC Ig moiety, which increases the circulating half-life of the fusion
XX CC protein. The serum half-life of the mutant fusion protein is improved
XX CC without affecting the interaction of the antibody moiety with the Fc
XX CC receptor (FcR) and Fc protection receptor (FcRp). The antibody-based
XX CC fusion proteins of the invention are useful to treat cancer, viral
XX CC infections, immune disorders, and to enhance growth (including
XX CC proliferation) of specific cell types. The present sequence is an
XX CC oligonucleotide used for generating mutant humanised KS antibody
XX CC (recognises epithelial cell adhesion molecule) and interleukin-2 fusion
XX CC protein with Pro to Leu substitution at the fusion junction
XX SQ Sequence 22 BP; 5 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
      Query Match      0.2%; Score 14.6; DB 1; Length 22;
      Best Local Similarity 81.0%; Pred. No. 2.4e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6998 GGGAAAGGAGATTTCTTCT 7018
DB 2 GGGACAGGGAGAGGCTTCT 22

RESULT 3403
AAC92055/c
ID AAC92055 standard; DNA; 22 BP.
XX AC AAC92055;
XX DT 21-MAR-2001 (first entry)

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XX Rat PER1 PCR primer #1.
DE DE
XX Rat; PER1; circadian rhythm; period protein; PCR primer; ss.
XX
XX Rattus sp.
OS
XX WO200075669-A1.
PN
XX 14-DEC-2000.
PD
XX
XX 07-JUN-2000; 2000WO-US015633.
PF
XX 08-JUN-1999; 99US-00327745.
PR
XX (AVET ) AVENTIS PHARM INC.
PA
XX Keesler G, Mondadori C, Yao Z, Camacho F;
PI
XX WPI; 2001-061769/07.
DR
XX
XX Identifying compounds that alter circadian rhythm of a mammal by altering
PT the phosphorylation or degradation of human period proteins, comprises
PT adding test compound to screening system comprising period proteins.
XX
XX Example 10; Page 33; 55pp; English.
PS
XX The present invention relates to a method for determining the ability of
CC a test compound to alter the circadian rhythm of a mammal by its ability
CC to alter phosphorylation or degradation of one or more period proteins.
CC The present sequence is a PCR primer for one such period protein (rat
CC PER1), that was used in the method of the present invention
XX
XX Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3239 TTTTGGAGCGCTTAATCAGA 3259
DB 21 TTGTGACGAGCCTTAACACAGA 1
RESULT 3404
AAFS876/c
ID AAF58870 standard; DNA; 22 BP.
XX
XX AAF58870;
AC
XX
XX 06-JUN-2001 (first entry)
DT
XX
XX Human metastasis-associated antigen C4-4A PCR primer #2.
DE
XX
XX Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200123553-A2.
PN
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-EP009567.
PF
XX
XX 29-SEP-1999; 99US-00407784.
PR
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Zoeller M, Roessel M, Wuerfel J;
PI
XX WPI; 2001-258133/26.
DR
XX New nucleic acid encoding rat or human metastasis-associated antigen
PT

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```

PT C4.4A for treating cell proliferative disorder associated with a
PT metastasizing tumor.
XX
XX Example 1; Page 29; 63pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of the
CC human and rat metastasis-associated antigen C4.4A. The protein is
CC expressed rarely in the adult, except on metastasizing cancer cells.
CC Because of this, the sequences are useful in cancer diagnosis and
CC treatment of cell proliferation diseases. The present sequence is a PCR
CC primer used to isolate the human C4.4A coding sequence
XX
XX Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3611 CTTTGGGGAATGGGCTGGGCG 3631
DB 21 CTTTGGAGCGTGGGCTGGGCTG 1
RESULT 3405
AAFS876/c
ID AAF58876 standard; DNA; 22 BP.
XX
XX AAF58876;
AC
XX
XX 06-JUN-2001 (first entry)
DT
XX
XX Human metastasis-associated antigen C4-4A PCR primer #4.
DE
XX
XX Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200123553-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-EP009567.
PF
XX
XX 29-SEP-1999; 99US-00407784.
PR
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Zoeller M, Roessel M, Wuerfel J;
PI
XX WPI; 2001-258133/26.
DR
XX
XX New nucleic acid encoding rat or human metastasis-associated antigen
PT C4.4A for treating cell proliferative disorder associated with a
PT metastasizing tumor.
XX
XX Example 1; Page 31; 63pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of the
CC human and rat metastasis-associated antigen C4.4A. The protein is
CC expressed rarely in the adult, except on metastasizing cancer cells.
CC Because of this, the sequences are useful in cancer diagnosis and
CC treatment of cell proliferation diseases. The present sequence is a PCR
CC primer used to isolate the human C4.4A coding sequence
XX
XX Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3611 CTTTGGGGAATGGGCTGGGCG 3631
DB 21 CTTTGGAGCGTGGGCTGGGCTG 1

```

RESULT 3406
AAFS8878/C
ID AAF58878 standard; DNA; 22 BP.
XX
XX
AC AAF58878;
XX
XX
DT 06-JUN-2001 (first entry)
XX
XX
DE Human metastasis-associated antigen C4-4A PCR primer #6.
XX
XX
KW Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200123553-A2.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000MO-EP009567.
XX
PR 29-SEP-1999; 99US-00407784.
XX
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zoeller M, Roedel M, Wuerfel J;
XX
DR WPI; 2001-258133/26.
XX
PT New nucleic acid encoding rat or human metastasis-associated antigen
PT C4.4A for treating cell proliferative disorder associated with a
PT metastasizing tumor.
XX
XX
PS Example 1; Page 32; 63pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and rat metastasis-associated antigen C4.4A. The protein is
CC expressed rarely in the adult, except on metastasizing cancer cells.
CC Because of this, the sequences are useful in cancer diagnosis and
CC treatment of cell proliferation diseases. The present sequence is a PCR
CC primer used to isolate the human C4.4A coding sequence
XX
SQ Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3611 CTTTGGGGAATGGGCTGGGG 3631
DB 21 CTTTGGAGCGTGGGCTGGTG 1

RESULT 3407
AAF99703
ID AAF99703 standard; DNA; 22 BP.
XX
XX
AC AAF99703;
XX
XX
DT 12-JUN-2001 (first entry)
XX
XX
DE Immunostimulatory nucleic acid #819.
XX
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumor; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX

PD 05-APR-2001.
XX
XX
PF 25-SEP-2000; 2000MO-US026383.
XX
XX
PR 25-SEP-1999; 99US-0156113P.
XX
PR 27-SEP-1999; 99US-0156135P.
XX
PR 23-AUG-2000; 2000US-0227436P.
XX
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C., Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC T12 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5328 CTCTCTTGGCTCACTCTCTC 5348
DB 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 3408
AAH79377/C
ID AAH79377 standard; DNA; 22 BP.
XX
XX
AC AAH79377;
XX
XX
DT 04-DEC-2001 (first entry)
XX
XX
DE Human RNA uncoiling enzyme 44 coding sequence PCR primer #1.
XX
XX
KW Human; RNA uncoiling enzyme 44; cancer; nervous system disease;
KW gene therapy; PCR primer; ss.
XX
XX
OS Homo sapiens.
XX
PN CN1302893-A.
XX
PD 11-JUL-2001.
XX
PF 29-OCT-1999; 99CN-00119928.
XX
PR 29-OCT-1999; 99CN-00119928.
XX
XX
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX

DR WPI; 2001-566052/64.
 XX
 PT Polypeptide-human RNA uncoiling enzyme 44 and polynucleotide for coding
 PT it.
 XX
 PS Example 3; Page 14(Disclosure); 24pp; Chinese.
 CC The present invention provides the protein and coding sequences of human
 CC RNA uncoiling enzyme 44. The sequences can be used in the treatment of
 CC cancer and nervous system diseases. The present sequence is a PCR primer
 CC for the coding sequence of the invention
 XX
 SO Sequence 22 BP; 9 A; 0 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4405 TTTACAAATGATTTTCC 4425
 DB 21 TTTTCAAAAACAAATTTCC 1
 RESULT 3409
 AAH74500
 ID AAH74500 standard; DNA; 22 BP.
 AC AAH74500;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE PCR primer used to amplify a marker SW782 from pig genome.
 XX
 KW Pig; boar taint; genetic marker; SW1057; SW782; S0121; SW322;
 KM chromosome 6; SW857; SW2496; SW295; SW210; S0007; SW761; SW1557;
 KM chromosome 14; PCR primer; ss.
 XX
 OS Sue sp.
 XX
 PN WO200157250-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-GB000448.
 XX
 PR 04-FEB-2000; 2000GB-00002451.
 XX
 PA (ROSL-) ROSLIN INST.
 XX
 PI Haley CS, Archibald AL;
 XX
 DX WPI; 2001-496928/54.
 XX
 PT Determining if a pig is predisposed to boar taint for exhibiting
 PT desirable flavor properties, involves assaying for the presence of
 PT alleles conveying susceptibility to boar taint using specific genetic
 PT markers.
 XX
 PS Example 1; Page 32; 71pp; English.
 XX
 CC PCR primers AAH74499-AAH74500 were used to amplify a fragment of the pig
 CC genome, comprising the marker SW782. The primers were used in the method
 CC of the invention. The specification describes a method for determining if
 CC a pig is predisposed to a boar taint. The method comprises assaying for
 CC the presence of alleles conveying susceptibility to boar taint using
 CC genetic markers selected from SW1057, SW782, S0121, SW322 or regions of
 CC chromosome 6 spanning in between, or SW857, SW2496, SW295, SW210, S0007,
 CC SW761, SW1557 or regions of chromosome 14 spanning in between. The method
 CC is useful for determining the predisposition of pigs to boar taint which
 CC is a strong unpleasant odour given off upon heating or cooking of meat
 CC from uncastrated male pigs, and for exhibiting desirable flavour
 CC properties
 XX

SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4435 ACTAGGCGATGCGGTGGTG 4455
 DB 1 AATAGGCGATGAGGGTGTG 21
 RESULT 3410
 AAH74340
 ID AAH74340 standard; DNA; 22 BP.
 AC AAH74340;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE PCR primer used to amplify a fragment of the human ATIP gene.
 XX
 KW Human; ATIP; hATIP2; hATIP3; hATIP4; hATIP5; hATIP6; AT2 receptor;
 KM angiotensin II receptor; anticonogenic; 8p21.3-p22; cancer; PCR primer;
 KM ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157209-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 07-FEB-2001; 2001WO-FR000359.
 XX
 PR 07-FEB-2000; 2000FR-00001504.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Nahmias C, Strosberg AD, Nouet S;
 XX
 DX WPI; 2001-488880/53.
 XX
 PT New protein family, designated hATIP, which interacts with the AT2
 PT receptor of angiotensin II are anti-oncogenic and useful to detect and
 PT treat cancer or precancerous conditions.
 XX
 PS Claim 7; Page 100; 118pp; French.
 XX
 CC PCR primers AAH74330-41 were used to amplify a fragment of the human ATIP
 CC gene. ATIP has isoforms designated hATIP2, hATIP3, hATIP4, hATIP5 and
 CC hATIP6. All ATIP proteins comprise in their C-terminal a common fragment
 CC which interacts with the angiotensin II (AT2) receptor. ATIP proteins
 CC have anticonogenic functions. The human ATIP gene has 17 exons, and is
 CC located at chromosome region 8p21.3-p22. ATIP polynucleotides and
 CC polypeptides are used to detect, evaluate or give prognosis for a cancer
 CC condition, and as an anti-tumour medicament
 XX
 SO Sequence 22 BP; 11 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7401 AGCAAGCAATCAGCAGCG 7421
 DB 2 AACAGACACATTAAGCAGCG 22
 RESULT 3411
 AAH78021
 ID AAH78021 standard; DNA; 22 BP.
 AC AAH78021;
 XX

```

DT 26-NOV-2001 (first entry)
XX PCR primer for human alpha subunit of prollyl 4-hydroxylase cDNA.
DE
XX
XX Human; alpha subunit; prollyl 4-hydroxylase; alpha (III) subunit;
KW collagen; kidney fibrosis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX MO200168868-A2.
XX
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001MO-US008267.
XX
XX 15-MAR-2000; 2000US-0189373P.
XX
XX (FIBR-) FIBROGEN INC.
XX
XX Kivirikko K, Myllyharju J, Kukkola L, Hietala R;
XX WPI; 2001-570871/64.
XX
XX
XX New alpha subunit of prollyl 4-hydroxylase and polynucleotide encoding the
PT subunit, useful for diagnosis, prevention and treatment of diseases and
PT disorders associated with increased or decreased expression of the
XX subunit.
XX
XX Example 1; Page 52; 75pp; English.
XX
XX PCR primers AAH78021-22 were used to amplify cDNA encoding a human alpha
CC subunit of prollyl 4-hydroxylase, designated alpha (III) subunit. The
CC alpha (III) subunit is useful for the production of recombinant collagen,
CC and for the diagnosis, prevention and treatment of various diseases and
CC disorders associated with decreased or increased production of the
CC subunit in specific tissues. The polynucleotide is a source of probes and
CC primers, which are useful for diagnosis, prevention and treatment of
CC diseases and disorders associated with increased or decreased expression
CC or activity of various prollyl 4-hydroxylase enzymes and to identify alpha
CC or beta prollyl 4-hydroxylase or fragments in tissue, e.g. biopsies from
CC specific tissues, etc or other biological samples. Small molecules that
CC modulate, regulate and inhibit prollyl 4-hydroxylase activity are useful
CC for treating and preventing kidney fibrosis and various other diseases
CC and disorders
XX
XX
XX Sequence 22 BP; 5 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 6437 TTACTAAGCAGCAGTGT 6457
XX ||||| ||||| |||||
DB 2 TTAGGATGCAGCACTGTTT 22
XX
XX
XX RESULT 3412
XX AAC84905
XX ID AAC84905 standard; DNA; 22 BP.
XX
XX AAC84905;
XX
XX 20-APR-2001 (first entry)
XX
XX
XX Primer Ag 36 (R) employed in expression analysis of SEC1 (3445452).
XX
XX
XX SECK; cytostatic; gynecological; gene therapy; screening assay; human;
KW chromosomal mapping; forensic biology; cell proliferation; cancer;
KW cell differentiation; immune associated disorder; gestational disease;
KW SEC1; PCR primer; ss.
XX
XX
XX Homo sapiens.
XX
XX

```

```

PN MO200078802-A2.
XX
XX PD -28-DEC-2000.
XX
XX 23-JUN-2000; 2000MO-US017328.
XX
XX
XX 23-JUN-1999; 99US-0140584P.
XX 20-JUN-1999; 99US-0144722P.
XX 16-SEP-1999; 99US-0154520P.
XX 22-JUN-2000; 2000US-00604286.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX
XX Shinkets RA, Fernandez E, Vernet C, Yang M, Boldog FL;
XX Herrmann JL;
XX WPI; 2001-071385/08.
XX
XX
XX Polynucleotides encoding SECK proteins useful for treating disease
PT characterized by an aberrant level of cell proliferation and/or
PT differentiation like cancer or immune associated disorders.
XX
XX
XX Example 10; Page 84; 132pp; English.
XX
XX
XX The invention relates to human SECK polypeptides and polynucleotides
CC encoding them. The SECK polypeptides can be expressed by standard
CC recombinant methodology. The SECK polypeptides are useful for treating or
CC preventing a SECK-associated disorder. The invention is useful in
CC screening assays; detection assays (e.g. chromosomal mapping, cell and
CC tissue typing, forensic biology); predictive medicine (diagnostic assays,
CC prognostic assays, monitoring clinical trials, and pharmacogenomics); and
CC methods of treatment (e.g. therapeutic and prophylactic), especially
CC disorders characterized by aberrant cell proliferation and/or
CC differentiation like cancer or immune associated disorders or gestational
CC disease. Sequences AAC94904-906 represent primer-probe sets employed in
CC the expression analysis of SEC1 clone
XX
XX
XX Sequence 22 BP; 5 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4299 CATCTTTTCTCTCCCTGGA 4319
XX ||||| ||||| |||||
DB 1 CATCTCTCTCTCCCAAGA 21
XX
XX
XX RESULT 3413
XX AAS11868/c
XX ID AAS11868 standard; DNA; 22 BP.
XX
XX AAS11868;
XX
XX 24-OCT-2001 (first entry)
XX
XX
XX Human PCNA random mutagenesis PCR primer #2.
XX
XX
XX Human; PCNA; PCR primer; HIS tag; iminodiscetic acid cellulose; IDAC;
KW immobilised protein; proliferating cell nuclear antigen; ss.
XX
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX US6232083-B1.
XX
XX
XX 15-MAY-2001.
XX
XX 12-MAR-1999; 99US-00268536.
XX
XX 12-MAR-1999; 99US-00268536.
XX
XX
XX (UTNY ) UNIV NEW YORK STATE RES FOUND.
XX
XX

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XX PI Fisher PA, Zaika A,
XX XX
XX DR WPI; 2001-440150/47.
XX PT Determining protein expression and function by genetically expressing
XX PT proteins having polypeptide regions, immobilizing the protein on metal
XX PT charged iminodiacetic acid cellulose and detecting protein or its
XX PT activity.
XX PS Example 5; Col 10; 23pp; English.
XX XX
XX CC The invention relates to determining expression or functional activity of
XX CC a protein, comprises expressing the protein having a polypeptide region
XX CC in genetically engineered cells, transferring the protein to metal
XX CC charged iminodiacetic acid cellulose (IDAC), immobilizing the protein on
XX CC the metal charged IDAC and detecting the protein or its functional
XX CC activity immobilised on the IDAC. The method is useful for determining
XX CC the expression of a protein and functional activity of a protein, which
XX CC includes binding specificity, enzyme activity, stimulation of enzyme
XX CC activity or stimulation of delta-polymerase activity. The protein is
XX CC especially human or Drosophila melanogaster proliferating cell nuclear
XX CC antigen (PCNA). Metal charged IDAC allows easy screening of a large
XX CC number of proteins following mutagenesis and can rapidly ascertain which
XX CC mutants have desired functional activity or binding capacity. The present
XX CC sequence is a mutagenic PCR primer for random mutagenesis of human PCNA
XX CC
XX SQ Sequence 22 BP; 5 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4743 GGAGGAGAGAGGCTTAATC 4763
XX 22 GGATGAGAGAGGATCTTAAC 2
XX
XX RESULT 3414
XX AAF76175/c
XX ID AAF76175 standard; DNA; 22 BP.
XX XX
XX AC AAF76175;
XX
XX DT 05-JUN-2001 (first entry)
XX
XX DE Human M-CSF PCR primer, SEQ ID NO:41.
XX
XX KM Transgenic mouse; immunodeficient; tissue recipient;
XX KM lymphocyte deficient; human cytokine; interleukin; IL-7; IL-6; SCF; LIF;
XX KM stem cell factor; leukemia inhibitory factor; GM-CSF; M-CSF;
XX KM granulocyte macrophage-colony stimulating factor;
XX KM macrophage-colony stimulating factor; human MHC class II; DR3;
XX KM major histocompatibility complex; allergenicity determination;
XX KM human monoclonal antibody generation; haematopoietic cell development;
XX KM human immune system animal model; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200115521-A1.
XX
XX PD 08-MAR-2001.
XX
XX PF 30-AUG-2000; 2000WO-US023971.
XX
XX PR 31-AUG-1999; 99US-0151688P.
XX
XX PA (GENM ) GENENCOR INT INC.
XX
XX PT Huang MA, Harding PA;
XX
XX WPI; 2001-169001/17.
XX

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PT PT New transgenic mice, useful as non-human mammalian models of human
PT disease, comprise recombination activation gene mutations and donor
PT specific transgenes encoding cytokines.
XX
XX PS Example 2; Page 37; 68pp; English.
XX XX
XX CC The invention relates to a transgenic immunodeficient recipient mouse
XX CC which is capable of supporting the growth of donor cells. In the mouse,
XX CC both alleles of a gene activated in early lymphocyte development are
XX CC disrupted, causing it to lack mature B and T cells. In particular, both
XX CC alleles of the recombination activation gene-2 (RAG-2) gene are
XX CC disrupted, which in turn prevents VDJ recombination. The mouse also
XX CC comprises donor (e.g., human) specific transgenes encoding the cytokines
XX CC interleukin-7 (IL-7), stem cell factor (SCF), leukemia inhibitory factor
XX CC (LIF), granulocyte macrophage-colony stimulating factor (GM-CSF),
XX CC macrophage-colony stimulating factor (M-CSF), and IL-6, which enable it
XX CC to support the growth of transplanted donor cells. In another embodiment
XX CC of the invention, the mouse comprises DNA encoding the human major
XX CC histocompatibility complex (MHC) class II DR3 molecule, where the
XX CC transgene has naturally linked Dab and Dqab alleles. The transgenic
XX CC mouse may be used as a model for determining the allergenicity of non-
XX CC donor, e.g., non-human, macromolecules, to determine the effect compounds
XX CC have on a human immune system; to generate fully human polyclonal or
XX CC monoclonal antibodies to specific antigens; to determine whether
XX CC humanised or other monoclonal antibodies will raise a response in a human
XX CC immune system; to investigate the human cell mediated response to
XX CC pathogens and other immunomodulatory compounds; and to determine the
XX CC factors involved in regulating the development and function of human
XX CC haematopoietic cells. The transgenic mouse supports the functional
XX CC properties of human haematopoietic cells, unlike previous animal models
XX CC which produce functionally impaired haematopoietic cells or are
XX CC immunologically dysfunctional. In addition the transgenic mouse provides
XX CC a unique model system which supports T cell development in a manner which
XX CC more closely resembles normal ontogeny, as they possess CD4+ T cells in
XX CC the periphery that exhibit MHC-restricted antigen- specific responses.
XX CC Sequences AAF76133-AAF76192 represent human cytokine PCR primers used in
XX CC the development of human cytokine-expressing transgenic mice
XX CC
XX SQ Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4803 CTGCCCTTGATGACCGGAT 4823
XX 22 CTGCCCTGTGAAGACTTGCT 2
XX
XX RESULT 3415
XX AAF31837/c
XX ID AAF31837 standard; DNA; 22 BP.
XX
XX AC AAF31837;
XX
XX DT 12-APR-2001 (first entry)
XX
XX DE Human MAT II beta subunit-specific PCR primer.
XX
XX KM Human; methionine adenosyltransferase II; MAT II; MAT II beta subunit;
XX KM cytosolic; immunosuppressive; gene therapy; antisense therapy;
XX KM livestock feed additive; cancer; autoimmune disease; transplantation;
XX KM PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200102420-A1.
XX
XX PD 11-JAN-2001.
XX
XX PF 30-JUN-2000; 2000WO-US018269.
XX
XX PR 01-JUL-1999; 99US-0142020P.
XX

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XX (UTTE-) UNIV TENNESSEE RES CORP.
XX
XX Koch M, Legros HL, Geller AM;
XX
XX WPI; 2001-080980/09.
XX
XX Nucleic acid encoding a biologically active methionine
XX PT adenosyltransferase II (MAT II) beta subunit, useful in screening assays
XX PT for identifying MAT II modulating compounds which can be used to treat
XX PT cancer and autoimmune diseases.
XX
XX Example 2; Page 92; 176pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
XX CC and purified nucleic acid encoding a biologically active methionine
XX CC adenosyltransferase II (MAT II) beta subunit polypeptide capable of
XX CC modulating MAT II biological activity. The MAT II beta subunit nucleic
XX CC acid and polypeptide are useful in screening assays for identifying
XX CC compounds that affect or modulate MAT II biological activity. The MAT
XX CC II beta subunit polypeptides have utility as feed additives for
XX CC livestock. The MAT II beta subunit polypeptide, anti-MAT II beta
XX CC subunit antibody and antisense oligonucleotide are useful for treating a
XX CC disorder associated with MAT II biological activity, e.g. cancer,
XX CC autoimmune diseases and transplantation
XX
XX Sequence 22 BP; 4 A; 3 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3379 TTGCTCTCCGCCAGCTGCCA 3399
XX Db 22 TTCTCTCCGACGACGCGACA 2
XX
XX RESULT 3416
XX ABA94871/C
XX ID ABA94871 standard; DNA; 22 BP.
XX
XX ABA94871;
XX AC
XX 08-MAY-2002 (first entry)
XX DT
XX
XX Unmethylated RASSF1A promoter fragment detecting reverse primer.
XX DE
XX Tumour suppressor gene; chromosome 3p21.3; Gene 26; PL6; Beta*; LUCA-1;
XX KM LUCA-2; 123F2; Fusi1; 101F6; Gene 21; SEM A3; cancer; tumour; BLU; human;
XX KM cytosolic; gene therapy; protein therapy; RASSF1A; PCR primer; ss.
XX OS
XX Homo sapiens.
XX OS
XX WO200204511-A2.
XX PN
XX 17-JAN-2002.
XX PD
XX 10-JUL-2001; 2001WO-US021781.
XX PF
XX 10-JUL-2000; 2000US-0217112P.
XX PR
XX (TEXA) UNIV TEXAS SYSTEM.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX J1 L, Minna J, Roth J, Lerman M;
XX P1
XX WPI; 2002-179699/23.
XX DR
XX New tumor suppressor genes and proteins, useful for detecting, diagnosing
XX PT and treating various human cancers, e.g. spleen cancer, kidney cancer,
XX PT lymph node cancer, small intestine cancer, blood cell cancer or
XX PT pancreatic cancer.

PS Example 15; Page 99; 206pp; English.
XX
XX The invention relates to tumour suppressor genes at chromosome 3p21.3
XX CC (Gene 26, PL6, Beta*, LUCA-1, LUCA-2, 123F2, Fusi1, 101F6, Gene 21, or
XX CC SEM A3). The tumour suppressor genes play a major role in the
XX CC pathogenesis of human lung cancer and other cancers. The polypeptide and
XX CC polynucleotides are useful for detecting, diagnosing and treating various
XX CC human cancers. These are particularly useful for inhibiting
XX CC tumorigenicity, suppressing tumour or restricting metastatic processes
XX CC in various tumours such as lung, colon, breast, stomach, cervix, and head
XX CC and neck, prostate or pancreas. In particular, the cancer is brain
XX CC cancer, lung cancer, liver cancer, spleen cancer, kidney cancer, lymph
XX CC node cancer, small intestine cancer, blood cell cancer, pancreatic
XX CC cancer, colon cancer, stomach cancer, cervix cancer, breast cancer,
XX CC endometrial cancer, prostate cancer, testicle cancer, ovarian cancer,
XX CC skin cancer, head and neck cancer, esophageal cancer, oral tissue cancer
XX CC or bone marrow cancer. The present sequence represents a primer for
XX CC detecting an unmethylated RASSF1A promoter fragment by methylation-
XX CC specific PCR
XX
XX Sequence 22 BP; 13 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3167 GTTAGGTTGGGTTTGACT 3187
XX Db 22 GTTGGTTGTTGGTTTGACT 2
XX
XX RESULT 3417
XX ABL92904
XX ID ABL92904 standard; DNA; 22 BP.
XX
XX ABL92904;
XX AC
XX 06-JUN-2002 (first entry)
XX DT
XX
XX G protein-coupled receptor GPCR23 PCR primer SEQ ID NO:386.
XX DE
XX Human; G protein-coupled receptor; antidiabetic; anorectic; cytosolic;
XX KM immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;
XX KM immunosuppressive; ophthalmological; antibacterial; virucide; fungicide;
XX KM protozoacide; hypertensive; hypotensive; analgesic; osteopathic;
XX KM antifungal; antistaphylococcal; antiallergic; anti-HIV; antiparasitic; vaccine;
XX KM antineoplastic; antineoplastic; haemostatic; cell signal processing;
XX KM cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;
XX KM gene therapy; PCR primer; ss.
XX OS
XX Homo sapiens.
XX OS
XX WO200212343-A2.
XX PN
XX 14-FEB-2002.
XX PD
XX 07-AUG-2001; 2001WO-US024787.
XX PF
XX 07-AUG-2000; 2000US-0223138P.
XX PR 07-AUG-2000; 2000US-0223472P.
XX PR 11-AUG-2000; 2000US-0224613P.
XX PR 11-AUG-2000; 2000US-0224815P.
XX PR 05-JAN-2001; 2001US-0260003P.
XX PR 05-JAN-2001; 2001US-0260072P.
XX PR 08-JAN-2001; 2001US-0260283P.
XX PR 09-JAN-2001; 2001US-0260450P.
XX PR 10-JAN-2001; 2001US-0261156P.
XX PR 22-JAN-2001; 2001US-0263338P.
XX PR 23-JAN-2001; 2001US-0263434P.
XX PR 01-FEB-2001; 2001US-0265704P.
XX PR 20-FEB-2001; 2001US-0265964P.
XX PR 09-MAR-2001; 2001US-0274873P.
XX PR 15-MAR-2001; 2001US-0276406P.

PR 01-MAY-2001; 2001US-0287916P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Spytek KA, Padigaru M, Zernhusen BD, Baumgartner JC, Li L;
 PI Casman SJ, Vernet CAM, Ballinger RA, Shenoy SG, Kekuda R;
 PI Burgess CE, Mezes PS, Grose WM, Alsbrook JP, Gorman L;
 PI Larochelle WJ, Taupier RJ, Colman SD, Szekeres ES;
 XX WPI; 2002-217180/27.
 DR
 XX
 PT New G-protein coupled receptor polypeptides and nucleic acids, useful for
 PT diagnosis, prevention or treatment of hematopoietic, neurodegenerative,
 PT immune and signal transduction pathway disorders.
 XX
 XX Example 2; Page 407; 492pp; English.
 XX
 CC The present invention describes novel human G protein-coupled receptors
 CC (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have
 CC activities such as: antidiabetic; anorectic; immunomodulator; cytostatic;
 CC neuroprotective; nootropic; antiparkinsonian; analgesic; osteopathic;
 CC immunosuppressive; metabolic; ophthalmological; antibacterial; virocidic;
 CC fungicide; protozoacide; hypertensive; hypotensive; anti-HIV; antiviral;
 CC antisthmatic; antidiabetic; antiallergic; antifertility; haemostatic;
 CC and antiinflammatory. They can be used in gene therapy and vaccine
 CC production. The GPCR proteins can be used for treating or preventing GPCR
 CC -associated disorders such as cardiomyopathy, atherosclerosis, or a
 CC disorder related to cell signal processing and metabolic pathway
 CC modulation, in humans. GPCR proteins and the polynucleotides encoding
 CC them are useful for determining the presence of or predisposition to a
 CC disease, especially cancer associated with altered levels of GPCR
 CC proteins and polynucleotides, by measuring the level of protein
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. GPCR
 CC proteins are also useful for identifying an agent, especially cellular
 CC receptor or a downstream effector that binds to GPCR, for screening of a
 CC candidate substance interacting with an olfactory receptor polypeptide,
 CC its fragments or variants. The present sequence represents a PCR primer
 CC used in the isolation of a novel human GPCR in the present invention
 XX
 XX Sequence 22 BP; 8 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3641 AGGTAGATGGGGAAGAATAC 3661
 DB 2 AGGTGCTGAGAGAAAGTAC 22
 RESULT 3418
 ABL92913 standard; DNA; 22 BP.
 ID ABL92913 standard; DNA; 22 BP.
 XX
 AC ABL92913;
 XX
 DT 06-JUN-2002 (first entry)
 XX
 XX G protein-coupled receptor GPCR25 PCR primer SEQ ID NO:395.
 DE
 XX
 XX Human; G protein-coupled receptor; antidiabetic; anorectic; cytostatic;
 KW immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;
 KW immunosuppressive; ophthalmological; antibacterial; virocidic; fungicide;
 KW protozoacide; hypertensive; hypotensive; analgesic; osteopathic;
 KW antiviral; antisthmatic; antidiabetic; antiallergic; anti-HIV; antifertility; vaccine;
 KW antifertility; antiinflammatory; haemostatic; cell signal processing;
 KW cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;
 KW gene therapy; PCR primer; 88.
 KW
 OS Homo sapiens.
 XX
 XX WO200212343-A2.

XX
 PD 14-FEB-2002.
 XX
 XX 07-AUG-2001; 2001WO-US024787.
 PF
 XX
 PR 07-AUG-2000; 2000US-0223138P.
 PR 07-AUG-2000; 2000US-0223472P.
 PR 11-AUG-2000; 2000US-0224613P.
 PR 11-AUG-2000; 2000US-0224815P.
 PR 05-JAN-2001; 2001US-0260003P.
 PR 05-JAN-2001; 2001US-0260072P.
 PR 08-JAN-2001; 2001US-0260283P.
 PR 09-JAN-2001; 2001US-0260450P.
 PR 10-JAN-2001; 2001US-0261156P.
 PR 22-JAN-2001; 2001US-0263138P.
 PR 23-JAN-2001; 2001US-0263434P.
 PR 01-FEB-2001; 2001US-0265704P.
 PR 20-FEB-2001; 2001US-0269964P.
 PR 09-MAR-2001; 2001US-0274873P.
 PR 15-MAR-2001; 2001US-0276406P.
 PR 01-MAY-2001; 2001US-0287916P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Spytek KA, Padigaru M, Zernhusen BD, Baumgartner JC, Li L;
 PI Casman SJ, Vernet CAM, Ballinger RA, Shenoy SG, Kekuda R;
 PI Burgess CE, Mezes PS, Grose WM, Alsbrook JP, Gorman L;
 PI Larochelle WJ, Taupier RJ, Colman SD, Szekeres ES;
 XX WPI; 2002-217180/27.
 DR
 XX
 PT New G-protein coupled receptor polypeptides and nucleic acids, useful for
 PT diagnosis, prevention or treatment of hematopoietic, neurodegenerative,
 PT immune and signal transduction pathway disorders.
 XX
 XX Example 2; Page 417; 492pp; English.
 XX
 CC The present invention describes novel human G protein-coupled receptors
 CC (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have
 CC activities such as: antidiabetic; anorectic; immunomodulator; cytostatic;
 CC neuroprotective; nootropic; antiparkinsonian; analgesic; osteopathic;
 CC immunosuppressive; metabolic; ophthalmological; antibacterial; virocidic;
 CC fungicide; protozoacide; hypertensive; hypotensive; anti-HIV; antiviral;
 CC antisthmatic; antidiabetic; antiallergic; antifertility; haemostatic;
 CC and antiinflammatory. They can be used in gene therapy and vaccine
 CC production. The GPCR proteins can be used for treating or preventing GPCR
 CC -associated disorders such as cardiomyopathy, atherosclerosis, or a
 CC disorder related to cell signal processing and metabolic pathway
 CC modulation, in humans. GPCR proteins and the polynucleotides encoding
 CC them are useful for determining the presence of or predisposition to a
 CC disease, especially cancer associated with altered levels of GPCR
 CC proteins and polynucleotides, by measuring the level of protein
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. GPCR
 CC proteins are also useful for identifying an agent, especially cellular
 CC receptor or a downstream effector that binds to GPCR, for screening of a
 CC candidate substance interacting with an olfactory receptor polypeptide,
 CC its fragments or variants. The present sequence represents a PCR primer
 CC used in the isolation of a novel human GPCR in the present invention
 XX
 XX Sequence 22 BP; 3 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5801 TGCCTGCTTCTGCTATGT 5821
 DB 1 TGCCTGCTTCTGCTATGT 21
 RESULT 3419
 ABL52319/c

ID ABK52319 standard; DNA; 22 BP.
 XX
 AC ABK52319;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Vascular smooth muscle cell proliferation associated PCR primer #7.
 XX
 KW Vascular smooth muscle; cell proliferation; proliferation inhibitor; PCR;
 KM primer; ss.
 XX
 OS Synthetic.
 XX
 PN JP2002112798-A.
 XX
 PD 16-APR-2002.
 XX
 PF 20-SEP-2000; 2000JP-00284973.
 XX
 PR 03-AUG-2000; 2000JP-00235459.
 XX
 PA (SUMO) SUMITOMO CHEM CO LTD.
 XX
 DR WPI; 2002-448760/48.
 XX
 PT Measurement of the inhibitory activity for vascular smooth muscle cell
 PT proliferation, and a method for screening a substance with inhibitory
 PT activity for vascular smooth muscle cell proliferation.
 XX
 PS Example 8; Page 22; 24pp; Japanese.
 XX
 CC The invention describes a measurement of inhibitory activity on vascular
 CC smooth muscle cell proliferation and a method for screening a substance
 CC having inhibitory activity on vascular smooth muscle cell proliferation.
 CC This sequence represents a PCR primer associated with the method of
 CC measuring, and screening for compounds responsible for, inhibition of
 CC vascular smooth muscle cell proliferation
 XX
 SQ Sequence 22 BP; 8 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4646 TGGATTTCCTCTTGGAGAG 4666
 DB 21 TGGATTTCCTCATTTGGAG 1
 RESULT 3420
 ID ABS58924/C
 ID ABS58924 standard; DNA; 22 BP.
 XX
 AC ABS58924;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human G-protein coupled receptor, reverse primer #24.
 XX
 KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
 KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
 KW adenocarcinoma; lymphoma; prostate cancer; uterine cancer; asthma;
 KW immune response; neurodegenerative disorder; inflammatory disorder;
 KW Crohn's disease; multiple sclerosis; Albritght hereditary osteodystrophy;
 KW primer; PCR; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200259313-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-DEC-2001; 2001WO-US049394.

XX
 PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0263669P.
 PR 08-FEB-2001; 2001US-0265746P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0299327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Ballinger RA, Padigaru M, Kehuda R, Colman SD, Spytek KA,
 PI Caaman SJ, Vernet CM, Shenoy SG, Gusev V, Malysankar UM, Edinger S,
 PI Gerlach V, Smithson G, Stone DU, Sclotre P, Macdougall JR, Gunther E,
 PI Peyman JA, Ellerman K, Gangoli EA, Millet I;
 XX
 DR WPI; 2002-599789/64.
 XX
 PT New G protein coupled receptor polypeptides and polynucleotides, useful
 PT in gene therapy, particularly for treating or preventing cardiomyopathy,
 PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
 PT in humans.
 XX
 PS Claim 9; Page 300; 685pp; English.
 XX
 CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
 CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
 CC and antibody are useful for treating, preventing or alleviating a GPCR-
 CC associated disorder or a pathological state in a subject, particularly a
 CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
 CC diabetes, or a disorder related to cell signal processing and metabolic
 CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
 CC for diagnosing the presence of or predisposition to a disease associated
 CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
 CC and polypeptide are especially useful in therapeutic or prophylactic
 CC applications for disorders associated with aberrant GPCR expression or
 CC activity. The DNA encoding the protein is useful in gene therapy for
 CC treating the above conditions. Furthermore, the nucleic acids and
 CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
 CC cancer, uterine cancer, immune response, neurodegenerative disorders,
 CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
 CC Albritght hereditary osteodystrophy. These are also useful in developing a
 CC powerful assay system for functional analysis of various human disorders,
 CC as well as in diagnostic applications. ABS58747-ABS59231 represent human
 CC GPCR coding sequences, primers and probes of the invention
 XX
 SQ Sequence 22 BP; 12 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3921 CTTTGCTCTTTCCTCCT 3941
 DB 21 CTTTGCTCTTTCCTCCT 1
 RESULT 3421
 ID AAD43245
 ID AAD43245 standard; DNA; 22 BP.
 XX
 AC AAD43245;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Antisense oligonucleotide R51A56.

```

XX Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;
KM hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;
KM leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;
KM inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;
KM antisense; phosphorothioate backbone; ss.
XX
XX Unidentified.
OS
XX Key Location/Qualifiers
FH modified_base 1..22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX US2002086840-A1.
XX
XX 04-JUL-2002.
XX
XX 26-JAN-2001; 2001US-00771355.
XX
XX 26-JAN-2000; 2000US-0178561P.
XX
XX (ZARL/) ZARLING D A.
XX (REDD/) REDDY G.
XX
XX Zarling DA, Reddy G;
XX WPI; 2002-635686/68.
XX
XX Inhibiting/reducing tumor cell proliferation in individual in vivo, for
PT treating cancer, arthritis, involves contacting tumor cell in vivo with
PT Rad51 inhibitor, and polynucleotide expressing functional p53 protein.
XX
XX Disclosure; Page 5; 12pp; English.
XX
XX The invention relates to a method for inhibiting or reducing tumor cell
XX proliferation in an individual in vivo. The method comprising contacting
XX a tumor cell in vivo with a Rad51 inhibitor and a polynucleotide capable
XX of expressing functional p53 protein. The method is useful for inhibiting
XX or reducing tumor cell proliferation in an individual in vivo. The
XX method is useful for treating hyperproliferative disorders, especially
XX cancer (such as Hodgkin's disease, squamous cell carcinoma and
XX leukemia), premature aging, autoimmune disease, arthritis, graft
XX rejection, inflammatory bowel disease, and proliferation induced after
XX medical procedures such as surgery and angioplasty. The invention is
XX useful in gene therapy. The present sequence is an antisense
XX oligonucleotide used to illustrate the method of the invention
XX
XX Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3477 CCTAGTAATCTTAAAGCAC 3497
XX |||||
XX 1 CCCAGTCATCTCTAAGCAC 21
XX
XX RESULT 3422
XX ABL35690
XX ID ABL35690 standard; DNA; 22 BP.
XX
XX ABL35690;
XX
XX 04-APR-2002 (first entry)
XX
XX Immunostimulatory oligonucleotide SEQ ID NO: 616.
XX
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KM infection; allergy; cancer; hypersensitivity; bio-warfare;
KM immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KM
OS Unidentified.

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KM immunosuppressive; protozoacide; virocid; hepatotropic; gene therapy;
KM antiinflammatory; antibacterial; ss.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH misc_RNA 1..22
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Kliman DM;
XX WPI; 2002-130570/17.
XX
XX Example 11; Page 63; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 22 BP; 0 A; 3 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4463 CTTTTTTTTTTTTTTTTTTT 4483
XX |||||
XX 2 CGTTGTCTCTTTT 22
XX
XX RESULT 3423
XX AAD38021
XX ID AAD38021 standard; DNA; 22 BP.
XX
XX AAD38021;
XX
XX 10-SEP-2002 (first entry)
XX
XX FGF10 amplifying reverse RT PCR primer.
XX
XX Lung cancer; homedomain; homeobox; HOX; wingless/int-1; WNT; tumour;
KM diagnosis; prognosis; therapeutic; real time PCR; RT-PCR; FGF10; primer;
KM ss.
XX
XX Unidentified.

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XX MO200231210-A1.
XX
XX 18-APR-2002.
XX
XX 11-OCT-2001; 2001WO-US031960.
XX
XX 11-OCT-2000; 2000US-0239596P.
XX
XX (UTRE-) UNIV TECHNOLOGY CORP.
XX
XX Drabkin HA, Gemm11 RM;
XX
XX WPI; 2002-454557/48.
XX
XX Evaluating a lung cell sample of a lung cancer patient for diagnosis to
PT determine clinical prognosis including tendency to metastasize comprises
PT screening for expression of homeodomain containing genes HOX or WNT.
XX
XX Example; Page 16; 37pp; English.
XX
XX The invention relates to evaluating a lung cell sample of a lung cancer
CC patient comprising screening for expression of a homeodomain containing
CC homeobox (HOX) or wingless/int-1 (WNT) gene and comparing the screen to a
CC sample of non-malignant lung cell. The method is useful for evaluating a
CC lung cell sample of a lung cancer patient. The method is useful for
CC determining the prognosis of a lung cancer and for assessing a lung
CC cancer for a tendency to metastasize, where decreased expression of a WNT
CC gene or HOXA1 gene, or increased expression of HOX gene other than HOXA1,
CC or both, indicates poor prognosis, increased rate of tumour growth, and
CC increased tendency to metastasize. The method is useful for obtaining
CC data for diagnosis, to determine clinical prognosis, including rate of
CC growth, tendency to metastasize, to assess the efficacy of treatment and
CC to determine the efficacy of a therapeutic agent. The present sequence is
CC a real time (RT)-PCR primer used to amplify FGF10. This sequence is used
CC in the exemplification of the invention
XX
XX
SQ Sequence 22 BP; 2 A; 10 C; 0 G; 10 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 5740 TCCCTTTCTCTATCACTC 5760
Db 1 TCCATTTCTCTATCTCTC 21
XX
XX
RESULT 3424
ABK78424
ID ABK78424 standard; DNA; 22 BP.
XX
XX ABK78424;
XX
XX 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #908.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiodiroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 35; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acid, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
CC wound granulation, intestinal adhesion, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
XX
SQ Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 5328 CTCCTTGGCTCCTCTCTC 5348
Db 1 CTCCTCTCTCTCTCTCTC 21
XX
XX
RESULT 3425
ABK97133
ID ABK97133 standard; DNA; 22 BP.
XX
XX ABK97133;
XX
XX 07-OCT-2002 (first entry)
XX
XX Alalfa mosaic virus DNA RT-PCR primer #1.
XX
XX Virus-encoded coat protein; primer; AMV; CVV; WGMV; leguminous plant;
KW viral replicase; intron ribonucleic acid; RNA; hairpin RNA; virucide;
KW pathogenic plant virus; SSU promoter; 35S promoter; gene therapy; RT-PCR;
KW reverse transcriptase PCR; ss.
XX
XX Alalfa mosaic virus.
XX
XX Synthetic.
XX
XX WO200239808-A1.
XX
XX 23-MAY-2002.
XX
XX 16-NOV-2001; 2001WO-AU001496.
XX
XX 17-NOV-2000; 2000AU-00001558.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (DAIR-) DAIRY RES & DEV CORP.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX
XX Chu PWG, Garrett RG, Kalla SR, Spangenberg GC, Larkin PJ,
PI Higgins TJ;

XX
DR WPI; 2002-519361/55.
XX
PT Conferring immunity to pathogenic plant virus on leguminous plant by
PT introducing nucleic acid sequence encoding virus-encoded coat protein,
PT dysfunctional viral replicase or tRNA comprising hairpin RNA, to plant.
XX
XX Example 1; Page 49; 283pp; English.
XX
CC The invention relates to a method for conferring immunity to a pathogenic
CC plant virus on a leguminous plant comprising introducing an isolated
CC nucleic acid molecule encoding a virus-encoded coat protein, a
CC dysfunctional viral replicase or an intron ribonucleic acid (tRNA)
CC comprising a hairpin RNA to the plant so the plant is immune to the plant
CC virus under field conditions. The invention also relates to a method for
CC transforming a leguminous plant by introducing to a leguminous plant
CC cell, tissue or organ, an isolated nucleic acid molecule comprising an
CC SSU promoter or a 35S promoter operably linked to a nucleic acid encoding
CC a virus-encoded coat protein and regenerating a transformed leguminous
CC plant from the plant cell, tissue or organ, where the transformed
CC leguminous plant is immune to a pathogenic plant virus. The method is
CC useful for producing a leguminous plant with enhanced viral resistance or
CC crossing two parent plants each having enhanced viral resistance or
CC immunity against one or more different viruses. This sequence represents
CC a reverse transcriptase PCR (RT-PCR) primer used in the method of the
CC invention
XX
SQ Sequence 22 BP; 5 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2238 CCAGATCTCCATATGAGCT 2258
DB 1 CCAGATCTCCATATGAGT 21
XX
RESULT 3426
ABN84449
ID ABN84449 standard; DNA; 22 BP.
XX
AC ABN84449;
XX
DT 21-OCT-2002 (first entry)
XX
DE Bcr/abl forward PCR primer used in whole cell RT-PCR.
XX
KM RNA polymer; ribonuclease; RNase; inhibitor; bcr; abl; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200259366-A2.
XX
PD 01-AUG-2002.
XX
PE 26-NOV-2001; 2001WO-US044644.
XX
PR 28-NOV-2000; 2000US-0253451P.
PR 28-NOV-2001; 2001US-00955912.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Schultz JW, Lewis MK, Andrews CA;
XX
DR WPI; 2002-599806/64.
XX
XX Reducing the activity of a ribonuclease, useful for inhibiting tumor
PT growth or for removing RNA binding proteins from a solution, comprises
PT mixing a sample containing an RNase with a preparation containing at
PT least one RNA polymer.
XX
XX Example 7; Page 45; 61pp; English.

XX
CC The present sequence is that of a bcr/abl forward PCR primer. The primer
CC was used in an example from the invention demonstrating the inhibition of
CC RNase enzymes in RT-PCR reactions using poly or polyI attached to
CC resins. RT-PCR was conducted without prior RNA isolation using K562
CC (human erythroleukemia cell line) whole cell lysates. The reverse primer
CC for the PCR is given in ABN84450. Results were compared with the effect
CC of adding RNASIN ribonuclease inhibitor. Addition of RNASIN to cells
CC during lysis allowed for the sensitive detection of the bcr/abl signal
CC down to as low as 1 cell, with increasing signal intensity with
CC increasing cell number. The addition of 1 uI, but not 3 uI, of poly
CC resin allowed detection of the bcr/abl signal down to approximately 1-10
CC cells (with or without spin). The signal in the presence of poly was
CC weaker than with RNASIN. It is concluded that RNA polymers can replace
CC RNASIN in single-tube, whole cell RT-PCR. The example illustrates the
CC present invention, which relates to compositions and methods for using
CC RNA polymers to inhibit RNase enzymes (e.g. those involved in
CC angiogenesis such as in tumour growth and proliferation, and in other
CC biological processes), for removing RNA binding proteins from a solution,
CC and for enhancing certain enzymatic reactions. The RNA polymers may also
CC be used in drug testing, or in screening for RNA binding proteins
CC involved in disease states
XX
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2539 GAGCTCCAGATCTGACGATC 2559
DB 2 GAGCTCCAGATCTGACCAAC 22
XX
RESULT 3427
ABS64779
ID ABS64779 standard; DNA; 22 BP.
XX
AC ABS64779;
XX
DT 15-NOV-2002 (first entry)
XX
DE GPCR15 real time forward PCR primer.
XX
KM G protein coupled receptor related protein; ss; primer; human; GPCR;
KM cardiomyopathy; atherosclerosis; diabetes; cancer; stroke; PCR;
KM Von Hippel-Lindau syndrome; Alzheimer's disease; tubercous sclerosis;
KM hypercalcaemia; Parkinson's disease; Huntington's disease;
KM cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis;
KM ataxia-telangiectasia; leukodystrophy; addiction; anxiety; depression;
KM pain; obesity; Crohn's disease; osteoporosis; haemophilia; asthma;
KM inflammatory bowel disease; infertility; hypertension; scleroderma;
KM arthritis; human immunodeficiency virus; autoimmune disease; HIV;
KM infection; graft-versus-host disease.
XX
OS Homo sapiens.
XX
PN WO200264793-A2.
XX
PD 22-AUG-2002.
XX
PE 03-JAN-2002; 2002WO-US000056.
XX
PR 03-JAN-2001; 2001US-0259552P.
PR 03-JAN-2001; 2001US-0260544P.
PR 20-MAR-2001; 2001US-0277405P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Casman SJ, Edinger SR, Ellerman K, Smithson G, Kekuda R;
PI Muralidhara P;
XX
DR WPI; 2002-643487/69.